(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
4 October 2001 (04.10.2001)

PCT

(10) International Publication Number
WO 01/73032 A2

(51) International Patent Classification[7]: C12N 15/12, C07K 14/47, C12N 1/21, 5/10, C07K 16/18, G01N 33/68, C07K 19/00, C12N 15/10, A61K 38/17, 31/70, 39/395, 35/14, C12Q 1/68

(21) International Application Number: PCT/US01/09919

(22) International Filing Date: 27 March 2001 (27.03.2001)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:

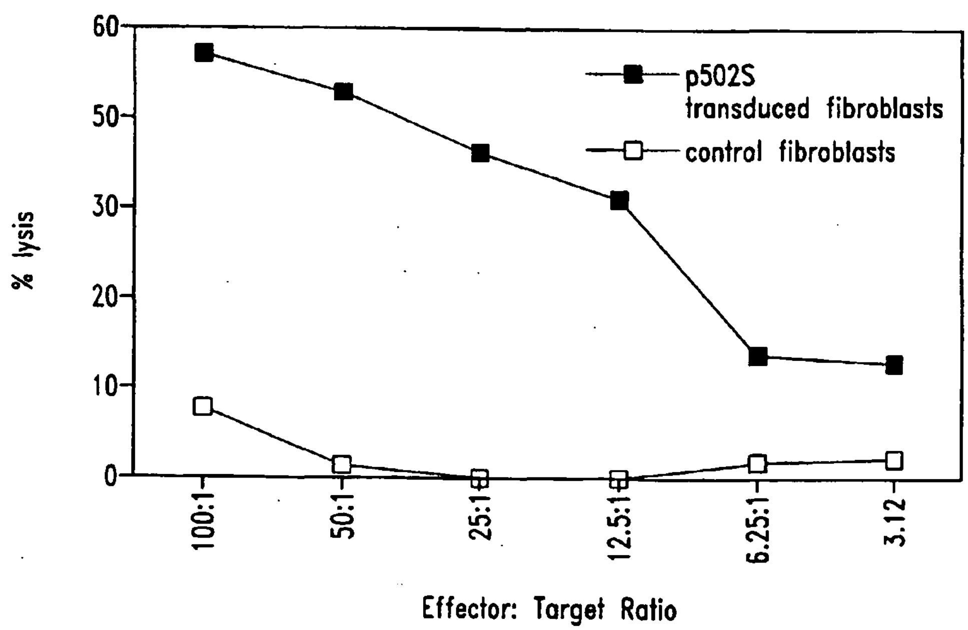
09/536,857	27 March 2000 (27.03.2000)	US
09/568,100	9 May 2000 (09.05.2000)	US
09/570,737	12 May 2000 (12.05.2000)	US
09/593,793	13 June 2000 (13.06.2000)	US
09/605,783	27 June 2000 (27.06.2000)	US
09/636,215	10 August 2000 (10.08.2000)	US
09/651,236	29 August 2000 (29.08.2000)	US
09/657,279	6 September 2000 (06.09.2000)	US
09/679,426	2 October 2000 (02.10.2000)	US
09/685,166	10 October 2000 (10.10.2000)	US
09/709,729	9 November 2000 (09.11.2000)	US

(71) Applicant *(for all designated States except US)*: **CORIXA CORPORATION** [US/US]; 1124 Columbia Street, Suite 200, Seattle, WA 98104 (US).

(72) Inventors; and
(75) Inventors/Applicants *(for US only)*: **XU, Jiangchun** [US/US]; 15805 S.E. 43rd Place, Bellevue, WA 98006 (US). **DILLON, Davin, C.** [US/US]; 18112 N.W. Montreux Drive, Issaquah, WA 98027 (US). **MITCHAM, Jennifer, L.** [US/US]; 16677 N.E. 88th Street, Redmond, WA 98052 (US). **HARLOCKER, Susan, L.** [US/US]; 7522 13th Avenue W., Seattle, WA 98117 (US). **JIANG, Yuqiu** [CN/US]; 5001 S. 232nd Street, Kent, WA 98032 (US). **KALOS, Michael, D.** [US/US]; 8116 Dayton Avenue N., Seattle, WA 98103 (US). **FANGER, Gary, Richard** [US/US]; 15906 29th Drive S.E., Mill Creek, WA 98012 (US). **RETTER, Marc, W.** [US/US]; 33402 N.E. 43rd Place, Carnation, WA 98104 (US). **STOLK, John, A.** [US/US]; 7436 N.E. 144th Place, Bothell, WA 98011 (US). **DAY, Craig, H.** [US/US]; 11501 Stone Avenue N., C122, Seattle, WA 98133 (US). **VEDVICK, Thomas, S.**

[Continued on next page]

(54) Title: COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF PROSTATE CANCER



(57) Abstract: Compositions and methods for the therapy and diagnosis of cancer, particularly prostate cancer, are disclosed. Illustrative compositions comprise one or more prostate-specific polypeptides, immunogenic portions thereof, polynucleotides that encode such polypeptides, antigen presenting cell that expresses such polypeptides, and T cells that are specific for cells expressing such polypeptides. The disclosed compositions are useful, for example, in the diagnosis, prevention and/or treatment of diseases, particularly prostate cancer.

WO 01/73032 A2

[US/US]; 124 S. 300th Place, Federal Way, WA 98003 (US). **CARTER, Darrick** [US/US]; 321 Summit Avenue E., Seattle, WA 98102 (US). **LI, Samuel, X.** [US/US]; 3608 175th Court N.E., Redmond, WA 98052 (US). **WANG, Aijun** [CN/US]; 3106 213th Place S.E., Issaquah, WA 98029 (US). **SKEIKY, Yasir, A., W.** [LB/US]; 15106 S.E. 47th Place, Bellevue, WA 98006 (US). **HEPLER, William, T.** [US/US]; 12034 38th Avenue N.E., Seattle, WA 98125 (US). **HENDERSON, Robert, A.** [US/US]; 8904 192nd Street S.W., Edmonds, WA 98026 (US).

(74) Agents: POTTER, Jane, E., R.; Seed Intellectual Property Law Group PLLC, Suite 6300, 701 Fifth Avenue, Seattle, WA 98104-7092 et al. (US).

(81) Designated States *(national)*: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.

(84) Designated States *(regional)*: ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

Published:

— *without international search report and to be republished upon receipt of that report*

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF PROSTATE CANCER

TECHNICAL FIELD OF THE INVENTION

The present invention relates generally to therapy and diagnosis of cancer, such as prostate cancer. The invention is more specifically related to polypeptides, comprising at least a portion of a prostate-specific protein, and to polynucleotides encoding such polypeptides. Such polypeptides and polynucleotides are useful in pharmaceutical compositions, *e.g.*, vaccines, and other compositions for the diagnosis and treatment of prostate cancer.

BACKGROUND OF THE INVENTION

Cancer is a significant health problem throughout the world. Although Cancer is a significant health problem throughout the world. Although advances have been made in detection and therapy of cancer, no vaccine or other universally successful method for prevention or treatment is currently available. Current therapies, which are generally based on a combination of chemotherapy or surgery and radiation, continue to prove inadequate in many patients.

Prostate cancer is the most common form of cancer among males, with an estimated incidence of 30% in men over the age of 50. Overwhelming clinical evidence shows that human prostate cancer has the propensity to metastasize to bone, and the disease appears to progress inevitably from androgen dependent to androgen refractory status, leading to increased patient mortality. This prevalent disease is currently the second leading cause of cancer death among men in the U.S.

In spite of considerable research into therapies for the disease, prostate cancer remains difficult to treat. Commonly, treatment is based on surgery and/or radiation therapy, but these methods are ineffective in a significant percentage of cases. Two previously identified prostate specific proteins - prostate specific antigen (PSA) and prostatic acid phosphatase (PAP) - have limited therapeutic and diagnostic potential. For example, PSA levels do not always correlate well with the presence of

prostate cancer, being positive in a percentage of non-prostate cancer cases, including benign prostatic hyperplasia (BPH). Furthermore, PSA measurements correlate with prostate volume, and do not indicate the level of metastasis.

In spite of considerable research into therapies for these and other cancers, prostate cancer remains difficult to diagnose and treat effectively. Accordingly, there is a need in the art for improved methods for detecting and treating such cancers. The present invention fulfills these needs and further provides other related advantages.

SUMMARY OF THE INVENTION

In one aspect, the present invention provides polynucleotide compositions comprising a sequence selected from the group consisting of:

(a) sequences provided in SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-705, 709-774, 777, 789, 817, 823, 824, 878, 880-882, 894, 896, 907, 908, 916-919, 929-931, 938, 939 and 942;

(b) complements of the sequences provided in SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-705, 709-774, 777, 789, 817, 823, 824, 878, 880-882, 894, 896, 907, 908, 916-919, 929-931, 938, 939 and 942;

(c) sequences consisting of at least 20 contiguous residues of a sequence provided in SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-705, 709-774, 777, 789, 817, 823, 824, 878, 880-882, 894, 896, 907, 908, 916-919, 929-931, 938, 939 and 942;

(d) sequences that hybridize to a sequence provided in SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-

606, 618-705, 709-774, 777, 789, 817, 823, 824, 878, 880-882, 894, 896, 907, 908, 916-919, 929-931, 938, 939 and 942, under moderately stringent conditions;

(e) sequences having at least 75% identity to a sequence of SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-705, 709-774, 777, 789, 817, 823, 824, 878, 880-882, 894, 896, 907, 908, 916-919, 929-931, 938, 939 and 942;

(f) sequences having at least 90% identity to a sequence of SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-705, 709-774, 777, 789, 817, 823, 824, 878, 880-882, 894, 896, 907, 908, 916-919, 929-931, 938, 939 and 942; and

(g) degenerate variants of a sequence provided in SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-705, 709-774, 777, 789, 817, 823, 824, 878, 880-882, 894, 896, 907, 908, 916-919, 929-931, 938, 939 and 942.

In one preferred embodiment, the polynucleotide compositions of the invention are expressed in at least about 20%, more preferably in at least about 30%, and most preferably in at least about 50% of prostate tissue samples tested, at a level that is at least about 2-fold, preferably at least about 5-fold, and most preferably at least about 10-fold higher than that for other normal tissues.

The present invention, in another aspect, provides polypeptide compositions comprising an amino acid sequence that is encoded by a polynucleotide sequence described above.

The present invention further provides polypeptide compositions comprising an amino acid sequence selected from the group consisting of sequences recited in SEQ ID NO: 112-114, 172, 176, 178, 327, 329, 331, 336, 339, 376-380, 383, 477-483, 496, 504, 505, 519, 520, 522, 525, 527, 532, 534, 537-551, 553-568, 573-586, 588-590, 592, 706-708, 775, 776, 778, 780, 781, 811, 814, 818, 826, 827, 853, 855,

858, 860-862, 866-877, 879, 883-893, 895, 897, 898, 909-915, 920-928, 932-934, 940, 941 and 943.

In certain preferred embodiments, the polypeptides and/or polynucleotides of the present invention are immunogenic, *i.e.*, they are capable of eliciting an immune response, particularly a humoral and/or cellular immune response, as further described herein.

The present invention further provides fragments, variants and/or derivatives of the disclosed polypeptide and/or polynucleotide sequences, wherein the fragments, variants and/or derivatives preferably have a level of immunogenic activity of at least about 50%, preferably at least about 70% and more preferably at least about 90% of the level of immunogenic activity of a polypeptide sequence set forth in SEQ ID NO: 112-114, 172, 176, 178, 327, 329, 331, 336, 339, 376-380, 383, 477-483, 496, 504, 505, 519, 520, 522, 525, 527, 532, 534, 537-551, 553-568, 573-586, 588-590, 592, 706-708, 775, 776, 778, 780, 781, 811, 814, 818, 826, 827, 853, 855, 858 or 860-862, or a polypeptide sequence encoded by a polynucleotide sequence set forth in SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-705, 709-774, 777, 789, 817, 823, 824, 878, 880-882, 894, 896, 907, 908, 916-919, 929-931, 938, 939 and 942.

The present invention further provides polynucleotides that encode a polypeptide described above, expression vectors comprising such polynucleotides and host cells transformed or transfected with such expression vectors.

Within other aspects, the present invention provides pharmaceutical compositions comprising a polypeptide or polynucleotide as described above and a physiologically acceptable carrier.

Within a related aspect of the present invention, pharmaceutical compositions, *e.g.*, vaccine compositions, are provided for prophylactic or therapeutic applications. Such compositions generally comprise an immunogenic polypeptide or polynucleotide of the invention and an immunostimulant, such as an adjuvant, together with a physiologically acceptable carrier.

The present invention further provides pharmaceutical compositions that comprise: (a) an antibody or antigen-binding fragment thereof that specifically binds to a polypeptide of the present invention, or a fragment thereof; and (b) a physiologically acceptable carrier.

Within further aspects, the present invention provides pharmaceutical compositions comprising: (a) an antigen presenting cell that expresses a polypeptide as described above and (b) a pharmaceutically acceptable carrier or excipient. Illustrative antigen presenting cells include dendritic cells, macrophages, monocytes, fibroblasts and B cells.

Within related aspects, pharmaceutical compositions are provided that comprise: (a) an antigen presenting cell that expresses a polypeptide as described above and (b) an immunostimulant.

The present invention further provides, in other aspects, fusion proteins that comprise at least one polypeptide as described above, as well as polynucleotides encoding such fusion proteins, typically in the form of pharmaceutical compositions, *e.g.*, vaccine compositions, comprising a physiologically acceptable carrier and/or an immunostimulant. The fusions proteins may comprise multiple immunogenic polypeptides or portions/variants thereof, as described herein, and may further comprise one or more polypeptide segments for facilitating and/or enhancing the expression, purification and/or immunogenicity of the polypeptide(s).

Within further aspects, the present invention provides methods for stimulating an immune response in a patient, preferably a T cell response in a human patient, comprising administering a pharmaceutical composition described herein. The patient may be afflicted with prostate cancer, in which case the methods provide treatment for the disease, or a patient considered to be at risk for such a disease may be treated prophylactically.

Within further aspects, the present invention provides methods for inhibiting the development of a cancer in a patient, comprising administering to a patient a pharmaceutical composition as recited above. The patient may be afflicted

with prostate cancer, in which case the methods provide treatment for the disease, or a patient considered to be at risk for such a disease may be treated prophylactically.

The present invention further provides, within other aspects, methods for removing tumor cells from a biological sample, comprising contacting a biological sample with T cells that specifically react with a polypeptide of the present invention, wherein the step of contacting is performed under conditions and for a time sufficient to permit the removal of cells expressing the polypeptide from the sample.

Within related aspects, methods are provided for inhibiting the development of a cancer in a patient, comprising administering to a patient a biological sample treated as described above.

Methods are further provided, within other aspects, for stimulating and/or expanding T cells specific for a polypeptide of the present invention, comprising contacting T cells with one or more of: (i) a polypeptide as described above; (ii) a polynucleotide encoding such a polypeptide; and (iii) an antigen presenting cell that expresses such a polypeptide; under conditions and for a time sufficient to permit the stimulation and/or expansion of T cells. Isolated T cell populations comprising T cells prepared as described above are also provided.

Within further aspects, the present invention provides methods for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a T cell population as described above.

The present invention further provides methods for inhibiting the development of a cancer in a patient, comprising the steps of: (a) incubating $CD4^+$ and/or $CD8^+$ T cells isolated from a patient with one or more of: (i) a polypeptide comprising at least an immunogenic portion of polypeptide disclosed herein; (ii) a polynucleotide encoding such a polypeptide; and (iii) an antigen-presenting cell that expressed such a polypeptide; and (b) administering to the patient an effective amount of the proliferated T cells, thereby inhibiting the development of a cancer in the patient. Proliferated cells may, but need not, be cloned prior to administration to the patient.

Within further aspects, the present invention provides methods for determining the presence or absence of a cancer, preferably a prostate cancer, in a

patient comprising: (a) contacting a biological sample obtained from a patient with a binding agent that binds to a polypeptide as recited above; (b) detecting in the sample an amount of polypeptide that binds to the binding agent; and (c) comparing the amount of polypeptide with a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient. Within preferred embodiments, the binding agent is an antibody, more preferably a monoclonal antibody.

The present invention also provides, within other aspects, methods for monitoring the progression of a cancer in a patient. Such methods comprise the steps of: (a) contacting a biological sample obtained from a patient at a first point in time with a binding agent that binds to a polypeptide as recited above; (b) detecting in the sample an amount of polypeptide that binds to the binding agent; (c) repeating steps (a) and (b) using a biological sample obtained from the patient at a subsequent point in time; and (d) comparing the amount of polypeptide detected in step (c) with the amount detected in step (b), and therefrom monitoring the progression of the cancer in the patient.

The present invention further provides, within other aspects, methods for determining the presence or absence of a cancer in a patient, comprising the steps of: (a) contacting a biological sample obtained from a patient with an oligonucleotide that hybridizes to a polynucleotide of the present invention; (b) detecting in the sample a level of a polynucleotide, preferably mRNA, that hybridizes to the oligonucleotide; and (c) comparing the level of polynucleotide that hybridizes to the oligonucleotide with a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient. Within certain embodiments, the amount of mRNA is detected via polymerase chain reaction using, for example, at least one oligonucleotide primer that hybridizes to a polynucleotide of the present invention, or a complement of such a polynucleotide. Within other embodiments, the amount of mRNA is detected using a hybridization technique, employing an oligonucleotide probe that hybridizes to an inventive polynucleotide, or a complement of such a polynucleotide.

In related aspects, methods are provided for monitoring the progression of a cancer in a patient, comprising the steps of: (a) contacting a biological sample

obtained from a patient with an oligonucleotide that hybridizes to a polynucleotide of the present invention; (b) detecting in the sample an amount of a polynucleotide that hybridizes to the oligonucleotide; (c) repeating steps (a) and (b) using a biological sample obtained from the patient at a subsequent point in time; and (d) comparing the amount of polynucleotide detected in step (c) with the amount detected in step (b), and therefrom monitoring the progression of the cancer in the patient.

Within further aspects, the present invention provides antibodies, such as monoclonal antibodies, that bind to a polypeptide as described above, as well as diagnostic kits comprising such antibodies. Diagnostic kits comprising one or more oligonucleotide probes or primers as described above are also provided.

These and other aspects of the present invention will become apparent upon reference to the following detailed description and attached drawings. All references disclosed herein are hereby incorporated by reference in their entirety as if each was incorporated individually.

BRIEF DESCRIPTION OF THE DRAWINGS AND SEQUENCE IDENTIFIERS

Figure 1 illustrates the ability of T cells to kill fibroblasts expressing the representative prostate-specific polypeptide P502S, as compared to control fibroblasts. The percentage lysis is shown as a series of effector:target ratios, as indicated.

Figures 2A and 2B illustrate the ability of T cells to recognize cells expressing the representative prostate-specific polypeptide P502S. In each case, the number of γ-interferon spots is shown for different numbers of responders. In Figure 2A, data is presented for fibroblasts pulsed with the P2S-12 peptide, as compared to fibroblasts pulsed with a control E75 peptide. In Figure 2B, data is presented for fibroblasts expressing P502S, as compared to fibroblasts expressing HER-2/*neu*.

Figure 3 represents a peptide competition binding assay showing that the P1S#10 peptide, derived from P501S, binds HLA-A2. Peptide P1S#10 inhibits HLA-A2 restricted presentation of fluM58 peptide to CTL clone D150M58 in TNF release bioassay. D150M58 CTL is specific for the HLA-A2 binding influenza matrix peptide fluM58.

Figure 4 illustrates the ability of T cell lines generated from P1S#10 immunized mice to specifically lyse P1S#10-pulsed Jurkat A2Kb targets and P501S-transduced Jurkat A2Kb targets, as compared to EGFP-transduced Jurkat A2Kb. The percent lysis is shown as a series of effector to target ratios, as indicated.

Figure 5 illustrates the ability of a T cell clone to recognize and specifically lyse Jurkat A2Kb cells expressing the representative prostate-specific polypeptide P501S, thereby demonstrating that the P1S#10 peptide may be a naturally processed epitope of the P501S polypeptide.

Figures 6A and 6B are graphs illustrating the specificity of a $CD8^+$ cell line (3A-1) for a representative prostate-specific antigen (P501S). Figure 6A shows the results of a ^{51}Cr release assay. The percent specific lysis is shown as a series of effector:target ratios, as indicated. Figure 6B shows the production of interferon-gamma by 3A-1 cells stimulated with autologous B-LCL transduced with P501S, at varying effector:target rations as indicated.

Figure 7 is a Western blot showing the expression of P501S in baculovirus.

Figure 8 illustrates the results of epitope mapping studies on P501S.

Figure 9 is a schematic representation of the P501S protein showing the location of transmembrane domains and predicted intracellular and extracellular domains.

Figure 10 is a genomic map showing the location of the prostate genes P775P, P704P, B305D, P712P and P774P within the Cat Eye Syndrome region of chromosome 22q11.2

Figure 11 shows the results of an ELISA assay to determine the specificity of rabbit polyclonal antisera raised against P501S.

Figures 12A(1), 12A(2), 12A(3), and B are the full-length cDNA (SEQ ID NO:777) and predicted amino acid (SEQ ID NO:778) sequences, respectively, for the clone P788P.

SEQ ID NO: 1 is the determined cDNA sequence for F1-13

SEQ ID NO: 2 is the determined 3' cDNA sequence for F1-12

SEQ ID NO: 3 is the determined 5' cDNA sequence for F1-12

SEQ ID NO: 4 is the determined 3' cDNA sequence for F1-16

SEQ ID NO: 5 is the determined 3' cDNA sequence for H1-1

SEQ ID NO: 6 is the determined 3' cDNA sequence for H1-9

SEQ ID NO: 7 is the determined 3' cDNA sequence for H1-4

SEQ ID NO: 8 is the determined 3' cDNA sequence for J1-17

SEQ ID NO: 9 is the determined 5' cDNA sequence for J1-17

SEQ ID NO: 10 is the determined 3' cDNA sequence for L1-12

SEQ ID NO: 11 is the determined 5' cDNA sequence for L1-12

SEQ ID NO: 12 is the determined 3' cDNA sequence for N1-1862

SEQ ID NO: 13 is the determined 5' cDNA sequence for N1-1862

SEQ ID NO: 14 is the determined 3' cDNA sequence for J1-13

SEQ ID NO: 15 is the determined 5' cDNA sequence for J1-13

SEQ ID NO: 16 is the determined 3' cDNA sequence for J1-19

SEQ ID NO: 17 is the determined 5' cDNA sequence for J1-19

SEQ ID NO: 18 is the determined 3' cDNA sequence for J1-25

SEQ ID NO: 19 is the determined 5' cDNA sequence for J1-25

SEQ ID NO: 20 is the determined 5' cDNA sequence for J1-24

SEQ ID NO: 21 is the determined 3' cDNA sequence for J1-24

SEQ ID NO: 22 is the determined 5' cDNA sequence for K1-58

SEQ ID NO: 23 is the determined 3' cDNA sequence for K1-58

SEQ ID NO: 24 is the determined 5' cDNA sequence for K1-63

SEQ ID NO: 25 is the determined 3' cDNA sequence for K1-63

SEQ ID NO: 26 is the determined 5' cDNA sequence for L1-4

SEQ ID NO: 27 is the determined 3' cDNA sequence for L1-4

SEQ ID NO: 28 is the determined 5' cDNA sequence for L1-14

SEQ ID NO: 29 is the determined 3' cDNA sequence for L1-14

SEQ ID NO: 30 is the determined 3' cDNA sequence for J1-12

SEQ ID NO: 31 is the determined 3' cDNA sequence for J1-16

SEQ ID NO: 32 is the determined 3' cDNA sequence for J1-21

SEQ ID NO: 33 is the determined 3' cDNA sequence for K1-48

SEQ ID NO: 34 is the determined 3' cDNA sequence for K1-55

SEQ ID NO: 35 is the determined 3' cDNA sequence for L1-2

SEQ ID NO: 36 is the determined 3' cDNA sequence for L1-6

SEQ ID NO: 37 is the determined 3' cDNA sequence for N1-1858

SEQ ID NO: 38 is the determined 3' cDNA sequence for N1-1860

SEQ ID NO: 39 is the determined 3' cDNA sequence for N1-1861

SEQ ID NO: 40 is the determined 3' cDNA sequence for N1-1864

SEQ ID NO: 41 is the determined cDNA sequence for P5

SEQ ID NO: 42 is the determined cDNA sequence for P8

SEQ ID NO: 43 is the determined cDNA sequence for P9

SEQ ID NO: 44 is the determined cDNA sequence for P18

SEQ ID NO: 45 is the determined cDNA sequence for P20

SEQ ID NO: 46 is the determined cDNA sequence for P29

SEQ ID NO: 47 is the determined cDNA sequence for P30

SEQ ID NO: 48 is the determined cDNA sequence for P34

SEQ ID NO: 49 is the determined cDNA sequence for P36

SEQ ID NO: 50 is the determined cDNA sequence for P38

SEQ ID NO: 51 is the determined cDNA sequence for P39

SEQ ID NO: 52 is the determined cDNA sequence for P42

SEQ ID NO: 53 is the determined cDNA sequence for P47

SEQ ID NO: 54 is the determined cDNA sequence for P49

SEQ ID NO: 55 is the determined cDNA sequence for P50

SEQ ID NO: 56 is the determined cDNA sequence for P53

SEQ ID NO: 57 is the determined cDNA sequence for P55

SEQ ID NO: 58 is the determined cDNA sequence for P60

SEQ ID NO: 59 is the determined cDNA sequence for P64

SEQ ID NO: 60 is the determined cDNA sequence for P65

SEQ ID NO: 61 is the determined cDNA sequence for P73

SEQ ID NO: 62 is the determined cDNA sequence for P75

SEQ ID NO: 63 is the determined cDNA sequence for P76

SEQ ID NO: 64 is the determined cDNA sequence for P79

SEQ ID NO: 65 is the determined cDNA sequence for P84

SEQ ID NO: 66 is the determined cDNA sequence for P68

SEQ ID NO: 67 is the determined cDNA sequence for P80 (also referred to as P704P)

SEQ ID NO: 68 is the determined cDNA sequence for P82

SEQ ID NO: 69 is the determined cDNA sequence for U1-3064

SEQ ID NO: 70 is the determined cDNA sequence for U1-3065

SEQ ID NO: 71 is the determined cDNA sequence for V1-3692

SEQ ID NO: 72 is the determined cDNA sequence for 1A-3905

SEQ ID NO: 73 is the determined cDNA sequence for V1-3686

SEQ ID NO: 74 is the determined cDNA sequence for R1-2330

SEQ ID NO: 75 is the determined cDNA sequence for 1B-3976

SEQ ID NO: 76 is the determined cDNA sequence for V1-3679

SEQ ID NO: 77 is the determined cDNA sequence for 1G-4736

SEQ ID NO: 78 is the determined cDNA sequence for 1G-4738

SEQ ID NO: 79 is the determined cDNA sequence for 1G-4741

SEQ ID NO: 80 is the determined cDNA sequence for 1G-4744

SEQ ID NO: 81 is the determined cDNA sequence for 1G-4734

SEQ ID NO: 82 is the determined cDNA sequence for 1H-4774

SEQ ID NO: 83 is the determined cDNA sequence for 1H-4781

SEQ ID NO: 84 is the determined cDNA sequence for 1H-4785

SEQ ID NO: 85 is the determined cDNA sequence for 1H-4787

SEQ ID NO: 86 is the determined cDNA sequence for 1H-4796

SEQ ID NO: 87 is the determined cDNA sequence for 1I-4807

SEQ ID NO: 88 is the determined cDNA sequence for 1I-4810

SEQ ID NO: 89 is the determined cDNA sequence for 1I-4811

SEQ ID NO: 90 is the determined cDNA sequence for 1J-4876

SEQ ID NO: 91 is the determined cDNA sequence for 1K-4884

SEQ ID NO: 92 is the determined cDNA sequence for 1K-4896

SEQ ID NO: 93 is the determined cDNA sequence for 1G-4761

SEQ ID NO: 94 is the determined cDNA sequence for 1G-4762

SEQ ID NO: 95 is the determined cDNA sequence for 1H-4766

SEQ ID NO: 96 is the determined cDNA sequence for 1H-4770

SEQ ID NO: 97 is the determined cDNA sequence for 1H-4771

SEQ ID NO: 98 is the determined cDNA sequence for 1H-4772

SEQ ID NO: 99 is the determined cDNA sequence for 1D-4297

SEQ ID NO: 100 is the determined cDNA sequence for 1D-4309

SEQ ID NO: 101 is the determined cDNA sequence for 1D.1-4278

SEQ ID NO: 102 is the determined cDNA sequence for 1D-4288

SEQ ID NO: 103 is the determined cDNA sequence for 1D-4283

SEQ ID NO: 104 is the determined cDNA sequence for 1D-4304

SEQ ID NO: 105 is the determined cDNA sequence for 1D-4296

SEQ ID NO: 106 is the determined cDNA sequence for 1D-4280

SEQ ID NO: 107 is the determined full length cDNA sequence for F1-12 (also referred to as P504S)

SEQ ID NO: 108 is the predicted amino acid sequence for F1-12

SEQ ID NO: 109 is the determined full length cDNA sequence for J1-17

SEQ ID NO: 110 is the determined full length cDNA sequence for L1-12 (also referred to as P501S)

SEQ ID NO: 111 is the determined full length cDNA sequence for N1-1862 (also referred to as P503S)

SEQ ID NO: 112 is the predicted amino acid sequence for J1-17

SEQ ID NO: 113 is the predicted amino acid sequence for L1-12 (also referred to as P501S)

SEQ ID NO: 114 is the predicted amino acid sequence for N1-1862 (also referred to as P503S)

SEQ ID NO: 115 is the determined cDNA sequence for P89

SEQ ID NO: 116 is the determined cDNA sequence for P90

SEQ ID NO: 117 is the determined cDNA sequence for P92
SEQ ID NO: 118 is the determined cDNA sequence for P95
SEQ ID NO: 119 is the determined cDNA sequence for P98
SEQ ID NO: 120 is the determined cDNA sequence for P102
SEQ ID NO: 121 is the determined cDNA sequence for P110
SEQ ID NO: 122 is the determined cDNA sequence for P111
SEQ ID NO: 123 is the determined cDNA sequence for P114
SEQ ID NO: 124 is the determined cDNA sequence for P115
SEQ ID NO: 125 is the determined cDNA sequence for P116
SEQ ID NO: 126 is the determined cDNA sequence for P124
SEQ ID NO: 127 is the determined cDNA sequence for P126
SEQ ID NO: 128 is the determined cDNA sequence for P130
SEQ ID NO: 129 is the determined cDNA sequence for P133
SEQ ID NO: 130 is the determined cDNA sequence for P138
SEQ ID NO: 131 is the determined cDNA sequence for P143
SEQ ID NO: 132 is the determined cDNA sequence for P151
SEQ ID NO: 133 is the determined cDNA sequence for P156
SEQ ID NO: 134 is the determined cDNA sequence for P157
SEQ ID NO: 135 is the determined cDNA sequence for P166
SEQ ID NO: 136 is the determined cDNA sequence for P176
SEQ ID NO: 137 is the determined cDNA sequence for P178
SEQ ID NO: 138 is the determined cDNA sequence for P179
SEQ ID NO: 139 is the determined cDNA sequence for P185
SEQ ID NO: 140 is the determined cDNA sequence for P192
SEQ ID NO: 141 is the determined cDNA sequence for P201
SEQ ID NO: 142 is the determined cDNA sequence for P204
SEQ ID NO: 143 is the determined cDNA sequence for P208
SEQ ID NO: 144 is the determined cDNA sequence for P211
SEQ ID NO: 145 is the determined cDNA sequence for P213
SEQ ID NO: 146 is the determined cDNA sequence for P219

SEQ ID NO: 147 is the determined cDNA sequence for P237

SEQ ID NO: 148 is the determined cDNA sequence for P239

SEQ ID NO: 149 is the determined cDNA sequence for P248

SEQ ID NO: 150 is the determined cDNA sequence for P251

SEQ ID NO: 151 is the determined cDNA sequence for P255

SEQ ID NO: 152 is the determined cDNA sequence for P256

SEQ ID NO: 153 is the determined cDNA sequence for P259

SEQ ID NO: 154 is the determined cDNA sequence for P260

SEQ ID NO: 155 is the determined cDNA sequence for P263

SEQ ID NO: 156 is the determined cDNA sequence for P264

SEQ ID NO: 157 is the determined cDNA sequence for P266

SEQ ID NO: 158 is the determined cDNA sequence for P270

SEQ ID NO: 159 is the determined cDNA sequence for P272

SEQ ID NO: 160 is the determined cDNA sequence for P278

SEQ ID NO: 161 is the determined cDNA sequence for P105

SEQ ID NO: 162 is the determined cDNA sequence for P107

SEQ ID NO: 163 is the determined cDNA sequence for P137

SEQ ID NO: 164 is the determined cDNA sequence for P194

SEQ ID NO: 165 is the determined cDNA sequence for P195

SEQ ID NO: 166 is the determined cDNA sequence for P196

SEQ ID NO: 167 is the determined cDNA sequence for P220

SEQ ID NO: 168 is the determined cDNA sequence for P234

SEQ ID NO: 169 is the determined cDNA sequence for P235

SEQ ID NO: 170 is the determined cDNA sequence for P243

SEQ ID NO: 171 is the determined cDNA sequence for P703P-DE1

SEQ ID NO: 172 is the predicted amino acid sequence for P703P-DE1

SEQ ID NO: 173 is the determined cDNA sequence for P703P-DE2

SEQ ID NO: 174 is the determined cDNA sequence for P703P-DE6

SEQ ID NO: 175 is the determined cDNA sequence for P703P-DE13

SEQ ID NO: 176 is the predicted amino acid sequence for P703P-DE13

SEQ ID NO: 177 is the determined cDNA sequence for P703P-DE14

SEQ ID NO: 178 is the predicted amino acid sequence for P703P-DE14

SEQ ID NO: 179 is the determined extended cDNA sequence for 1G-4736

SEQ ID NO: 180 is the determined extended cDNA sequence for 1G-4738

SEQ ID NO: 181 is the determined extended cDNA sequence for 1G-4741

SEQ ID NO: 182 is the determined extended cDNA sequence for 1G-4744

SEQ ID NO: 183 is the determined extended cDNA sequence for 1H-4774

SEQ ID NO: 184 is the determined extended cDNA sequence for 1H-4781

SEQ ID NO: 185 is the determined extended cDNA sequence for 1H-4785

SEQ ID NO: 186 is the determined extended cDNA sequence for 1H-4787

SEQ ID NO: 187 is the determined extended cDNA sequence for 1H-4796

SEQ ID NO: 188 is the determined extended cDNA sequence for 1I-4807

SEQ ID NO: 189 is the determined 3' cDNA sequence for 1I-4810

SEQ ID NO: 190 is the determined 3' cDNA sequence for 1I-4811

SEQ ID NO: 191 is the determined extended cDNA sequence for 1J-4876

SEQ ID NO: 192 is the determined extended cDNA sequence for 1K-4884

SEQ ID NO: 193 is the determined extended cDNA sequence for 1K-4896

SEQ ID NO: 194 is the determined extended cDNA sequence for 1G-4761

SEQ ID NO: 195 is the determined extended cDNA sequence for 1G-4762

SEQ ID NO: 196 is the determined extended cDNA sequence for 1H-4766

SEQ ID NO: 197 is the determined 3' cDNA sequence for 1H-4770

SEQ ID NO: 198 is the determined 3' cDNA sequence for 1H-4771

SEQ ID NO: 199 is the determined extended cDNA sequence for 1H-4772

SEQ ID NO: 200 is the determined extended cDNA sequence for 1D-4309

SEQ ID NO: 201 is the determined extended cDNA sequence for 1D.1-4278

SEQ ID NO: 202 is the determined extended cDNA sequence for 1D-4288

SEQ ID NO: 203 is the determined extended cDNA sequence for 1D-4283

SEQ ID NO: 204 is the determined extended cDNA sequence for 1D-4304

SEQ ID NO: 205 is the determined extended cDNA sequence for 1D-4296

SEQ ID NO: 206 is the determined extended cDNA sequence for 1D-4280

SEQ ID NO: 207 is the determined cDNA sequence for 10-d8fwd

SEQ ID NO: 208 is the determined cDNA sequence for 10-H10con

SEQ ID NO: 209 is the determined cDNA sequence for 11-C8rev

SEQ ID NO: 210 is the determined cDNA sequence for 7.g6fwd

SEQ ID NO: 211 is the determined cDNA sequence for 7.g6rev

SEQ ID NO: 212 is the determined cDNA sequence for 8-b5fwd

SEQ ID NO: 213 is the determined cDNA sequence for 8-b5rev

SEQ ID NO: 214 is the determined cDNA sequence for 8-b6fwd

SEQ ID NO: 215 is the determined cDNA sequence for 8-b6 rev

SEQ ID NO: 216 is the determined cDNA sequence for 8-d4fwd

SEQ ID NO: 217 is the determined cDNA sequence for 8-d9rev

SEQ ID NO: 218 is the determined cDNA sequence for 8-g3fwd

SEQ ID NO: 219 is the determined cDNA sequence for 8-g3rev

SEQ ID NO: 220 is the determined cDNA sequence for 8-h11rev

SEQ ID NO: 221 is the determined cDNA sequence for g-f12fwd

SEQ ID NO: 222 is the determined cDNA sequence for g-f3rev

SEQ ID NO: 223 is the determined cDNA sequence for P509S

SEQ ID NO: 224 is the determined cDNA sequence for P510S

SEQ ID NO: 225 is the determined cDNA sequence for P703DE5

SEQ ID NO: 226 is the determined cDNA sequence for 9-A11

SEQ ID NO: 227 is the determined cDNA sequence for 8-C6

SEQ ID NO: 228 is the determined cDNA sequence for 8-H7

SEQ ID NO: 229 is the determined cDNA sequence for JPTPN13

SEQ ID NO: 230 is the determined cDNA sequence for JPTPN14

SEQ ID NO: 231 is the determined cDNA sequence for JPTPN23

SEQ ID NO: 232 is the determined cDNA sequence for JPTPN24

SEQ ID NO: 233 is the determined cDNA sequence for JPTPN25

SEQ ID NO: 234 is the determined cDNA sequence for JPTPN30

SEQ ID NO: 235 is the determined cDNA sequence for JPTPN34

SEQ ID NO: 236 is the determined cDNA sequence for PTPN35

SEQ ID NO: 237 is the determined cDNA sequence for JPTPN36

SEQ ID NO: 238 is the determined cDNA sequence for JPTPN38

SEQ ID NO: 239 is the determined cDNA sequence for JPTPN39

SEQ ID NO: 240 is the determined cDNA sequence for JPTPN40

SEQ ID NO: 241 is the determined cDNA sequence for JPTPN41

SEQ ID NO: 242 is the determined cDNA sequence for JPTPN42

SEQ ID NO: 243 is the determined cDNA sequence for JPTPN45

SEQ ID NO: 244 is the determined cDNA sequence for JPTPN46

SEQ ID NO: 245 is the determined cDNA sequence for JPTPN51

SEQ ID NO: 246 is the determined cDNA sequence for JPTPN56

SEQ ID NO: 247 is the determined cDNA sequence for PTPN64

SEQ ID NO: 248 is the determined cDNA sequence for JPTPN65

SEQ ID NO: 249 is the determined cDNA sequence for JPTPN67

SEQ ID NO: 250 is the determined cDNA sequence for JPTPN76

SEQ ID NO: 251 is the determined cDNA sequence for JPTPN84

SEQ ID NO: 252 is the determined cDNA sequence for JPTPN85

SEQ ID NO: 253 is the determined cDNA sequence for JPTPN86

SEQ ID NO: 254 is the determined cDNA sequence for JPTPN87

SEQ ID NO: 255 is the determined cDNA sequence for JPTPN88

SEQ ID NO: 256 is the determined cDNA sequence for JP1F1

SEQ ID NO: 257 is the determined cDNA sequence for JP1F2

SEQ ID NO: 258 is the determined cDNA sequence for JP1C2

SEQ ID NO: 259 is the determined cDNA sequence for JP1B1

SEQ ID NO: 260 is the determined cDNA sequence for JP1B2

SEQ ID NO: 261 is the determined cDNA sequence for JP1D3

SEQ ID NO: 262 is the determined cDNA sequence for JP1A4

SEQ ID NO: 263 is the determined cDNA sequence for JP1F5

SEQ ID NO: 264 is the determined cDNA sequence for JP1E6

SEQ ID NO: 265 is the determined cDNA sequence for JP1D6

SEQ ID NO: 266 is the determined cDNA sequence for JP1B5

SEQ ID NO: 267 is the determined cDNA sequence for JP1A6

SEQ ID NO: 268 is the determined cDNA sequence for JP1E8

SEQ ID NO: 269 is the determined cDNA sequence for JP1D7

SEQ ID NO: 270 is the determined cDNA sequence for JP1D9

SEQ ID NO: 271 is the determined cDNA sequence for JP1C10

SEQ ID NO: 272 is the determined cDNA sequence for JP1A9

SEQ ID NO: 273 is the determined cDNA sequence for JP1F12

SEQ ID NO: 274 is the determined cDNA sequence for JP1E12

SEQ ID NO: 275 is the determined cDNA sequence for JP1D11

SEQ ID NO: 276 is the determined cDNA sequence for JP1C11

SEQ ID NO: 277 is the determined cDNA sequence for JP1C12

SEQ ID NO: 278 is the determined cDNA sequence for JP1B12

SEQ ID NO: 279 is the determined cDNA sequence for JP1A12

SEQ ID NO: 280 is the determined cDNA sequence for JP8G2

SEQ ID NO: 281 is the determined cDNA sequence for JP8H1

SEQ ID NO: 282 is the determined cDNA sequence for JP8H2

SEQ ID NO: 283 is the determined cDNA sequence for JP8A3

SEQ ID NO: 284 is the determined cDNA sequence for JP8A4

SEQ ID NO: 285 is the determined cDNA sequence for JP8C3

SEQ ID NO: 286 is the determined cDNA sequence for JP8G4

SEQ ID NO: 287 is the determined cDNA sequence for JP8B6

SEQ ID NO: 288 is the determined cDNA sequence for JP8D6

SEQ ID NO: 289 is the determined cDNA sequence for JP8F5

SEQ ID NO: 290 is the determined cDNA sequence for JP8A8

SEQ ID NO: 291 is the determined cDNA sequence for JP8C7

SEQ ID NO: 292 is the determined cDNA sequence for JP8D7

SEQ ID NO: 293 is the determined cDNA sequence for P8D8

SEQ ID NO: 294 is the determined cDNA sequence for JP8E7

SEQ ID NO: 295 is the determined cDNA sequence for JP8F8

SEQ ID NO: 296 is the determined cDNA sequence for JP8G8

SEQ ID NO: 297 is the determined cDNA sequence for JP8B10

SEQ ID NO: 298 is the determined cDNA sequence for JP8C10

SEQ ID NO: 299 is the determined cDNA sequence for JP8E9

SEQ ID NO: 300 is the determined cDNA sequence for JP8E10

SEQ ID NO: 301 is the determined cDNA sequence for JP8F9

SEQ ID NO: 302 is the determined cDNA sequence for JP8H9

SEQ ID NO: 303 is the determined cDNA sequence for JP8C12

SEQ ID NO: 304 is the determined cDNA sequence for JP8E11

SEQ ID NO: 305 is the determined cDNA sequence for JP8E12

SEQ ID NO: 306 is the amino acid sequence for the peptide PS2#12

SEQ ID NO: 307 is the determined cDNA sequence for P711P

SEQ ID NO: 308 is the determined cDNA sequence for P712P

SEQ ID NO: 309 is the determined cDNA sequence for CLONE23

SEQ ID NO: 310 is the determined cDNA sequence for P774P

SEQ ID NO: 311 is the determined cDNA sequence for P775P

SEQ ID NO: 312 is the determined cDNA sequence for P715P

SEQ ID NO: 313 is the determined cDNA sequence for P710P

SEQ ID NO: 314 is the determined cDNA sequence for P767P

SEQ ID NO: 315 is the determined cDNA sequence for P768P

SEQ ID NO: 316-325 are the determined cDNA sequences of previously isolated genes

SEQ ID NO: 326 is the determined cDNA sequence for P703PDE5

SEQ ID NO: 327 is the predicted amino acid sequence for P703PDE5

SEQ ID NO: 328 is the determined cDNA sequence for P703P6.26

SEQ ID NO: 329 is the predicted amino acid sequence for P703P6.26

SEQ ID NO: 330 is the determined cDNA sequence for P703PX-23

SEQ ID NO: 331 is the predicted amino acid sequence for P703PX-23

SEQ ID NO: 332 is the determined full length cDNA sequence for P509S

SEQ ID NO: 333 is the determined extended cDNA sequence for P707P (also referred to as 11-C9)

SEQ ID NO: 334 is the determined cDNA sequence for P714P

SEQ ID NO: 335 is the determined cDNA sequence for P705P (also referred to as 9-F3)

SEQ ID NO: 336 is the predicted amino acid sequence for P705P

SEQ ID NO: 337 is the amino acid sequence of the peptide P1S#10

SEQ ID NO: 338 is the amino acid sequence of the peptide p5

SEQ ID NO: 339 is the predicted amino acid sequence of P509S

SEQ ID NO: 340 is the determined cDNA sequence for P778P

SEQ ID NO: 341 is the determined cDNA sequence for P786P

SEQ ID NO: 342 is the determined cDNA sequence for P789P

SEQ ID NO: 343 is the determined cDNA sequence for a clone showing homology to Homo sapiens MM46 mRNA

SEQ ID NO: 344 is the determined cDNA sequence for a clone showing homology to Homo sapiens TNF-alpha stimulated ABC protein (ABC50) mRNA

SEQ ID NO: 345 is the determined cDNA sequence for a clone showing homology to Homo sapiens mRNA for E-cadherin

SEQ ID NO: 346 is the determined cDNA sequence for a clone showing homology to Human nuclear-encoded mitochondrial serine hydroxymethyltransferase (SHMT)

SEQ ID NO: 347 is the determined cDNA sequence for a clone showing homology to Homo sapiens natural resistance-associated macrophage protein2 (NRAMP2)

SEQ ID NO: 348 is the determined cDNA sequence for a clone showing homology to Homo sapiens phosphoglucomutase-related protein (PGMRP)

SEQ ID NO: 349 is the determined cDNA sequence for a clone showing homology to Human mRNA for proteosome subunit p40

SEQ ID NO: 350 is the determined cDNA sequence for P777P

SEQ ID NO: 351 is the determined cDNA sequence for P779P

SEQ ID NO: 352 is the determined cDNA sequence for P790P

SEQ ID NO: 353 is the determined cDNA sequence for P784P

SEQ ID NO: 354 is the determined cDNA sequence for P776P

SEQ ID NO: 355 is the determined cDNA sequence for P780P

SEQ ID NO: 356 is the determined cDNA sequence for P544S

SEQ ID NO: 357 is the determined cDNA sequence for P745S

SEQ ID NO: 358 is the determined cDNA sequence for P782P

SEQ ID NO: 359 is the determined cDNA sequence for P783P

SEQ ID NO: 360 is the determined cDNA sequence for unknown 17984

SEQ ID NO: 361 is the determined cDNA sequence for P787P

SEQ ID NO: 362 is the determined cDNA sequence for P788P

SEQ ID NO: 363 is the determined cDNA sequence for unknown 17994

SEQ ID NO: 364 is the determined cDNA sequence for P781P

SEQ ID NO: 365 is the determined cDNA sequence for P785P

SEQ ID NO: 366-375 are the determined cDNA sequences for splice variants of B305D.

SEQ ID NO: 376 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: 366.

SEQ ID NO: 377 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: 372.

SEQ ID NO: 378 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: 373.

SEQ ID NO: 379 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: 374.

SEQ ID NO: 380 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: 375.

SEQ ID NO: 381 is the determined cDNA sequence for B716P.

SEQ ID NO: 382 is the determined full-length cDNA sequence for P711P.

SEQ ID NO: 383 is the predicted amino acid sequence for P711P.

SEQ ID NO: 384 is the cDNA sequence for P1000C.

SEQ ID NO: 385 is the cDNA sequence for CGI-82.

SEQ ID NO:386 is the cDNA sequence for 23320.

SEQ ID NO:387 is the cDNA sequence for CGI-69.

SEQ ID NO:388 is the cDNA sequence for L-iditol-2-dehydrogenase.

SEQ ID NO:389 is the cDNA sequence for 23379.

SEQ ID NO:390 is the cDNA sequence for 23381.

SEQ ID NO:391 is the cDNA sequence for KIAA0122.

SEQ ID NO:392 is the cDNA sequence for 23399.

SEQ ID NO:393 is the cDNA sequence for a previously identified gene.

SEQ ID NO:394 is the cDNA sequence for HCLBP.

SEQ ID NO:395 is the cDNA sequence for transglutaminase.

SEQ ID NO:396 is the cDNA sequence for a previously identified gene.

SEQ ID NO:397 is the cDNA sequence for PAP.

SEQ ID NO:398 is the cDNA sequence for Ets transcription factor PDEF.

SEQ ID NO:399 is the cDNA sequence for hTGR.

SEQ ID NO:400 is the cDNA sequence for KIAA0295.

SEQ ID NO:401 is the cDNA sequence for 22545.

SEQ ID NO:402 is the cDNA sequence for 22547.

SEQ ID NO:403 is the cDNA sequence for 22548.

SEQ ID NO:404 is the cDNA sequence for 22550.

SEQ ID NO:405 is the cDNA sequence for 22551.

SEQ ID NO:406 is the cDNA sequence for 22552.

SEQ ID NO:407 is the cDNA sequence for 22553 (also known as P1020C).

SEQ ID NO:408 is the cDNA sequence for 22558.

SEQ ID NO:409 is the cDNA sequence for 22562.

SEQ ID NO:410 is the cDNA sequence for 22565.

SEQ ID NO:411 is the cDNA sequence for 22567.

SEQ ID NO:412 is the cDNA sequence for 22568.

SEQ ID NO:413 is the cDNA sequence for 22570.

SEQ ID NO:414 is the cDNA sequence for 22571.

SEQ ID NO:415 is the cDNA sequence for 22572.

SEQ ID NO:416 is the cDNA sequence for 22573.

SEQ ID NO:417 is the cDNA sequence for 22573.

SEQ ID NO:418 is the cDNA sequence for 22575.

SEQ ID NO:419 is the cDNA sequence for 22580.

SEQ ID NO:420 is the cDNA sequence for 22581.

SEQ ID NO:421 is the cDNA sequence for 22582.

SEQ ID NO:422 is the cDNA sequence for 22583.

SEQ ID NO:423 is the cDNA sequence for 22584.

SEQ ID NO:424 is the cDNA sequence for 22585.

SEQ ID NO:425 is the cDNA sequence for 22586.

SEQ ID NO:426 is the cDNA sequence for 22587.

SEQ ID NO:427 is the cDNA sequence for 22588.

SEQ ID NO:428 is the cDNA sequence for 22589.

SEQ ID NO:429 is the cDNA sequence for 22590.

SEQ ID NO:430 is the cDNA sequence for 22591.

SEQ ID NO:431 is the cDNA sequence for 22592.

SEQ ID NO:432 is the cDNA sequence for 22593.

SEQ ID NO:433 is the cDNA sequence for 22594.

SEQ ID NO:434 is the cDNA sequence for 22595.

SEQ ID NO:435 is the cDNA sequence for 22596.

SEQ ID NO:436 is the cDNA sequence for 22847.

SEQ ID NO:437 is the cDNA sequence for 22848.

SEQ ID NO:438 is the cDNA sequence for 22849.

SEQ ID NO:439 is the cDNA sequence for 22851.

SEQ ID NO:440 is the cDNA sequence for 22852.

SEQ ID NO:441 is the cDNA sequence for 22853.

SEQ ID NO:442 is the cDNA sequence for 22854.

SEQ ID NO:443 is the cDNA sequence for 22855.

SEQ ID NO:444 is the cDNA sequence for 22856.

SEQ ID NO:445 is the cDNA sequence for 22857.

SEQ ID NO:446 is the cDNA sequence for 23601.

SEQ ID NO:447 is the cDNA sequence for 23602.

SEQ ID NO:448 is the cDNA sequence for 23605.

SEQ ID NO:449 is the cDNA sequence for 23606.

SEQ ID NO:450 is the cDNA sequence for 23612.

SEQ ID NO:451 is the cDNA sequence for 23614.

SEQ ID NO:452 is the cDNA sequence for 23618.

SEQ ID NO:453 is the cDNA sequence for 23622.

SEQ ID NO:454 is the cDNA sequence for folate hydrolase.

SEQ ID NO:455 is the cDNA sequence for LIM protein.

SEQ ID NO:456 is the cDNA sequence for a known gene.

SEQ ID NO:457 is the cDNA sequence for a known gene.

SEQ ID NO:458 is the cDNA sequence for a previously identified gene.

SEQ ID NO:459 is the cDNA sequence for 23045.

SEQ ID NO:460 is the cDNA sequence for 23032.

SEQ ID NO:461 is the cDNA sequence for clone 23054.

SEQ ID NO:462-467 are cDNA sequences for known genes.

SEQ ID NO:468-471 are cDNA sequences for P710P.

SEQ ID NO:472 is a cDNA sequence for P1001C.

SEQ ID NO: 473 is the determined cDNA sequence for a first splice variant of P775P (referred to as 27505).

SEQ ID NO: 474 is the determined cDNA sequence for a second splice variant of P775P (referred to as 19947).

SEQ ID NO: 475 is the determined cDNA sequence for a third splice variant of P775P (referred to as 19941).

SEQ ID NO: 476 is the determined cDNA sequence for a fourth splice variant of P775P (referred to as 19937).

SEQ ID NO: 477 is a first predicted amino acid sequence encoded by the sequence of SEQ ID NO: 474.

SEQ ID NO: 478 is a second predicted amino acid sequence encoded by the sequence of SEQ ID NO: 474.

SEQ ID NO: 479 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: 475.

SEQ ID NO: 480 is a first predicted amino acid sequence encoded by the sequence of SEQ ID NO: 473.

SEQ ID NO: 481 is a second predicted amino acid sequence encoded by the sequence of SEQ ID NO: 473.

SEQ ID NO: 482 is a third predicted amino acid sequence encoded by the sequence of SEQ ID NO: 473.

SEQ ID NO: 483 is a fourth predicted amino acid sequence encoded by the sequence of SEQ ID NO: 473.

SEQ ID NO: 484 is the first 30 amino acids of the *M. tuberculosis* antigen Ra12.

SEQ ID NO: 485 is the PCR primer AW025.

SEQ ID NO: 486 is the PCR primer AW003.

SEQ ID NO: 487 is the PCR primer AW027.

SEQ ID NO: 488 is the PCR primer AW026.

SEQ ID NO: 489-501 are peptides employed in epitope mapping studies.

SEQ ID NO: 502 is the determined cDNA sequence of the complementarity determining region for the anti-P503S monoclonal antibody 20D4.

SEQ ID NO: 503 is the determined cDNA sequence of the complementarity determining region for the anti-P503S monoclonal antibody JA1.

SEQ ID NO: 504 & 505 are peptides employed in epitope mapping studies.

SEQ ID NO: 506 is the determined cDNA sequence of the complementarity determining region for the anti-P703P monoclonal antibody 8H2.

SEQ ID NO: 507 is the determined cDNA sequence of the complementarity determining region for the anti-P703P monoclonal antibody 7H8.

SEQ ID NO: 508 is the determined cDNA sequence of the complementarity determining region for the anti-P703P monoclonal antibody 2D4.

SEQ ID NO: 509-522 are peptides employed in epitope mapping studies.

SEQ ID NO: 523 is a mature form of P703P used to raise antibodies against P703P.

SEQ ID NO: 524 is the putative full-length cDNA sequence of P703P.

SEQ ID NO: 525 is the predicted amino acid sequence encoded by SEQ ID NO: 524.

SEQ ID NO: 526 is the full-length cDNA sequence for P790P.

SEQ ID NO: 527 is the predicted amino acid sequence for P790P.

SEQ ID NO: 528 & 529 are PCR primers.

SEQ ID NO: 530 is the cDNA sequence of a splice variant of SEQ ID NO: 366.

SEQ ID NO: 531 is the cDNA sequence of the open reading frame of SEQ ID NO: 530.

SEQ ID NO: 532 is the predicted amino acid encoded by the sequence of SEQ ID NO: 531.

SEQ ID NO: 533 is the DNA sequence of a putative ORF of P775P.

SEQ ID NO: 534 is the predicted amino acid sequence encoded by SEQ ID NO: 533.

SEQ ID NO: 535 is a first full-length cDNA sequence for P510S.

SEQ ID NO: 536 is a second full-length cDNA sequence for P510S.

SEQ ID NO: 537 is the predicted amino acid sequence encoded by SEQ ID NO: 535.

SEQ ID NO: 538 is the predicted amino acid sequence encoded by SEQ ID NO: 536.

SEQ ID NO: 539 is the peptide P501S-370.

SEQ ID NO: 540 is the peptide P501S-376.

SEQ ID NO: 541-551 are epitopes of P501S.

SEQ ID NO: 552 is an extended cDNA sequence for P712P.

SEQ ID NO: 553-568 are the amino acid sequences encoded by predicted open reading frames within SEQ ID NO: 552.

SEQ ID NO: 569 is an extended cDNA sequence for P776P.

SEQ ID NO: 570 is the determined cDNA sequence for a splice variant of P776P referred to as contig 6.

SEQ ID NO: 571 is the determined cDNA sequence for a splice variant of P776P referred to as contig 7.

SEQ ID NO: 572 is the determined cDNA sequence for a splice variant of P776P referred to as contig 14.

SEQ ID NO: 573 is the amino acid sequence encoded by a first predicted ORF of SEQ ID NO: 570.

SEQ ID NO: 574 is the amino acid sequence encoded by a second predicted ORF of SEQ ID NO: 570.

SEQ ID NO: 575 is the amino acid sequence encoded by a predicted ORF of SEQ ID NO: 571.

SEQ ID NO: 576-586 are amino acid sequences encoded by predicted ORFs of SEQ ID NO: 569.

SEQ ID NO: 587 is a DNA consensus sequence of the sequences of P767P and P777P.

SEQ ID NO: 588-590 are amino acid sequences encoded by predicted ORFs of SEQ ID NO: 587.

SEQ ID NO: 591 is an extended cDNA sequence for P1020C.

SEQ ID NO: 592 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: P1020C.

SEQ ID NO: 593 is a splice variant of P775P referred to as 50748.

SEQ ID NO: 594 is a splice variant of P775P referred to as 50717.SEQ ID NO: 595 is a splice variant of P775P referred to as 45985.

SEQ ID NO: 596 is a splice variant of P775P referred to as 38769.

SEQ ID NO: 597 is a splice variant of P775P referred to as 37922.

SEQ ID NO: 598 is a splice variant of P510S referred to as 49274.

SEQ ID NO: 599 is a splice variant of P510S referred to as 39487.

SEQ ID NO: 600 is a splice variant of P504S referred to as 5167.16.

SEQ ID NO: 601 is a splice variant of P504S referred to as 5167.1.

SEQ ID NO: 602 is a splice variant of P504S referred to as 5163.46.

SEQ ID NO: 603 is a splice variant of P504S referred to as 5163.42.

SEQ ID NO: 604 is a splice variant of P504S referred to as 5163.34.

SEQ ID NO: 605 is a splice variant of P504S referred to as 5163.17.

SEQ ID NO: 606 is a splice variant of P501S referred to as 10640.

SEQ ID NO: 607-615 are the sequences of PCR primers.

SEQ ID NO: 616 is the determined cDNA sequence of a fusion of P703P and PSA.

SEQ ID NO: 617 is the amino acid sequence of the fusion of P703P and PSA.

SEQ ID NO: 618-689 are determined cDNA sequences of prostate-specific clones.

SEQ ID NO: 690 is the cDNA sequence of the gene DD3.

SEQ ID NO: 691-697 are determined cDNA sequences of prostate-specific clones.

SEQ ID NO: 698 is an extended cDNA sequence for P714P.

SEQ ID NO: 699-701 are the cDNA sequences for splice variants of P704P.

SEQ ID NO: 702 is the cDNA sequence of a spliced variant of P553S referred to as P553S-14.

SEQ ID NO: 703 is the cDNA sequence of a spliced variant of P553S referred to as P553S-12.

SEQ ID NO: 704 is the cDNA sequence of a spliced variant of P553S referred to as P553S-10.

SEQ ID NO: 705 is the cDNA sequence of a spliced variant of P553S referred to as P553S-6.

SEQ ID NO: 706 is the amino acid sequence encoded by SEQ ID NO: 705.

SEQ ID NO: 707 is the amino acid sequence encoded by SEQ ID NO: 702 SEQ ID NO: 708 is a second amino acid sequence encoded by SEQ ID NO: 702.

SEQ ID NO: 709-772 are determined cDNA sequences of prostate-specific clones.

SEQ ID NO: 773 is a first full-length cDNA sequence for prostate-specific transglutaminase gene (also referred to herein as P558S).

SEQ ID NO: 774 is a second full-length cDNA sequence for prostate-specific transglutaminase gene.

SEQ ID NO: 775 is the amino acid sequence encoded by the sequence of SEQ ID NO: 773.

SEQ ID NO: 776 is the amino acid sequence encoded by the sequence of SEQ ID NO: 774.

SEQ ID NO: 777 is the full-length cDNA sequence for P788P.

SEQ ID NO: 778 is the amino acid sequence encoded by SEQ ID NO: 777.

SEQ ID NO: 779 is the determined cDNA sequence for a polymorphic variant of P788P.

SEQ ID NO: 780 is the amino acid sequence encoded by SEQ ID NO: 779.

SEQ ID NO: 781 is the amino acid sequence of peptide 4 from P703P.

SEQ ID NO: 782 is the cDNA sequence that encodes peptide 4 from P703P.

SEQ ID NO: 783-798 are the cDNA sequence encoding epitopes of P703P.

SEQ ID NO: 799-814 are the amino acid sequences of epitopes of P703P.

SEQ ID NO: 815 and 816 are PCR primers.

SEQ ID NO: 817 is the cDNA sequence encoding an N-terminal portion of P788P expressed in *E. coli*.

SEQ ID NO: 818 is the amino acid sequence of the N-terminal portion of P788P expressed in *E. coli*.

SEQ ID NO: 819 is the amino acid sequence of the *M. tuberculosis* antigen Ra12.

SEQ ID NO: 820 and 821 are PCR primers.

SEQ ID NO: 822 is the cDNA sequence for the Ra12-P510S-C construct.

SEQ ID NO: 823 is the cDNA sequence for the P510S-C construct.

SEQ ID NO: 824 is the cDNA sequence for the P510S-E3 construct.

SEQ ID NO: 825 is the amino acid sequence for the Ra12-P510S-C construct.

SEQ ID NO: 826 is the amino acid sequence for the P510S-C construct.

SEQ ID NO: 827 is the amino acid sequence for the P510S-E3 construct.

SEQ ID NO: 828-833 are PCR primers.

SEQ ID NO: 834 is the cDNA sequence of the construct Ra12-P775P-ORF3.

SEQ ID NO: 835 is the amino acid sequence of the construct Ra12-P775P-ORF3.

SEQ ID NO: 836 and 837 are PCR primers.

SEQ ID NO: 838 is the determined amino acid sequence for a P703P His tag fusion protein.

SEQ ID NO: 839 is the determined cDNA sequence for a P703P His tag fusion protein.

SEQ ID NO: 840 and 841 are PCR primers.

SEQ ID NO: 842 is the determined amino acid sequence for a P705P His tag fusion protein.

SEQ ID NO: 843 is the determined cDNA sequence for a P705P His tag fusion protein.

SEQ ID NO: 844 and 845 are PCR primers.

SEQ ID NO: 846 is the determined amino acid sequence for a P711P His tag fusion protein.

SEQ ID NO: 847 is the determined cDNA sequence for a P711P His tag fusion protein.

SEQ ID NO: 848 is the amino acid sequence of the *M. tuberculosis* antigen Ra12.

SEQ ID NO: 849 and 850 are PCR primers.

SEQ ID NO: 851 is the determined cDNA sequence for the construct Ra12-P501S-E2.

SEQ ID NO: 852 is the determined amino acid sequence for the construct Ra12-P501S-E2.

SEQ ID NO: 853 is the amino acid sequence for an epitope of P501S.

SEQ ID NO: 854 is the DNA sequence encoding SEQ ID NO: 853.

SEQ ID NO: 855 is the amino acid sequence for an epitope of P501S.

SEQ ID NO: 856 is the DNA sequence encoding SEQ ID NO: 855.

SEQ ID NO: 857 is a peptide employed in epitope mapping studies.

SEQ ID NO: 858 is the amino acid sequence for an epitope of P501S.

SEQ ID NO: 859 is the DNA sequence encoding SEQ ID NO: 858.

SEQ ID NO: 860-862 are the amino acid sequences for CD4 epitopes of P501S.

SEQ ID NO: 863-865 are the DNA sequences encoding the sequences of SEQ ID NO: 860-862.

SEQ ID NO: 866-877 are the amino acid sequences for putative CTL epitopes of P703P.

SEQ ID NO: 878 is the full-length cDNA sequence for P789P.

SEQ ID NO: 879 is the amino acid sequence encoded by SEQ ID NO: 878.

SEQ ID NO: 880 is the determined full-length cDNA sequence for the splice variant of P776P referred to as contig 6.

SEQ ID NO: 881-882 are determined full-length cDNA sequences for the splice variant of P776P referred to as contig 7.

SEQ ID NO: 883-887 are amino acid sequences encoded by SEQ ID NO: 880.

SEQ ID NO: 888-893 are amino acid sequences encoded by the splice variant of P776P referred to as contig 7.

SEQ ID NO: 894 is the full-length cDNA sequence for human transmembrane protease serine 2.

SEQ ID NO: 895 is the amino acid sequence encoded by SEQ ID NO: 894.

SEQ ID NO: 896 is the cDNA sequence encoding the first 209 amino acids of human transmembrane protease serine 2.

SEQ ID NO: 897 is the first 209 amino acids of human transmembrane protease serine 2.

SEQ ID NO: 898 is the amino acid sequence of peptide 296-322 of P501S.

SEQ ID NO: 899-902 are PCR primers.

SEQ ID NO: 903 is the determined cDNA sequence of the Vb chain of a T cell receptor for the P501S-specific T cell clone 4E5.

SEQ ID NO: 904 is the determined cDNA sequence of the Va chain of a T cell receptor for the P501S-specific T cell clone 4E5.

SEQ ID NO: 905 is the amino acid sequence encoded by SEQ ID NO 903.

SEQ ID NO: 906 is the amino acid sequence encoded by SEQ ID NO 904.

SEQ ID NO: 907 is the full-length open reading frame for P768P including stop codon.

SEQ ID NO: 908 is the full-length open reading frame for P768P without stop codon.

SEQ ID NO: 909 is the amino acid sequence encoded by SEQ ID NO: 908.

SEQ ID NO: 910-915 are the amino acid sequences for predicted domains of P768P.

SEQ ID NO: 916 is the full-length cDNA sequence of P835P.

SEQ ID NO: 917 is the cDNA sequence of the previously identified clone FLJ13581.

SEQ ID NO: 918 is the cDNA sequence of the open reading frame for P835P with stop codon.

SEQ ID NO: 919 is the cDNA sequence of the open reading frame for P835P without stop codon.

SEQ ID NO: 920 is the full-length amino acid sequence for P835P.

SEQ ID NO: 921-928 are the amino acid sequences of extracellular and intracellular domains of P835P.

SEQ ID NO: 929 is the full-length cDNA sequence for P1000C.

SEQ ID NO: 930 is the cDNA sequence of the open reading frame for P1000C, including stop codon.

SEQ ID NO: 931 is the cDNA sequence of the open reading frame for P1000C, without stop codon.

SEQ ID NO: 932 is the full-length amino acid sequence for P1000C.

SEQ ID NO: 933 is amino acids 1-100 of SEQ ID NO: 932.

SEQ ID NO: 934 is amino acids 100-492 of SEQ ID NO: 932.

SEQ ID NO: 935-937 are PCR primers.

SEQ ID NO: 938 is the cDNA sequence of the expressed full-length P767P coding region.

SEQ ID NO: 939 is the cDNA sequence of an expressed truncated P767P coding region.

SEQ ID NO: 940 is the amino acid sequence encoded by SEQ ID NO: 939.

SEQ ID NO: 941 is the amino acid sequence encoded by SEQ ID NO: 938.

SEQ ID NO: 942 is the DNA sequence of a CD4 epitope of P703P.

SEQ ID NO: 943 is the amino acid sequence of a CD4 epitope of P703P.

DETAILED DESCRIPTION OF THE INVENTION

The present invention is directed generally to compositions and their use in the therapy and diagnosis of cancer, particularly prostate cancer. As described further below, illustrative compositions of the present invention include, but are not restricted to, polypeptides, particularly immunogenic polypeptides, polynucleotides encoding such polypeptides, antibodies and other binding agents, antigen presenting cells (APCs) and immune system cells (*e.g.,* T cells).

The practice of the present invention will employ, unless indicated specifically to the contrary, conventional methods of virology, immunology, microbiology, molecular biology and recombinant DNA techniques within the skill of the art, many of which are described below for the purpose of illustration. Such techniques are explained fully in the literature. See, *e.g.*, Sambrook, et al. Molecular Cloning: A Laboratory Manual (2nd Edition, 1989); Maniatis et al. Molecular Cloning: A Laboratory Manual (1982); DNA Cloning: A Practical Approach, vol. I & II (D. Glover, ed.); Oligonucleotide Synthesis (N. Gait, ed., 1984); Nucleic Acid Hybridization (B. Hames & S. Higgins, eds., 1985); Transcription and Translation (B. Hames & S. Higgins, eds., 1984); Animal Cell Culture (R. Freshney, ed., 1986); Perbal, A Practical Guide to Molecular Cloning (1984).

All publications, patents and patent applications cited herein, whether supra or infra, are hereby incorporated by reference in their entirety.

As used in this specification and the appended claims, the singular forms "a," "an" and "the" include plural references unless the content clearly dictates otherwise.

Polypeptide Compositions

As used herein, the term "polypeptide" " is used in its conventional meaning, *i.e.*, as a sequence of amino acids. The polypeptides are not limited to a specific length of the product; thus, peptides, oligopeptides, and proteins are included within the definition of polypeptide, and such terms may be used interchangeably herein unless specifically indicated otherwise. This term also does not refer to or exclude post-

expression modifications of the polypeptide, for example, glycosylations, acetylations, phosphorylations and the like, as well as other modifications known in the art, both naturally occurring and non-naturally occurring. A polypeptide may be an entire protein, or a subsequence thereof. Particular polypeptides of interest in the context of this invention are amino acid subsequences comprising epitopes, *i.e.*, antigenic determinants substantially responsible for the immunogenic properties of a polypeptide and being capable of evoking an immune response.

Particularly illustrative polypeptides of the present invention comprise those encoded by a polynucleotide sequence set forth in any one of SEQ ID NOs: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-705, 709-774, 777, 789, 817, 823, 824, 878, 880-882, 894, 896, 907, 908, 916-919, 929-931, 938, 939 and 942, or a sequence that hybridizes under moderately stringent conditions, or, alternatively, under highly stringent conditions, to a polynucleotide sequence set forth in any one of SEQ ID NOs: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-705, 709-774, 777, 789, 817, 823, 824, 878, 880-882, 894, 896, 907, 908, 916-919, 929-931, 938, 939 and 942. In specific embodiments, the polypeptides of the invention comprise amino acid sequences as set forth in any one of SEQ ID NO: 112-114, 172, 176, 178, 327, 329, 331, 336, 339, 376-380, 383, 477-483, 496, 504, 505, 519, 520, 522, 525, 527, 532, 534, 537-551, 553-568, 573-586, 588-590, 592, 706-708, 775, 776, 778, 780, 781, 811, 814, 818, 826, 827, 853, 855, 858, 860-862, 866-877, 879, 883-893, 895, 897, 898, 909-915, 920-928, 932-934, 940, 941 and 943.

The polypeptides of the present invention are sometimes herein referred to as prostate-specific proteins or prostate-specific polypeptides, as an indication that their identification has been based at least in part upon their increased levels of expression in prostate tissue samples. Thus, a "prostate-specific polypeptide" or "prostate-specific protein," refers generally to a polypeptide sequence of the present invention, or a polynucleotide sequence encoding such a polypeptide, that is expressed

in a substantial proportion of prostate tissue samples, for example preferably greater than about 20%, more preferably greater than about 30%, and most preferably greater than about 50% or more of prostate tissue samples tested, at a level that is at least two fold, and preferably at least five fold, greater than the level of expression in other normal tissues, as determined using a representative assay provided herein. A prostate-specific polypeptide sequence of the invention, based upon its increased level of expression in tumor cells, has particular utility both as a diagnostic marker as well as a therapeutic target, as further described below.

In certain preferred embodiments, the polypeptides of the invention are immunogenic, *i.e.*, they react detectably within an immunoassay (such as an ELISA or T-cell stimulation assay) with antisera and/or T-cells from a patient with prostate cancer. Screening for immunogenic activity can be performed using techniques well known to the skilled artisan. For example, such screens can be performed using methods such as those described in Harlow and Lane, *Antibodies: A Laboratory Manual,* Cold Spring Harbor Laboratory, 1988. In one illustrative example, a polypeptide may be immobilized on a solid support and contacted with patient sera to allow binding of antibodies within the sera to the immobilized polypeptide. Unbound sera may then be removed and bound antibodies detected using, for example, ^{125}I-labeled Protein A.

As would be recognized by the skilled artisan, immunogenic portions of the polypeptides disclosed herein are also encompassed by the present invention. An "immunogenic portion," as used herein, is a fragment of an immunogenic polypeptide of the invention that itself is immunologically reactive (*i.e.,* specifically binds) with the B-cells and/or T-cell surface antigen receptors that recognize the polypeptide. Immunogenic portions may generally be identified using well known techniques, such as those summarized in Paul, *Fundamental Immunology*, 3rd ed., 243-247 (Raven Press, 1993) and references cited therein. Such techniques include screening polypeptides for the ability to react with antigen-specific antibodies, antisera and/or T-cell lines or clones. As used herein, antisera and antibodies are "antigen-specific" if they specifically bind to an antigen (*i.e.,* they react with the protein in an ELISA or other

immunoassay, and do not react detectably with unrelated proteins). Such antisera and antibodies may be prepared as described herein, and using well-known techniques.

In one preferred embodiment, an immunogenic portion of a polypeptide of the present invention is a portion that reacts with antisera and/or T-cells at a level that is not substantially less than the reactivity of the full-length polypeptide (*e.g.*, in an ELISA and/or T-cell reactivity assay). Preferably, the level of immunogenic activity of the immunogenic portion is at least about 50%, preferably at least about 70% and most preferably greater than about 90% of the immunogenicity for the full-length polypeptide. In some instances, preferred immunogenic portions will be identified that have a level of immunogenic activity greater than that of the corresponding full-length polypeptide, *e.g.*, having greater than about 100% or 150% or more immunogenic activity.

In certain other embodiments, illustrative immunogenic portions may include peptides in which an N-terminal leader sequence and/or transmembrane domain has been deleted. Other illustrative immunogenic portions will contain a small N- and/or C-terminal deletion (*e.g.*, 1-30 amino acids, preferably 5-15 amino acids), relative to the mature protein.

In another embodiment, a polypeptide composition of the invention may also comprise one or more polypeptides that are immunologically reactive with T cells and/or antibodies generated against a polypeptide of the invention, particularly a polypeptide having an amino acid sequence disclosed herein, or to an immunogenic fragment or variant thereof.

In another embodiment of the invention, polypeptides are provided that comprise one or more polypeptides that are capable of eliciting T cells and/or antibodies that are immunologically reactive with one or more polypeptides described herein, or one or more polypeptides encoded by contiguous nucleic acid sequences contained in the polynucleotide sequences disclosed herein, or immunogenic fragments or variants thereof, or to one or more nucleic acid sequences which hybridize to one or more of these sequences under conditions of moderate to high stringency.

The present invention, in another aspect, provides polypeptide fragments comprising at least about 5, 10, 15, 20, 25, 50, or 100 contiguous amino acids, or more, including all intermediate lengths, of a polypeptide composition set forth herein, such as those set forth in SEQ ID NO: 112-114, 172, 176, 178, 327, 329, 331, 336, 339, 376-380, 383, 477-483, 496, 504, 505, 519, 520, 522, 525, 527, 532, 534, 537-551, 553-568, 573-586, 588-590, 592, 706-708, 775, 776, 778, 780, 781, 811, 814, 818, 826, 827, 853, 855, 858, 860-862, 866-877, 879, 883-893, 895, 897, 898, 909-915, 920-928, 932-934, 940, 941 and 943, or those encoded by a polynucleotide sequence set forth in a sequence of SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-705, 709-774, 777, 789, 817, 823, 824, 878, 880-882, 894, 896, 907, 908, 916-919, 929-931, 938, 939 and 942.

In another aspect, the present invention provides variants of the polypeptide compositions described herein. Polypeptide variants generally encompassed by the present invention will typically exhibit at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% or more identity (determined as described below), along its length, to a polypeptide sequence set forth herein.

In one preferred embodiment, the polypeptide fragments and variants provided by the present invention are immunologically reactive with an antibody and/or T-cell that reacts with a full-length polypeptide specifically set forth herein.

In another preferred embodiment, the polypeptide fragments and variants provided by the present invention exhibit a level of immunogenic activity of at least about 50%, preferably at least about 70%, and most preferably at least about 90% or more of that exhibited by a full-length polypeptide sequence specifically set forth herein.

A polypeptide "variant," as the term is used herein, is a polypeptide that typically differs from a polypeptide specifically disclosed herein in one or more substitutions, deletions, additions and/or insertions. Such variants may be naturally occurring or may be synthetically generated, for example, by modifying one or more of

the above polypeptide sequences of the invention and evaluating their immunogenic activity as described herein using any of a number of techniques well known in the art.

For example, certain illustrative variants of the polypeptides of the invention include those in which one or more portions, such as an N-terminal leader sequence or transmembrane domain, have been removed. Other illustrative variants include variants in which a small portion (*e.g.,* 1-30 amino acids, preferably 5-15 amino acids) has been removed from the N- and/or C-terminal of the mature protein.

In many instances, a variant will contain conservative substitutions. A "conservative substitution" is one in which an amino acid is substituted for another amino acid that has similar properties, such that one skilled in the art of peptide chemistry would expect the secondary structure and hydropathic nature of the polypeptide to be substantially unchanged. As described above, modifications may be made in the structure of the polynucleotides and polypeptides of the present invention and still obtain a functional molecule that encodes a variant or derivative polypeptide with desirable characteristics, *e.g.*, with immunogenic characteristics. When it is desired to alter the amino acid sequence of a polypeptide to create an equivalent, or even an improved, immunogenic variant or portion of a polypeptide of the invention, one skilled in the art will typically change one or more of the codons of the encoding DNA sequence according to Table 1.

For example, certain amino acids may be substituted for other amino acids in a protein structure without appreciable loss of interactive binding capacity with structures such as, for example, antigen-binding regions of antibodies or binding sites on substrate molecules. Since it is the interactive capacity and nature of a protein that defines that protein's biological functional activity, certain amino acid sequence substitutions can be made in a protein sequence, and, of course, its underlying DNA coding sequence, and nevertheless obtain a protein with like properties. It is thus contemplated that various changes may be made in the peptide sequences of the disclosed compositions, or corresponding DNA sequences which encode said peptides without appreciable loss of their biological utility or activity.

TABLE 1

Amino Acids			Codons					
Alanine	Ala	A	GCA	GCC	GCG	GCU		
Cysteine	Cys	C	UGC	UGU				
Aspartic acid	Asp	D	GAC	GAU				
Glutamic acid	Glu	E	GAA	GAG				
Phenylalanine	Phe	F	UUC	UUU				
Glycine	Gly	G	GGA	GGC	GGG	GGU		
Histidine	His	H	CAC	CAU				
Isoleucine	Ile	I	AUA	AUC	AUU			
Lysine	Lys	K	AAA	AAG				
Leucine	Leu	L	UUA	UUG	CUA	CUC	CUG	CUU
Methionine	Met	M	AUG					
Asparagine	Asn	N	AAC	AAU				
Proline	Pro	P	CCA	CCC	CCG	CCU		
Glutamine	Gln	Q	CAA	CAG				
Arginine	Arg	R	AGA	AGG	CGA	CGC	CGG	CGU
Serine	Ser	S	AGC	AGU	UCA	UCC	UCG	UCU
Threonine	Thr	T	ACA	ACC	ACG	ACU		
Valine	Val	V	GUA	GUC	GUG	GUU		
Tryptophan	Trp	W	UGG					
Tyrosine	Tyr	Y	UAC	UAU				

In making such changes, the hydropathic index of amino acids may be considered. The importance of the hydropathic amino acid index in conferring interactive biologic function on a protein is generally understood in the art (Kyte and Doolittle, 1982, incorporated herein by reference). It is accepted that the relative hydropathic character of the amino acid contributes to the secondary structure of the resultant protein, which in turn defines the interaction of the protein with other molecules, for example, enzymes, substrates, receptors, DNA, antibodies, antigens, and the like. Each amino acid has been assigned a hydropathic index on the basis of its

hydrophobicity and charge characteristics (Kyte and Doolittle, 1982). These values are: isoleucine (+4.5); valine (+4.2); leucine (+3.8); phenylalanine (+2.8); cysteine/cystine (+2.5); methionine (+1.9); alanine (+1.8); glycine (–0.4); threonine (–0.7); serine (–0.8); tryptophan (–0.9); tyrosine (–1.3); proline (–1.6); histidine (–3.2); glutamate (–3.5); glutamine (–3.5); aspartate (–3.5); asparagine (–3.5); lysine (–3.9); and arginine (–4.5).

It is known in the art that certain amino acids may be substituted by other amino acids having a similar hydropathic index or score and still result in a protein with similar biological activity, *i.e.* still obtain a biological functionally equivalent protein. In making such changes, the substitution of amino acids whose hydropathic indices are within ±2 is preferred, those within ±1 are particularly preferred, and those within ±0.5 are even more particularly preferred. It is also understood in the art that the substitution of like amino acids can be made effectively on the basis of hydrophilicity. U. S. Patent 4,554,101 (specifically incorporated herein by reference in its entirety), states that the greatest local average hydrophilicity of a protein, as governed by the hydrophilicity of its adjacent amino acids, correlates with a biological property of the protein.

As detailed in U. S. Patent 4,554,101, the following hydrophilicity values have been assigned to amino acid residues: arginine (+3.0); lysine (+3.0); aspartate (+3.0 ± 1); glutamate (+3.0 ± 1); serine (+0.3); asparagine (+0.2); glutamine (+0.2); glycine (0); threonine (–0.4); proline (–0.5 ± 1); alanine (–0.5); histidine (–0.5); cysteine (–1.0); methionine (–1.3); valine (–1.5); leucine (–1.8); isoleucine (–1.8); tyrosine (–2.3); phenylalanine (–2.5); tryptophan (–3.4). It is understood that an amino acid can be substituted for another having a similar hydrophilicity value and still obtain a biologically equivalent, and in particular, an immunologically equivalent protein. In such changes, the substitution of amino acids whose hydrophilicity values are within ±2 is preferred, those within ±1 are particularly preferred, and those within ±0.5 are even more particularly preferred.

As outlined above, amino acid substitutions are generally therefore based on the relative similarity of the amino acid side-chain substituents, for example, their hydrophobicity, hydrophilicity, charge, size, and the like. Exemplary substitutions that take various of the foregoing characteristics into consideration are well known to those

of skill in the art and include: arginine and lysine; glutamate and aspartate; serine and threonine; glutamine and asparagine; and valine, leucine and isoleucine.

In addition, any polynucleotide may be further modified to increase stability *in vivo*. Possible modifications include, but are not limited to, the addition of flanking sequences at the 5' and/or 3' ends; the use of phosphorothioate or 2' O-methyl rather than phosphodiesterase linkages in the backbone; and/or the inclusion of nontraditional bases such as inosine, queosine and wybutosine, as well as acetyl-methyl-, thio- and other modified forms of adenine, cytidine, guanine, thymine and uridine.

Amino acid substitutions may further be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity and/or the amphipathic nature of the residues. For example, negatively charged amino acids include aspartic acid and glutamic acid; positively charged amino acids include lysine and arginine; and amino acids with uncharged polar head groups having similar hydrophilicity values include leucine, isoleucine and valine; glycine and alanine; asparagine and glutamine; and serine, threonine, phenylalanine and tyrosine. Other groups of amino acids that may represent conservative changes include: (1) ala, pro, gly, glu, asp, gln, asn, ser, thr; (2) cys, ser, tyr, thr; (3) val, ile, leu, met, ala, phe; (4) lys, arg, his; and (5) phe, tyr, trp, his. A variant may also, or alternatively, contain nonconservative changes. In a preferred embodiment, variant polypeptides differ from a native sequence by substitution, deletion or addition of five amino acids or fewer. Variants may also (or alternatively) be modified by, for example, the deletion or addition of amino acids that have minimal influence on the immunogenicity, secondary structure and hydropathic nature of the polypeptide.

As noted above, polypeptides may comprise a signal (or leader) sequence at the N-terminal end of the protein, which co-translationally or post-translationally directs transfer of the protein. The polypeptide may also be conjugated to a linker or other sequence for ease of synthesis, purification or identification of the polypeptide (*e.g.,* poly-His), or to enhance binding of the polypeptide to a solid support. For example, a polypeptide may be conjugated to an immunoglobulin Fc region.

When comparing polypeptide sequences, two sequences are said to be "identical" if the sequence of amino acids in the two sequences is the same when aligned for maximum correspondence, as described below. Comparisons between two sequences are typically performed by comparing the sequences over a comparison window to identify and compare local regions of sequence similarity. A "comparison window" as used herein, refers to a segment of at least about 20 contiguous positions, usually 30 to about 75, 40 to about 50, in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned.

Optimal alignment of sequences for comparison may be conducted using the Megalign program in the Lasergene suite of bioinformatics software (DNASTAR, Inc., Madison, WI), using default parameters. This program embodies several alignment schemes described in the following references: Dayhoff, M.O. (1978) A model of evolutionary change in proteins – Matrices for detecting distant relationships. In Dayhoff, M.O. (ed.) Atlas of Protein Sequence and Structure, National Biomedical Research Foundation, Washington DC Vol. 5, Suppl. 3, pp. 345-358; Hein J. (1990) Unified Approach to Alignment and Phylogenes pp. 626-645 *Methods in Enzymology* vol. 183, Academic Press, Inc., San Diego, CA; Higgins, D.G. and Sharp, P.M. (1989) *CABIOS 5*:151-153; Myers, E.W. and Muller W. (1988) *CABIOS 4*:11-17; Robinson, E.D. (1971) *Comb. Theor 11*:105; Santou, N. Nes, M. (1987) *Mol. Biol. Evol. 4*:406-425; Sneath, P.H.A. and Sokal, R.R. (1973) *Numerical Taxonomy – the Principles and Practice of Numerical Taxonomy*, Freeman Press, San Francisco, CA; Wilbur, W.J. and Lipman, D.J. (1983) *Proc. Natl. Acad., Sci. USA 80*:726-730.

Alternatively, optimal alignment of sequences for comparison may be conducted by the local identity algorithm of Smith and Waterman (1981) *Add. APL. Math* 2:482, by the identity alignment algorithm of Needleman and Wunsch (1970) *J. Mol. Biol.* 48:443, by the search for similarity methods of Pearson and Lipman (1988) *Proc. Natl. Acad. Sci. USA* 85: 2444, by computerized implementations of these algorithms (GAP, BESTFIT, BLAST, FASTA, and TFASTA in the Wisconsin Genetics

Software Package, Genetics Computer Group (GCG), 575 Science Dr., Madison, WI), or by inspection.

One preferred example of algorithms that are suitable for determining percent sequence identity and sequence similarity are the BLAST and BLAST 2.0 algorithms, which are described in Altschul et al. (1977) *Nucl. Acids Res.* 25:3389-3402 and Altschul et al. (1990) *J. Mol. Biol.* 215:403-410, respectively. BLAST and BLAST 2.0 can be used, for example with the parameters described herein, to determine percent sequence identity for the polynucleotides and polypeptides of the invention. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information. For amino acid sequences, a scoring matrix can be used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T and X determine the sensitivity and speed of the alignment.

In one preferred approach, the "percentage of sequence identity" is determined by comparing two optimally aligned sequences over a window of comparison of at least 20 positions, wherein the portion of the polypeptide sequence in the comparison window may comprise additions or deletions (*i.e.*, gaps) of 20 percent or less, usually 5 to 15 percent, or 10 to 12 percent, as compared to the reference sequences (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the reference sequence (*i.e.*, the window size) and multiplying the results by 100 to yield the percentage of sequence identity.

Within other illustrative embodiments, a polypeptide may be a fusion polypeptide that comprises multiple polypeptides as described herein, or that comprises at least one polypeptide as described herein and an unrelated sequence, such as a known

tumor protein. A fusion partner may, for example, assist in providing T helper epitopes (an immunological fusion partner), preferably T helper epitopes recognized by humans, or may assist in expressing the protein (an expression enhancer) at higher yields than the native recombinant protein. Certain preferred fusion partners are both immunological and expression enhancing fusion partners. Other fusion partners may be selected so as to increase the solubility of the polypeptide or to enable the polypeptide to be targeted to desired intracellular compartments. Still further fusion partners include affinity tags, which facilitate purification of the polypeptide.

Fusion polypeptides may generally be prepared using standard techniques, including chemical conjugation. Preferably, a fusion polypeptide is expressed as a recombinant polypeptide, allowing the production of increased levels, relative to a non-fused polypeptide, in an expression system. Briefly, DNA sequences encoding the polypeptide components may be assembled separately, and ligated into an appropriate expression vector. The 3' end of the DNA sequence encoding one polypeptide component is ligated, with or without a peptide linker, to the 5' end of a DNA sequence encoding the second polypeptide component so that the reading frames of the sequences are in phase. This permits translation into a single fusion polypeptide that retains the biological activity of both component polypeptides.

A peptide linker sequence may be employed to separate the first and second polypeptide components by a distance sufficient to ensure that each polypeptide folds into its secondary and tertiary structures. Such a peptide linker sequence is incorporated into the fusion polypeptide using standard techniques well known in the art. Suitable peptide linker sequences may be chosen based on the following factors: (1) their ability to adopt a flexible extended conformation; (2) their inability to adopt a secondary structure that could interact with functional epitopes on the first and second polypeptides; and (3) the lack of hydrophobic or charged residues that might react with the polypeptide functional epitopes. Preferred peptide linker sequences contain Gly, Asn and Ser residues. Other near neutral amino acids, such as Thr and Ala may also be used in the linker sequence. Amino acid sequences which may be usefully employed as linkers include those disclosed in Maratea et al., *Gene 40*:39-46, 1985; Murphy et al.,

Proc. Natl. Acad. Sci. USA 83:8258-8262, 1986; U.S. Patent No. 4,935,233 and U.S. Patent No. 4,751,180. The linker sequence may generally be from 1 to about 50 amino acids in length. Linker sequences are not required when the first and second polypeptides have non-essential N-terminal amino acid regions that can be used to separate the functional domains and prevent steric interference.

The ligated DNA sequences are operably linked to suitable transcriptional or translational regulatory elements. The regulatory elements responsible for expression of DNA are located only 5' to the DNA sequence encoding the first polypeptides. Similarly, stop codons required to end translation and transcription termination signals are only present 3' to the DNA sequence encoding the second polypeptide.

The fusion polypeptide can comprise a polypeptide as described herein together with an unrelated immunogenic protein, such as an immunogenic protein capable of eliciting a recall response. Examples of such proteins include tetanus, tuberculosis and hepatitis proteins (*see*, for example, Stoute et al. *New Engl. J. Med.*, *336*:86-91, 1997).

In one preferred embodiment, the immunological fusion partner is derived from a Mycobacterium sp., such as a *Mycobacterium tuberculosis*-derived Ra12 fragment. Ra12 compositions and methods for their use in enhancing the expression and/or immunogenicity of heterologous polynucleotide/polypeptide sequences is described in U.S. Patent Application 60/158,585, the disclosure of which is incorporated herein by reference in its entirety. Briefly, Ra12 refers to a polynucleotide region that is a subsequence of a *Mycobacterium tuberculosis* MTB32A nucleic acid. MTB32A is a serine protease of 32 KD molecular weight encoded by a gene in virulent and avirulent strains of *M. tuberculosis*. The nucleotide sequence and amino acid sequence of MTB32A have been described (for example, U.S. Patent Application 60/158,585; see also, Skeiky *et al., Infection and Immun.* (1999) 67:3998-4007, incorporated herein by reference). C-terminal fragments of the MTB32A coding sequence express at high levels and remain as a soluble polypeptides throughout the purification process. Moreover, Ra12 may enhance the immunogenicity of heterologous

immunogenic polypeptides with which it is fused. One preferred Ra12 fusion polypeptide comprises a 14 KD C-terminal fragment corresponding to amino acid residues 192 to 323 of MTB32A. Other preferred Ra12 polynucleotides generally comprise at least about 15 consecutive nucleotides, at least about 30 nucleotides, at least about 60 nucleotides, at least about 100 nucleotides, at least about 200 nucleotides, or at least about 300 nucleotides that encode a portion of a Ra12 polypeptide. Ra12 polynucleotides may comprise a native sequence (*i.e.*, an endogenous sequence that encodes a Ra12 polypeptide or a portion thereof) or may comprise a variant of such a sequence. Ra12 polynucleotide variants may contain one or more substitutions, additions, deletions and/or insertions such that the biological activity of the encoded fusion polypeptide is not substantially diminished, relative to a fusion polypeptide comprising a native Ra12 polypeptide. Variants preferably exhibit at least about 70% identity, more preferably at least about 80% identity and most preferably at least about 90% identity to a polynucleotide sequence that encodes a native Ra12 polypeptide or a portion thereof.

Within other preferred embodiments, an immunological fusion partner is derived from protein D, a surface protein of the gram-negative bacterium Haemophilus influenza B (WO 91/18926). Preferably, a protein D derivative comprises approximately the first third of the protein (*e.g.*, the first N-terminal 100-110 amino acids), and a protein D derivative may be lipidated. Within certain preferred embodiments, the first 109 residues of a Lipoprotein D fusion partner is included on the N-terminus to provide the polypeptide with additional exogenous T-cell epitopes and to increase the expression level in *E. coli* (thus functioning as an expression enhancer). The lipid tail ensures optimal presentation of the antigen to antigen presenting cells. Other fusion partners include the non-structural protein from influenzae virus, NS1 (hemaglutinin). Typically, the N-terminal 81 amino acids are used, although different fragments that include T-helper epitopes may be used.

In another embodiment, the immunological fusion partner is the protein known as LYTA, or a portion thereof (preferably a C-terminal portion). LYTA is derived from *Streptococcus pneumoniae*, which synthesizes an N-acetyl-L-alanine

amidase known as amidase LYTA (encoded by the LytA gene; *Gene 43*:265-292, 1986). LYTA is an autolysin that specifically degrades certain bonds in the peptidoglycan backbone. The C-terminal domain of the LYTA protein is responsible for the affinity to the choline or to some choline analogues such as DEAE. This property has been exploited for the development of *E. coli* C-LYTA expressing plasmids useful for expression of fusion proteins. Purification of hybrid proteins containing the C-LYTA fragment at the amino terminus has been described (*see Biotechnology 10*:795-798, 1992). Within a preferred embodiment, a repeat portion of LYTA may be incorporated into a fusion polypeptide. A repeat portion is found in the C-terminal region starting at residue 178. A particularly preferred repeat portion incorporates residues 188-305.

Yet another illustrative embodiment involves fusion polypeptides, and the polynucleotides encoding them, wherein the fusion partner comprises a targeting signal capable of directing a polypeptide to the endosomal/lysosomal compartment, as described in U.S. Patent No. 5,633,234. An immunogenic polypeptide of the invention, when fused with this targeting signal, will associate more efficiently with MHC class II molecules and thereby provide enhanced in vivo stimulation of $CD4^+$ T-cells specific for the polypeptide.

Polypeptides of the invention are prepared using any of a variety of well known synthetic and/or recombinant techniques, the latter of which are further described below. Polypeptides, portions and other variants generally less than about 150 amino acids can be generated by synthetic means, using techniques well known to those of ordinary skill in the art. In one illustrative example, such polypeptides are synthesized using any of the commercially available solid-phase techniques, such as the Merrifield solid-phase synthesis method, where amino acids are sequentially added to a growing amino acid chain. *See* Merrifield, *J. Am. Chem. Soc. 85*:2149-2146, 1963. Equipment for automated synthesis of polypeptides is commercially available from suppliers such as Perkin Elmer/Applied BioSystems Division (Foster City, CA), and may be operated according to the manufacturer's instructions.

In general, polypeptide compositions (including fusion polypeptides) of the invention are isolated. An "isolated" polypeptide is one that is removed from its

original environment. For example, a naturally-occurring protein or polypeptide is isolated if it is separated from some or all of the coexisting materials in the natural system. Preferably, such polypeptides are also purified, *e.g.*, are at least about 90% pure, more preferably at least about 95% pure and most preferably at least about 99% pure.

Polynucleotide Compositions

The present invention, in other aspects, provides polynucleotide compositions. The terms "DNA" and "polynucleotide" are used essentially interchangeably herein to refer to a DNA molecule that has been isolated free of total genomic DNA of a particular species. "Isolated," as used herein, means that a polynucleotide is substantially away from other coding sequences, and that the DNA molecule does not contain large portions of unrelated coding DNA, such as large chromosomal fragments or other functional genes or polypeptide coding regions. Of course, this refers to the DNA molecule as originally isolated, and does not exclude genes or coding regions later added to the segment by the hand of man.

As will be understood by those skilled in the art, the polynucleotide compositions of this invention can include genomic sequences, extra-genomic and plasmid-encoded sequences and smaller engineered gene segments that express, or may be adapted to express, proteins, polypeptides, peptides and the like. Such segments may be naturally isolated, or modified synthetically by the hand of man.

As will be also recognized by the skilled artisan, polynucleotides of the invention may be single-stranded (coding or antisense) or double-stranded, and may be DNA (genomic, cDNA or synthetic) or RNA molecules. RNA molecules may include HnRNA molecules, which contain introns and correspond to a DNA molecule in a one-to-one manner, and mRNA molecules, which do not contain introns. Additional coding or non-coding sequences may, but need not, be present within a polynucleotide of the present invention, and a polynucleotide may, but need not, be linked to other molecules and/or support materials.

Polynucleotides may comprise a native sequence (*i.e.,* an endogenous sequence that encodes a polypeptide/protein of the invention or a portion thereof) or may comprise a sequence that encodes a variant or derivative, preferably an immunogenic variant or derivative, of such a sequence.

Therefore, according to another aspect of the present invention, polynucleotide compositions are provided that comprise some or all of a polynucleotide sequence set forth in any one of SEQ ID NOs: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-705, 709-774, 777, 789, 817, 823, 824, 878, 880-882, 894, 896, 907, 908, 916-919, 929-931, 938, 939 and 942, complements of a polynucleotide sequence set forth in any one of SEQ ID NOs: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-705, 709-774, 777, 789, 817, 823, 824, 878, 880-882, 894, 896, 907, 908, 916-919, 929-931, 938, 939 and 942, and degenerate variants of a polynucleotide sequence set forth in any one of SEQ ID NOs: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-705, 709-774, 777, 789, 817, 823, 824, 878, 880-882, 894, 896, 907, 908, 916-919, 929-931, 938, 939 and 942. In certain preferred embodiments, the polynucleotide sequences set forth herein encode immunogenic polypeptides, as described above.

In other related embodiments, the present invention provides polynucleotide variants having substantial identity to the sequences disclosed herein in SEQ ID NOs: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-705, 709-774, 777, 789, 817, 823, 824, 878, 880-882, 894, 896, 907, 908, 916-919, 929-931, 938, 939 and 942, for example those comprising at least 70% sequence identity, preferably at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% or higher, sequence identity compared to a polynucleotide sequence of this invention using the methods described herein, (*e.g.*, BLAST analysis using standard

parameters, as described below). One skilled in this art will recognize that these values can be appropriately adjusted to determine corresponding identity of proteins encoded by two nucleotide sequences by taking into account codon degeneracy, amino acid similarity, reading frame positioning and the like.

Typically, polynucleotide variants will contain one or more substitutions, additions, deletions and/or insertions, preferably such that the immunogenicity of the polypeptide encoded by the variant polynucleotide is not substantially diminished relative to a polypeptide encoded by a polynucleotide sequence specifically set forth herein). The term "variants" should also be understood to encompasses homologous genes of xenogenic origin.

In additional embodiments, the present invention provides polynucleotide fragments comprising various lengths of contiguous stretches of sequence identical to, or complementary to, one or more of the sequences disclosed herein. For example, polynucleotides are provided by this invention that comprise at least about 10, 15, 20, 30, 40, 50, 75, 100, 150, 200, 300, 400, 500 or 1000 or more contiguous nucleotides of one or more of the sequences disclosed herein as well as all intermediate lengths there between. It will be readily understood that "intermediate lengths", in this context, means any length between the quoted values, such as 16, 17, 18, 19, *etc.*; 21, 22, 23, *etc.*; 30, 31, 32, *etc.*; 50, 51, 52, 53, *etc.*; 100, 101, 102, 103, *etc.*; 150, 151, 152, 153, *etc.*; including all integers through 200-500; 500-1,000, and the like.

In another embodiment of the invention, polynucleotide compositions are provided that are capable of hybridizing under moderate to high stringency conditions to a polynucleotide sequence provided herein, or a fragment thereof, or a complementary sequence thereof. Hybridization techniques are well known in the art of molecular biology. For purposes of illustration, suitable moderately stringent conditions for testing the hybridization of a polynucleotide of this invention with other polynucleotides include prewashing in a solution of 5 X SSC, 0.5% SDS, 1.0 mM EDTA (pH 8.0); hybridizing at 50°C-60°C, 5 X SSC, overnight; followed by washing twice at 65°C for 20 minutes with each of 2X, 0.5X and 0.2X SSC containing 0.1% SDS. One skilled in

the art will understand that the stringency of hybridization can be readily manipulated, such as by altering the salt content of the hybridization solution and/or the temperature at which the hybridization is performed. For example, in another embodiment, suitable highly stringent hybridization conditions include those described above, with the exception that the temperature of hybridization is increased, *e.g.*, to 60-65°C or 65-70°C.

In certain preferred embodiments, the polynucleotides described above, *e.g.*, polynucleotide variants, fragments and hybridizing sequences, encode polypeptides that are immunologically cross-reactive with a polypeptide sequence specifically set forth herein. In other preferred embodiments, such polynucleotides encode polypeptides that have a level of immunogenic activity of at least about 50%, preferably at least about 70%, and more preferably at least about 90% of that for a polypeptide sequence specifically set forth herein.

The polynucleotides of the present invention, or fragments thereof, regardless of the length of the coding sequence itself, may be combined with other DNA sequences, such as promoters, polyadenylation signals, additional restriction enzyme sites, multiple cloning sites, other coding segments, and the like, such that their overall length may vary considerably. It is therefore contemplated that a nucleic acid fragment of almost any length may be employed, with the total length preferably being limited by the ease of preparation and use in the intended recombinant DNA protocol. For example, illustrative polynucleotide segments with total lengths of about 10,000, about 5000, about 3000, about 2,000, about 1,000, about 500, about 200, about 100, about 50 base pairs in length, and the like, (including all intermediate lengths) are contemplated to be useful in many implementations of this invention.

When comparing polynucleotide sequences, two sequences are said to be "identical" if the sequence of nucleotides in the two sequences is the same when aligned for maximum correspondence, as described below. Comparisons between two sequences are typically performed by comparing the sequences over a comparison window to identify and compare local regions of sequence similarity. A "comparison window" as used herein, refers to a segment of at least about 20 contiguous positions,

usually 30 to about 75, preferably 40 to about 50, in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned.

Optimal alignment of sequences for comparison may be conducted using the Megalign program in the Lasergene suite of bioinformatics software (DNASTAR, Inc., Madison, WI), using default parameters. This program embodies several alignment schemes described in the following references: Dayhoff, M.O. (1978) A model of evolutionary change in proteins – Matrices for detecting distant relationships. In Dayhoff, M.O. (ed.) Atlas of Protein Sequence and Structure, National Biomedical Research Foundation, Washington DC Vol. 5, Suppl. 3, pp. 345-358; Hein J. (1990) Unified Approach to Alignment and Phylogenes pp. 626-645 *Methods in Enzymology* vol. 183, Academic Press, Inc., San Diego, CA; Higgins, D.G. and Sharp, P.M. (1989) *CABIOS 5*:151-153; Myers, E.W. and Muller W. (1988) *CABIOS 4*:11-17; Robinson, E.D. (1971) *Comb. Theor 11*:105; Santou, N. Nes, M. (1987) *Mol. Biol. Evol. 4*:406-425; Sneath, P.H.A. and Sokal, R.R. (1973) *Numerical Taxonomy – the Principles and Practice of Numerical Taxonomy*, Freeman Press, San Francisco, CA; Wilbur, W.J. and Lipman, D.J. (1983) *Proc. Natl. Acad., Sci. USA 80*:726-730.

Alternatively, optimal alignment of sequences for comparison may be conducted by the local identity algorithm of Smith and Waterman (1981) *Add. APL. Math* 2:482, by the identity alignment algorithm of Needleman and Wunsch (1970) *J. Mol. Biol.* 48:443, by the search for similarity methods of Pearson and Lipman (1988) *Proc. Natl. Acad. Sci. USA* 85: 2444, by computerized implementations of these algorithms (GAP, BESTFIT, BLAST, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group (GCG), 575 Science Dr., Madison, WI), or by inspection.

One preferred example of algorithms that are suitable for determining percent sequence identity and sequence similarity are the BLAST and BLAST 2.0 algorithms, which are described in Altschul et al. (1977) *Nucl. Acids Res.* 25:3389-3402 and Altschul et al. (1990) *J. Mol. Biol.* 215:403-410, respectively. BLAST and BLAST 2.0 can be used, for example with the parameters described herein, to determine percent

sequence identity for the polynucleotides of the invention. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information. In one illustrative example, cumulative scores can be calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always >0) and N (penalty score for mismatching residues; always <0). Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, and expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff and Henikoff (1989) *Proc. Natl. Acad. Sci. USA* 89:10915) alignments, (B) of 50, expectation (E) of 10, M=5, N=-4 and a comparison of both strands.

Preferably, the "percentage of sequence identity" is determined by comparing two optimally aligned sequences over a window of comparison of at least 20 positions, wherein the portion of the polynucleotide sequence in the comparison window may comprise additions or deletions (*i.e.*, gaps) of 20 percent or less, usually 5 to 15 percent, or 10 to 12 percent, as compared to the reference sequences (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid bases occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the reference sequence (*i.e.*, the window size) and multiplying the results by 100 to yield the percentage of sequence identity.

It will be appreciated by those of ordinary skill in the art that, as a result of the degeneracy of the genetic code, there are many nucleotide sequences that encode a polypeptide as described herein. Some of these polynucleotides bear minimal homology to the nucleotide sequence of any native gene. Nonetheless, polynucleotides that vary due to differences in codon usage are specifically contemplated by the present

invention. Further, alleles of the genes comprising the polynucleotide sequences provided herein are within the scope of the present invention. Alleles are endogenous genes that are altered as a result of one or more mutations, such as deletions, additions and/or substitutions of nucleotides. The resulting mRNA and protein may, but need not, have an altered structure or function. Alleles may be identified using standard techniques (such as hybridization, amplification and/or database sequence comparison).

Therefore, in another embodiment of the invention, a mutagenesis approach, such as site-specific mutagenesis, is employed for the preparation of immunogenic variants and/or derivatives of the polypeptides described herein. By this approach, specific modifications in a polypeptide sequence can be made through mutagenesis of the underlying polynucleotides that encode them. These techniques provides a straightforward approach to prepare and test sequence variants, for example, incorporating one or more of the foregoing considerations, by introducing one or more nucleotide sequence changes into the polynucleotide.

Site-specific mutagenesis allows the production of mutants through the use of specific oligonucleotide sequences which encode the DNA sequence of the desired mutation, as well as a sufficient number of adjacent nucleotides, to provide a primer sequence of sufficient size and sequence complexity to form a stable duplex on both sides of the deletion junction being traversed. Mutations may be employed in a selected polynucleotide sequence to improve, alter, decrease, modify, or otherwise change the properties of the polynucleotide itself, and/or alter the properties, activity, composition, stability, or primary sequence of the encoded polypeptide.

In certain embodiments of the present invention, the inventors contemplate the mutagenesis of the disclosed polynucleotide sequences to alter one or more properties of the encoded polypeptide, such as the immunogenicity of a polypeptide vaccine. The techniques of site-specific mutagenesis are well-known in the art, and are widely used to create variants of both polypeptides and polynucleotides. For example, site-specific mutagenesis is often used to alter a specific portion of a DNA molecule. In such embodiments, a primer comprising typically about 14 to about 25

nucleotides or so in length is employed, with about 5 to about 10 residues on both sides of the junction of the sequence being altered.

As will be appreciated by those of skill in the art, site-specific mutagenesis techniques have often employed a phage vector that exists in both a single stranded and double stranded form. Typical vectors useful in site-directed mutagenesis include vectors such as the M13 phage. These phage are readily commercially-available and their use is generally well-known to those skilled in the art. Double-stranded plasmids are also routinely employed in site directed mutagenesis that eliminates the step of transferring the gene of interest from a plasmid to a phage.

In general, site-directed mutagenesis in accordance herewith is performed by first obtaining a single-stranded vector or melting apart of two strands of a double-stranded vector that includes within its sequence a DNA sequence that encodes the desired peptide. An oligonucleotide primer bearing the desired mutated sequence is prepared, generally synthetically. This primer is then annealed with the single-stranded vector, and subjected to DNA polymerizing enzymes such as *E. coli* polymerase I Klenow fragment, in order to complete the synthesis of the mutation-bearing strand. Thus, a heteroduplex is formed wherein one strand encodes the original non-mutated sequence and the second strand bears the desired mutation. This heteroduplex vector is then used to transform appropriate cells, such as *E. coli* cells, and clones are selected which include recombinant vectors bearing the mutated sequence arrangement.

The preparation of sequence variants of the selected peptide-encoding DNA segments using site-directed mutagenesis provides a means of producing potentially useful species and is not meant to be limiting as there are other ways in which sequence variants of peptides and the DNA sequences encoding them may be obtained. For example, recombinant vectors encoding the desired peptide sequence may be treated with mutagenic agents, such as hydroxylamine, to obtain sequence variants. Specific details regarding these methods and protocols are found in the teachings of Maloy *et al.*, 1994; Segal, 1976; Prokop and Bajpai, 1991; Kuby, 1994; and Maniatis *et al.*, 1982, each incorporated herein by reference, for that purpose.

As used herein, the term "oligonucleotide directed mutagenesis procedure" refers to template-dependent processes and vector-mediated propagation which result in an increase in the concentration of a specific nucleic acid molecule relative to its initial concentration, or in an increase in the concentration of a detectable signal, such as amplification. As used herein, the term "oligonucleotide directed mutagenesis procedure" is intended to refer to a process that involves the template-dependent extension of a primer molecule. The term template dependent process refers to nucleic acid synthesis of an RNA or a DNA molecule wherein the sequence of the newly synthesized strand of nucleic acid is dictated by the well-known rules of complementary base pairing (see, for example, Watson, 1987). Typically, vector mediated methodologies involve the introduction of the nucleic acid fragment into a DNA or RNA vector, the clonal amplification of the vector, and the recovery of the amplified nucleic acid fragment. Examples of such methodologies are provided by U. S. Patent No. 4,237,224, specifically incorporated herein by reference in its entirety.

In another approach for the production of polypeptide variants of the present invention, recursive sequence recombination, as described in U.S. Patent No. 5,837,458, may be employed. In this approach, iterative cycles of recombination and screening or selection are performed to "evolve" individual polynucleotide variants of the invention having, for example, enhanced immunogenic activity.

In other embodiments of the present invention, the polynucleotide sequences provided herein can be advantageously used as probes or primers for nucleic acid hybridization. As such, it is contemplated that nucleic acid segments that comprise a sequence region of at least about 15 contiguous nucleotides that has the same sequence as, or is complementary to, a 15 nucleotide long contiguous sequence disclosed herein will find particular utility. Longer contiguous identical or complementary sequences, *e.g.*, those of about 20, 30, 40, 50, 100, 200, 500, 1000 (including all intermediate lengths) and even up to full length sequences will also be of use in certain embodiments.

The ability of such nucleic acid probes to specifically hybridize to a sequence of interest will enable them to be of use in detecting the presence of

complementary sequences in a given sample. However, other uses are also envisioned, such as the use of the sequence information for the preparation of mutant species primers, or primers for use in preparing other genetic constructions.

Polynucleotide molecules having sequence regions consisting of contiguous nucleotide stretches of 10-14, 15-20, 30, 50, or even of 100-200 nucleotides or so (including intermediate lengths as well), identical or complementary to a polynucleotide sequence disclosed herein, are particularly contemplated as hybridization probes for use in, *e.g.*, Southern and Northern blotting. This would allow a gene product, or fragment thereof, to be analyzed, both in diverse cell types and also in various bacterial cells. The total size of fragment, as well as the size of the complementary stretch(es), will ultimately depend on the intended use or application of the particular nucleic acid segment. Smaller fragments will generally find use in hybridization embodiments, wherein the length of the contiguous complementary region may be varied, such as between about 15 and about 100 nucleotides, but larger contiguous complementarity stretches may be used, according to the length complementary sequences one wishes to detect.

The use of a hybridization probe of about 15-25 nucleotides in length allows the formation of a duplex molecule that is both stable and selective. Molecules having contiguous complementary sequences over stretches greater than 15 bases in length are generally preferred, though, in order to increase stability and selectivity of the hybrid, and thereby improve the quality and degree of specific hybrid molecules obtained. One will generally prefer to design nucleic acid molecules having gene-complementary stretches of 15 to 25 contiguous nucleotides, or even longer where desired.

Hybridization probes may be selected from any portion of any of the sequences disclosed herein. All that is required is to review the sequences set forth herein, or to any continuous portion of the sequences, from about 15-25 nucleotides in length up to and including the full length sequence, that one wishes to utilize as a probe or primer. The choice of probe and primer sequences may be governed by various

factors. For example, one may wish to employ primers from towards the termini of the total sequence.

Small polynucleotide segments or fragments may be readily prepared by, for example, directly synthesizing the fragment by chemical means, as is commonly practiced using an automated oligonucleotide synthesizer. Also, fragments may be obtained by application of nucleic acid reproduction technology, such as the PCR™ technology of U. S. Patent 4,683,202 (incorporated herein by reference), by introducing selected sequences into recombinant vectors for recombinant production, and by other recombinant DNA techniques generally known to those of skill in the art of molecular biology.

The nucleotide sequences of the invention may be used for their ability to selectively form duplex molecules with complementary stretches of the entire gene or gene fragments of interest. Depending on the application envisioned, one will typically desire to employ varying conditions of hybridization to achieve varying degrees of selectivity of probe towards target sequence. For applications requiring high selectivity, one will typically desire to employ relatively stringent conditions to form the hybrids, *e.g.*, one will select relatively low salt and/or high temperature conditions, such as provided by a salt concentration of from about 0.02 M to about 0.15 M salt at temperatures of from about 50°C to about 70°C. Such selective conditions tolerate little, if any, mismatch between the probe and the template or target strand, and would be particularly suitable for isolating related sequences.

Of course, for some applications, for example, where one desires to prepare mutants employing a mutant primer strand hybridized to an underlying template, less stringent (reduced stringency) hybridization conditions will typically be needed in order to allow formation of the heteroduplex. In these circumstances, one may desire to employ salt conditions such as those of from about 0.15 M to about 0.9 M salt, at temperatures ranging from about 20°C to about 55°C. Cross-hybridizing species can thereby be readily identified as positively hybridizing signals with respect to control hybridizations. In any case, it is generally appreciated that conditions can be rendered more stringent by the addition of increasing amounts of formamide, which serves to

destabilize the hybrid duplex in the same manner as increased temperature. Thus, hybridization conditions can be readily manipulated, and thus will generally be a method of choice depending on the desired results.

According to another embodiment of the present invention, polynucleotide compositions comprising antisense oligonucleotides are provided. Antisense oligonucleotides have been demonstrated to be effective and targeted inhibitors of protein synthesis, and, consequently, provide a therapeutic approach by which a disease can be treated by inhibiting the synthesis of proteins that contribute to the disease. The efficacy of antisense oligonucleotides for inhibiting protein synthesis is well established. For example, the synthesis of polygalactauronase and the muscarine type 2 acetylcholine receptor are inhibited by antisense oligonucleotides directed to their respective mRNA sequences (U. S. Patent 5,739,119 and U. S. Patent 5,759,829). Further, examples of antisense inhibition have been demonstrated with the nuclear protein cyclin, the multiple drug resistance gene (MDG1), ICAM-1, E-selectin, STK-1, striatal $GABA_A$ receptor and human EGF (Jaskulski *et al.*, Science. 1988 Jun 10;240(4858):1544-6; Vasanthakumar and Ahmed, Cancer Commun. 1989;1(4):225-32; Peris *et al.*, Brain Res Mol Brain Res. 1998 Jun 15;57(2):310-20; U. S. Patent 5,801,154; U.S. Patent 5,789,573; U. S. Patent 5,718,709 and U.S. Patent 5,610,288). Antisense constructs have also been described that inhibit and can be used to treat a variety of abnormal cellular proliferations, *e.g.* cancer (U. S. Patent 5,747,470; U. S. Patent 5,591,317 and U. S. Patent 5,783,683).

Therefore, in certain embodiments, the present invention provides oligonucleotide sequences that comprise all, or a portion of, any sequence that is capable of specifically binding to polynucleotide sequence described herein, or a complement thereof. In one embodiment, the antisense oligonucleotides comprise DNA or derivatives thereof. In another embodiment, the oligonucleotides comprise RNA or derivatives thereof. In a third embodiment, the oligonucleotides are modified DNAs comprising a phosphorothioated modified backbone. In a fourth embodiment, the oligonucleotide sequences comprise peptide nucleic acids or derivatives thereof. In each case, preferred compositions comprise a sequence region that is complementary,

and more preferably substantially-complementary, and even more preferably, completely complementary to one or more portions of polynucleotides disclosed herein. Selection of antisense compositions specific for a given gene sequence is based upon analysis of the chosen target sequence and determination of secondary structure, T_m, binding energy, and relative stability. Antisense compositions may be selected based upon their relative inability to form dimers, hairpins, or other secondary structures that would reduce or prohibit specific binding to the target mRNA in a host cell. Highly preferred target regions of the mRNA, are those which are at or near the AUG translation initiation codon, and those sequences which are substantially complementary to 5' regions of the mRNA. These secondary structure analyses and target site selection considerations can be performed, for example, using v.4 of the OLIGO primer analysis software and/or the BLASTN 2.0.5 algorithm software (Altschul *et al.,* Nucleic Acids Res. 1997 Sep 1;25(17):3389-402).

The use of an antisense delivery method employing a short peptide vector, termed MPG (27 residues), is also contemplated. The MPG peptide contains a hydrophobic domain derived from the fusion sequence of HIV gp41 and a hydrophilic domain from the nuclear localization sequence of SV40 T-antigen (Morris *et al.*, Nucleic Acids Res. 1997 Jul 15;25(14):2730-6). It has been demonstrated that several molecules of the MPG peptide coat the antisense oligonucleotides and can be delivered into cultured mammalian cells in less than 1 hour with relatively high efficiency (90%). Further, the interaction with MPG strongly increases both the stability of the oligonucleotide to nuclease and the ability to cross the plasma membrane.

According to another embodiment of the invention, the polynucleotide compositions described herein are used in the design and preparation of ribozyme molecules for inhibiting expression of the tumor polypeptides and proteins of the present invention in tumor cells. Ribozymes are RNA-protein complexes that cleave nucleic acids in a site-specific fashion. Ribozymes have specific catalytic domains that possess endonuclease activity (Kim and Cech, Proc Natl Acad Sci U S A. 1987 Dec;84(24):8788-92; Forster and Symons, Cell. 1987 Apr 24;49(2):211-20). For example, a large number of ribozymes accelerate phosphoester transfer reactions with a

high degree of specificity, often cleaving only one of several phosphoesters in an oligonucleotide substrate (Cech *et al.*, Cell. 1981 Dec;27(3 Pt 2):487-96; Michel and Westhof, J Mol Biol. 1990 Dec 5;216(3):585-610; Reinhold-Hurek and Shub, Nature. 1992 May 14;357(6374):173-6). This specificity has been attributed to the requirement that the substrate bind via specific base-pairing interactions to the internal guide sequence ("IGS") of the ribozyme prior to chemical reaction.

Six basic varieties of naturally-occurring enzymatic RNAs are known presently. Each can catalyze the hydrolysis of RNA phosphodiester bonds *in trans* (and thus can cleave other RNA molecules) under physiological conditions. In general, enzymatic nucleic acids act by first binding to a target RNA. Such binding occurs through the target binding portion of a enzymatic nucleic acid which is held in close proximity to an enzymatic portion of the molecule that acts to cleave the target RNA. Thus, the enzymatic nucleic acid first recognizes and then binds a target RNA through complementary base-pairing, and once bound to the correct site, acts enzymatically to cut the target RNA. Strategic cleavage of such a target RNA will destroy its ability to direct synthesis of an encoded protein. After an enzymatic nucleic acid has bound and cleaved its RNA target, it is released from that RNA to search for another target and can repeatedly bind and cleave new targets.

The enzymatic nature of a ribozyme is advantageous over many technologies, such as antisense technology (where a nucleic acid molecule simply binds to a nucleic acid target to block its translation) since the concentration of ribozyme necessary to affect a therapeutic treatment is lower than that of an antisense oligonucleotide. This advantage reflects the ability of the ribozyme to act enzymatically. Thus, a single ribozyme molecule is able to cleave many molecules of target RNA. In addition, the ribozyme is a highly specific inhibitor, with the specificity of inhibition depending not only on the base pairing mechanism of binding to the target RNA, but also on the mechanism of target RNA cleavage. Single mismatches, or base-substitutions, near the site of cleavage can completely eliminate catalytic activity of a ribozyme. Similar mismatches in antisense molecules do not prevent their action (Woolf *et al.*, Proc Natl Acad Sci U S A. 1992 Aug 15;89(16):7305-9). Thus, the

specificity of action of a ribozyme is greater than that of an antisense oligonucleotide binding the same RNA site.

The enzymatic nucleic acid molecule may be formed in a hammerhead, hairpin, a hepatitis δ virus, group I intron or RNaseP RNA (in association with an RNA guide sequence) or Neurospora VS RNA motif. Examples of hammerhead motifs are described by Rossi *et al.* Nucleic Acids Res. 1992 Sep 11;20(17):4559-65. Examples of hairpin motifs are described by Hampel *et al.* (Eur. Pat. Appl. Publ. No. EP 0360257), Hampel and Tritz, Biochemistry 1989 Jun 13;28(12):4929-33; Hampel *et al.,* Nucleic Acids Res. 1990 Jan 25;18(2):299-304 and U. S. Patent 5,631,359. An example of the hepatitis δ virus motif is described by Perrotta and Been, Biochemistry. 1992 Dec 1;31(47):11843-52; an example of the RNaseP motif is described by Guerrier-Takada *et al.,* Cell. 1983 Dec;35(3 Pt 2):849-57; Neurospora VS RNA ribozyme motif is described by Collins (Saville and Collins, Cell. 1990 May 18;61(4):685-96; Saville and Collins, Proc Natl Acad Sci U S A. 1991 Oct 1;88(19):8826-30; Collins and Olive, Biochemistry. 1993 Mar 23;32(11):2795-9); and an example of the Group I intron is described in (U. S. Patent 4,987,071). All that is important in an enzymatic nucleic acid molecule of this invention is that it has a specific substrate binding site which is complementary to one or more of the target gene RNA regions, and that it have nucleotide sequences within or surrounding that substrate binding site which impart an RNA cleaving activity to the molecule. Thus the ribozyme constructs need not be limited to specific motifs mentioned herein.

Ribozymes may be designed as described in Int. Pat. Appl. Publ. No. WO 93/23569 and Int. Pat. Appl. Publ. No. WO 94/02595, each specifically incorporated herein by reference) and synthesized to be tested *in vitro* and *in vivo,* as described. Such ribozymes can also be optimized for delivery. While specific examples are provided, those in the art will recognize that equivalent RNA targets in other species can be utilized when necessary.

Ribozyme activity can be optimized by altering the length of the ribozyme binding arms, or chemically synthesizing ribozymes with modifications that prevent their degradation by serum ribonucleases (see *e.g.*, Int. Pat. Appl. Publ. No. WO

92/07065; Int. Pat. Appl. Publ. No. WO 93/15187; Int. Pat. Appl. Publ. No. WO 91/03162; Eur. Pat. Appl. Publ. No. 92110298.4; U. S. Patent 5,334,711; and Int. Pat. Appl. Publ. No. WO 94/13688, which describe various chemical modifications that can be made to the sugar moieties of enzymatic RNA molecules), modifications which enhance their efficacy in cells, and removal of stem II bases to shorten RNA synthesis times and reduce chemical requirements.

Sullivan *et al.* (Int. Pat. Appl. Publ. No. WO 94/02595) describes the general methods for delivery of enzymatic RNA molecules. Ribozymes may be administered to cells by a variety of methods known to those familiar to the art, including, but not restricted to, encapsulation in liposomes, by iontophoresis, or by incorporation into other vehicles, such as hydrogels, cyclodextrins, biodegradable nanocapsules, and bioadhesive microspheres. For some indications, ribozymes may be directly delivered *ex vivo* to cells or tissues with or without the aforementioned vehicles. Alternatively, the RNA/vehicle combination may be locally delivered by direct inhalation, by direct injection or by use of a catheter, infusion pump or stent. Other routes of delivery include, but are not limited to, intravascular, intramuscular, subcutaneous or joint injection, aerosol inhalation, oral (tablet or pill form), topical, systemic, ocular, intraperitoneal and/or intrathecal delivery. More detailed descriptions of ribozyme delivery and administration are provided in Int. Pat. Appl. Publ. No. WO 94/02595 and Int. Pat. Appl. Publ. No. WO 93/23569, each specifically incorporated herein by reference.

Another means of accumulating high concentrations of a ribozyme(s) within cells is to incorporate the ribozyme-encoding sequences into a DNA expression vector. Transcription of the ribozyme sequences are driven from a promoter for eukaryotic RNA polymerase I (pol I), RNA polymerase II (pol II), or RNA polymerase III (pol III). Transcripts from pol II or pol III promoters will be expressed at high levels in all cells; the levels of a given pol II promoter in a given cell type will depend on the nature of the gene regulatory sequences (enhancers, silencers, *etc.*) present nearby. Prokaryotic RNA polymerase promoters may also be used, providing that the prokaryotic RNA polymerase enzyme is expressed in the appropriate cells Ribozymes

expressed from such promoters have been shown to function in mammalian cells. Such transcription units can be incorporated into a variety of vectors for introduction into mammalian cells, including but not restricted to, plasmid DNA vectors, viral DNA vectors (such as adenovirus or adeno-associated vectors), or viral RNA vectors (such as retroviral, semliki forest virus, sindbis virus vectors).

In another embodiment of the invention, peptide nucleic acids (PNAs) compositions are provided. PNA is a DNA mimic in which the nucleobases are attached to a pseudopeptide backbone (Good and Nielsen, Antisense Nucleic Acid Drug Dev. 1997 7(4) 431-37). PNA is able to be utilized in a number methods that traditionally have used RNA or DNA. Often PNA sequences perform better in techniques than the corresponding RNA or DNA sequences and have utilities that are not inherent to RNA or DNA. A review of PNA including methods of making, characteristics of, and methods of using, is provided by Corey (*Trends Biotechnol* 1997 Jun;15(6):224-9). As such, in certain embodiments, one may prepare PNA sequences that are complementary to one or more portions of the ACE mRNA sequence, and such PNA compositions may be used to regulate, alter, decrease, or reduce the translation of ACE-specific mRNA, and thereby alter the level of ACE activity in a host cell to which such PNA compositions have been administered.

PNAs have 2-aminoethyl-glycine linkages replacing the normal phosphodiester backbone of DNA (Nielsen *et al.*, *Science* 1991 Dec 6;254(5037):1497-500; Hanvey *et al.*, Science. 1992 Nov 27;258(5087):1481-5; Hyrup and Nielsen, Bioorg Med Chem. 1996 Jan;4(1):5-23). This chemistry has three important consequences: firstly, in contrast to DNA or phosphorothioate oligonucleotides, PNAs are neutral molecules; secondly, PNAs are achiral, which avoids the need to develop a stereoselective synthesis; and thirdly, PNA synthesis uses standard Boc or Fmoc protocols for solid-phase peptide synthesis, although other methods, including a modified Merrifield method, have been used.

PNA monomers or ready-made oligomers are commercially available from PerSeptive Biosystems (Framingham, MA). PNA syntheses by either Boc or Fmoc protocols are straightforward using manual or automated protocols (Norton *et al.*,

Bioorg Med Chem. 1995 Apr;3(4):437-45). The manual protocol lends itself to the production of chemically modified PNAs or the simultaneous synthesis of families of closely related PNAs.

As with peptide synthesis, the success of a particular PNA synthesis will depend on the properties of the chosen sequence. For example, while in theory PNAs can incorporate any combination of nucleotide bases, the presence of adjacent purines can lead to deletions of one or more residues in the product. In expectation of this difficulty, it is suggested that, in producing PNAs with adjacent purines, one should repeat the coupling of residues likely to be added inefficiently. This should be followed by the purification of PNAs by reverse-phase high-pressure liquid chromatography, providing yields and purity of product similar to those observed during the synthesis of peptides.

Modifications of PNAs for a given application may be accomplished by coupling amino acids during solid-phase synthesis or by attaching compounds that contain a carboxylic acid group to the exposed N-terminal amine. Alternatively, PNAs can be modified after synthesis by coupling to an introduced lysine or cysteine. The ease with which PNAs can be modified facilitates optimization for better solubility or for specific functional requirements. Once synthesized, the identity of PNAs and their derivatives can be confirmed by mass spectrometry. Several studies have made and utilized modifications of PNAs (for example, Norton *et al.*, Bioorg Med Chem. 1995 Apr;3(4):437-45; Petersen *et al.*, J Pept Sci. 1995 May-Jun;1(3):175-83; Orum *et al.*, Biotechniques. 1995 Sep;19(3):472-80; Footer *et al.*, Biochemistry. 1996 Aug 20;35(33):10673-9; Griffith *et al.*, Nucleic Acids Res. 1995 Aug 11;23(15):3003-8; Pardridge *et al.*, Proc Natl Acad Sci U S A. 1995 Jun 6;92(12):5592-6; Boffa *et al.*, Proc Natl Acad Sci U S A. 1995 Mar 14;92(6):1901-5; Gambacorti-Passerini *et al.*, Blood. 1996 Aug 15;88(4):1411-7; Armitage *et al.*, Proc Natl Acad Sci U S A. 1997 Nov 11;94(23):12320-5; Seeger *et al.*, Biotechniques. 1997 Sep;23(3):512-7). U.S. Patent No. 5,700,922 discusses PNA-DNA-PNA chimeric molecules and their uses in diagnostics, modulating protein in organisms, and treatment of conditions susceptible to therapeutics.

Methods of characterizing the antisense binding properties of PNAs are discussed in Rose (Anal Chem. 1993 Dec 15;65(24):3545-9) and Jensen *et al.* (Biochemistry. 1997 Apr 22;36(16):5072-7). Rose uses capillary gel electrophoresis to determine binding of PNAs to their complementary oligonucleotide, measuring the relative binding kinetics and stoichiometry. Similar types of measurements were made by Jensen *et al.* using BIAcore™ technology.

Other applications of PNAs that have been described and will be apparent to the skilled artisan include use in DNA strand invasion, antisense inhibition, mutational analysis, enhancers of transcription, nucleic acid purification, isolation of transcriptionally active genes, blocking of transcription factor binding, genome cleavage, biosensors, *in situ* hybridization, and the like.

Polynucleotide Identification, Characterization and Expression

Polynucleotide compositions of the present invention may be identified, prepared and/or manipulated using any of a variety of well established techniques (see generally, Sambrook et al., *Molecular Cloning: A Laboratory Manual,* Cold Spring Harbor Laboratories, Cold Spring Harbor, NY, 1989, and other like references). For example, a polynucleotide may be identified, as described in more detail below, by screening a microarray of cDNAs for tumor-associated expression (*i.e.,* expression that is at least two fold greater in a tumor than in normal tissue, as determined using a representative assay provided herein). Such screens may be performed, for example, using the microarray technology of Affymetrix, Inc. (Santa Clara, CA) according to the manufacturer's instructions (and essentially as described by Schena et al., *Proc. Natl. Acad. Sci. USA 93*:10614-10619, 1996 and Heller et al., *Proc. Natl. Acad. Sci. USA 94*:2150-2155, 1997). Alternatively, polynucleotides may be amplified from cDNA prepared from cells expressing the proteins described herein, such as tumor cells.

Many template dependent processes are available to amplify a target sequences of interest present in a sample. One of the best known amplification methods is the polymerase chain reaction (PCR™) which is described in detail in U.S. Patent Nos. 4,683,195, 4,683,202 and 4,800,159, each of which is incorporated herein by

reference in its entirety. Briefly, in PCR™, two primer sequences are prepared which are complementary to regions on opposite complementary strands of the target sequence. An excess of deoxynucleoside triphosphates is added to a reaction mixture along with a DNA polymerase (*e.g.*, *Taq* polymerase). If the target sequence is present in a sample, the primers will bind to the target and the polymerase will cause the primers to be extended along the target sequence by adding on nucleotides. By raising and lowering the temperature of the reaction mixture, the extended primers will dissociate from the target to form reaction products, excess primers will bind to the target and to the reaction product and the process is repeated. Preferably reverse transcription and PCR™ amplification procedure may be performed in order to quantify the amount of mRNA amplified. Polymerase chain reaction methodologies are well known in the art.

Any of a number of other template dependent processes, many of which are variations of the PCR ™ amplification technique, are readily known and available in the art. Illustratively, some such methods include the ligase chain reaction (referred to as LCR), described, for example, in Eur. Pat. Appl. Publ. No. 320,308 and U.S. Patent No. 4,883,750; Qbeta Replicase, described in PCT Intl. Pat. Appl. Publ. No. PCT/US87/00880; Strand Displacement Amplification (SDA) and Repair Chain Reaction (RCR). Still other amplification methods are described in Great Britain Pat. Appl. No. 2 202 328, and in PCT Intl. Pat. Appl. Publ. No. PCT/US89/01025. Other nucleic acid amplification procedures include transcription-based amplification systems (TAS) (PCT Intl. Pat. Appl. Publ. No. WO 88/10315), including nucleic acid sequence based amplification (NASBA) and 3SR. Eur. Pat. Appl. Publ. No. 329,822 describes a nucleic acid amplification process involving cyclically synthesizing single-stranded RNA ("ssRNA"), ssDNA, and double-stranded DNA (dsDNA). PCT Intl. Pat. Appl. Publ. No. WO 89/06700 describes a nucleic acid sequence amplification scheme based on the hybridization of a promoter/primer sequence to a target single-stranded DNA ("ssDNA") followed by transcription of many RNA copies of the sequence. Other amplification methods such as "RACE" (Frohman, 1990), and "one-sided PCR" (Ohara, 1989) are also well-known to those of skill in the art.

An amplified portion of a polynucleotide of the present invention may be used to isolate a full length gene from a suitable library (*e.g.*, a tumor cDNA library) using well known techniques. Within such techniques, a library (cDNA or genomic) is screened using one or more polynucleotide probes or primers suitable for amplification. Preferably, a library is size-selected to include larger molecules. Random primed libraries may also be preferred for identifying 5' and upstream regions of genes. Genomic libraries are preferred for obtaining introns and extending 5' sequences.

For hybridization techniques, a partial sequence may be labeled (*e.g.*, by nick-translation or end-labeling with ^{32}P) using well known techniques. A bacterial or bacteriophage library is then generally screened by hybridizing filters containing denatured bacterial colonies (or lawns containing phage plaques) with the labeled probe (*see* Sambrook et al., *Molecular Cloning: A Laboratory Manual,* Cold Spring Harbor Laboratories, Cold Spring Harbor, NY, 1989). Hybridizing colonies or plaques are selected and expanded, and the DNA is isolated for further analysis. cDNA clones may be analyzed to determine the amount of additional sequence by, for example, PCR using a primer from the partial sequence and a primer from the vector. Restriction maps and partial sequences may be generated to identify one or more overlapping clones. The complete sequence may then be determined using standard techniques, which may involve generating a series of deletion clones. The resulting overlapping sequences can then assembled into a single contiguous sequence. A full length cDNA molecule can be generated by ligating suitable fragments, using well known techniques.

Alternatively, amplification techniques, such as those described above, can be useful for obtaining a full length coding sequence from a partial cDNA sequence. One such amplification technique is inverse PCR (*see* Triglia et al., *Nucl. Acids Res. 16*:8186, 1988), which uses restriction enzymes to generate a fragment in the known region of the gene. The fragment is then circularized by intramolecular ligation and used as a template for PCR with divergent primers derived from the known region. Within an alternative approach, sequences adjacent to a partial sequence may be retrieved by amplification with a primer to a linker sequence and a primer specific to a known region. The amplified sequences are typically subjected to a second round of

amplification with the same linker primer and a second primer specific to the known region. A variation on this procedure, which employs two primers that initiate extension in opposite directions from the known sequence, is described in WO 96/38591. Another such technique is known as "rapid amplification of cDNA ends" or RACE. This technique involves the use of an internal primer and an external primer, which hybridizes to a polyA region or vector sequence, to identify sequences that are 5' and 3' of a known sequence. Additional techniques include capture PCR (Lagerstrom et al., *PCR Methods Applic. 1*:111-19, 1991) and walking PCR (Parker et al., *Nucl. Acids. Res. 19*:3055-60, 1991). Other methods employing amplification may also be employed to obtain a full length cDNA sequence.

In certain instances, it is possible to obtain a full length cDNA sequence by analysis of sequences provided in an expressed sequence tag (EST) database, such as that available from GenBank. Searches for overlapping ESTs may generally be performed using well known programs (*e.g.,* NCBI BLAST searches), and such ESTs may be used to generate a contiguous full length sequence. Full length DNA sequences may also be obtained by analysis of genomic fragments.

In other embodiments of the invention, polynucleotide sequences or fragments thereof which encode polypeptides of the invention, or fusion proteins or functional equivalents thereof, may be used in recombinant DNA molecules to direct expression of a polypeptide in appropriate host cells. Due to the inherent degeneracy of the genetic code, other DNA sequences that encode substantially the same or a functionally equivalent amino acid sequence may be produced and these sequences may be used to clone and express a given polypeptide.

As will be understood by those of skill in the art, it may be advantageous in some instances to produce polypeptide-encoding nucleotide sequences possessing non-naturally occurring codons. For example, codons preferred by a particular prokaryotic or eukaryotic host can be selected to increase the rate of protein expression or to produce a recombinant RNA transcript having desirable properties, such as a half-life which is longer than that of a transcript generated from the naturally occurring sequence.

Moreover, the polynucleotide sequences of the present invention can be engineered using methods generally known in the art in order to alter polypeptide encoding sequences for a variety of reasons, including but not limited to, alterations which modify the cloning, processing, and/or expression of the gene product. For example, DNA shuffling by random fragmentation and PCR reassembly of gene fragments and synthetic oligonucleotides may be used to engineer the nucleotide sequences. In addition, site-directed mutagenesis may be used to insert new restriction sites, alter glycosylation patterns, change codon preference, produce splice variants, or introduce mutations, and so forth.

In another embodiment of the invention, natural, modified, or recombinant nucleic acid sequences may be ligated to a heterologous sequence to encode a fusion protein. For example, to screen peptide libraries for inhibitors of polypeptide activity, it may be useful to encode a chimeric protein that can be recognized by a commercially available antibody. A fusion protein may also be engineered to contain a cleavage site located between the polypeptide-encoding sequence and the heterologous protein sequence, so that the polypeptide may be cleaved and purified away from the heterologous moiety.

Sequences encoding a desired polypeptide may be synthesized, in whole or in part, using chemical methods well known in the art (see Caruthers, M. H. et al. (1980) *Nucl. Acids Res. Symp. Ser.* 215-223, Horn, T. et al. (1980) *Nucl. Acids Res. Symp. Ser.* 225-232). Alternatively, the protein itself may be produced using chemical methods to synthesize the amino acid sequence of a polypeptide, or a portion thereof. For example, peptide synthesis can be performed using various solid-phase techniques (Roberge, J. Y. et al. (1995) *Science 269*:202-204) and automated synthesis may be achieved, for example, using the ABI 431A Peptide Synthesizer (Perkin Elmer, Palo Alto, CA).

A newly synthesized peptide may be substantially purified by preparative high performance liquid chromatography (*e.g.*, Creighton, T. (1983) Proteins, Structures and Molecular Principles, WH Freeman and Co., New York, N.Y.) or other comparable techniques available in the art. The composition of the synthetic peptides may be

confirmed by amino acid analysis or sequencing (*e.g.*, the Edman degradation procedure). Additionally, the amino acid sequence of a polypeptide, or any part thereof, may be altered during direct synthesis and/or combined using chemical methods with sequences from other proteins, or any part thereof, to produce a variant polypeptide.

In order to express a desired polypeptide, the nucleotide sequences encoding the polypeptide, or functional equivalents, may be inserted into appropriate expression vector, *i.e.*, a vector which contains the necessary elements for the transcription and translation of the inserted coding sequence. Methods which are well known to those skilled in the art may be used to construct expression vectors containing sequences encoding a polypeptide of interest and appropriate transcriptional and translational control elements. These methods include *in vitro* recombinant DNA techniques, synthetic techniques, and *in vivo* genetic recombination. Such techniques are described, for example, in Sambrook, J. et al. (1989) Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Press, Plainview, N.Y., and Ausubel, F. M. et al. (1989) Current Protocols in Molecular Biology, John Wiley & Sons, New York. N.Y.

A variety of expression vector/host systems may be utilized to contain and express polynucleotide sequences. These include, but are not limited to, microorganisms such as bacteria transformed with recombinant bacteriophage, plasmid, or cosmid DNA expression vectors; yeast transformed with yeast expression vectors; insect cell systems infected with virus expression vectors (*e.g.*, baculovirus); plant cell systems transformed with virus expression vectors (*e.g.*, cauliflower mosaic virus, CaMV; tobacco mosaic virus, TMV) or with bacterial expression vectors (*e.g.*, Ti or pBR322 plasmids); or animal cell systems.

The "control elements" or "regulatory sequences" present in an expression vector are those non-translated regions of the vector--enhancers, promoters, 5' and 3' untranslated regions--which interact with host cellular proteins to carry out transcription and translation. Such elements may vary in their strength and specificity. Depending on the vector system and host utilized, any number of suitable transcription and translation elements, including constitutive and inducible promoters, may be used.

For example, when cloning in bacterial systems, inducible promoters such as the hybrid lacZ promoter of the PBLUESCRIPT phagemid (Stratagene, La Jolla, Calif.) or PSPORT1 plasmid (Gibco BRL, Gaithersburg, MD) and the like may be used. In mammalian cell systems, promoters from mammalian genes or from mammalian viruses are generally preferred. If it is necessary to generate a cell line that contains multiple copies of the sequence encoding a polypeptide, vectors based on SV40 or EBV may be advantageously used with an appropriate selectable marker.

In bacterial systems, any of a number of expression vectors may be selected depending upon the use intended for the expressed polypeptide. For example, when large quantities are needed, for example for the induction of antibodies, vectors which direct high level expression of fusion proteins that are readily purified may be used. Such vectors include, but are not limited to, the multifunctional *E. coli* cloning and expression vectors such as BLUESCRIPT (Stratagene), in which the sequence encoding the polypeptide of interest may be ligated into the vector in frame with sequences for the amino-terminal Met and the subsequent 7 residues of .beta.-galactosidase so that a hybrid protein is produced; pIN vectors (Van Heeke, G. and S. M. Schuster (1989) *J. Biol. Chem. 264*:5503-5509); and the like. pGEX Vectors (Promega, Madison, Wis.) may also be used to express foreign polypeptides as fusion proteins with glutathione S-transferase (GST). In general, such fusion proteins are soluble and can easily be purified from lysed cells by adsorption to glutathione-agarose beads followed by elution in the presence of free glutathione. Proteins made in such systems may be designed to include heparin, thrombin, or factor XA protease cleavage sites so that the cloned polypeptide of interest can be released from the GST moiety at will.

In the yeast, Saccharomyces cerevisiae, a number of vectors containing constitutive or inducible promoters such as alpha factor, alcohol oxidase, and PGH may be used. For reviews, see Ausubel et al. (supra) and Grant et al. (1987) *Methods Enzymol.* 153:516-544.

In cases where plant expression vectors are used, the expression of sequences encoding polypeptides may be driven by any of a number of promoters. For

example, viral promoters such as the 35S and 19S promoters of CaMV may be used alone or in combination with the omega leader sequence from TMV (Takamatsu, N. (1987) *EMBO J. 6*:307-311. Alternatively, plant promoters such as the small subunit of RUBISCO or heat shock promoters may be used (Coruzzi, G. et al. (1984) *EMBO J. 3*:1671-1680; Broglie, R. et al. (1984) *Science 224*:838-843; and Winter, J. et al. (1991) *Results Probl. Cell Differ. 17*:85-105). These constructs can be introduced into plant cells by direct DNA transformation or pathogen-mediated transfection. Such techniques are described in a number of generally available reviews (see, for example, Hobbs, S. or Murry, L. E. in McGraw Hill Yearbook of Science and Technology (1992) McGraw Hill, New York, N.Y.; pp. 191-196).

An insect system may also be used to express a polypeptide of interest. For example, in one such system, Autographa californica nuclear polyhedrosis virus (AcNPV) is used as a vector to express foreign genes in Spodoptera frugiperda cells or in Trichoplusia larvae. The sequences encoding the polypeptide may be cloned into a non-essential region of the virus, such as the polyhedrin gene, and placed under control of the polyhedrin promoter. Successful insertion of the polypeptide-encoding sequence will render the polyhedrin gene inactive and produce recombinant virus lacking coat protein. The recombinant viruses may then be used to infect, for example, S. frugiperda cells or Trichoplusia larvae in which the polypeptide of interest may be expressed (Engelhard, E. K. et al. (1994) *Proc. Natl. Acad. Sci. 91* :3224-3227).

In mammalian host cells, a number of viral-based expression systems are generally available. For example, in cases where an adenovirus is used as an expression vector, sequences encoding a polypeptide of interest may be ligated into an adenovirus transcription/translation complex consisting of the late promoter and tripartite leader sequence. Insertion in a non-essential E1 or E3 region of the viral genome may be used to obtain a viable virus which is capable of expressing the polypeptide in infected host cells (Logan, J. and Shenk, T. (1984) *Proc. Natl. Acad. Sci. 81*:3655-3659). In addition, transcription enhancers, such as the Rous sarcoma virus (RSV) enhancer, may be used to increase expression in mammalian host cells.

Specific initiation signals may also be used to achieve more efficient translation of sequences encoding a polypeptide of interest. Such signals include the ATG initiation codon and adjacent sequences. In cases where sequences encoding the polypeptide, its initiation codon, and upstream sequences are inserted into the appropriate expression vector, no additional transcriptional or translational control signals may be needed. However, in cases where only coding sequence, or a portion thereof, is inserted, exogenous translational control signals including the ATG initiation codon should be provided. Furthermore, the initiation codon should be in the correct reading frame to ensure translation of the entire insert. Exogenous translational elements and initiation codons may be of various origins, both natural and synthetic. The efficiency of expression may be enhanced by the inclusion of enhancers which are appropriate for the particular cell system which is used, such as those described in the literature (Scharf, D. et al. (1994) *Results Probl. Cell Differ. 20*:125-162).

In addition, a host cell strain may be chosen for its ability to modulate the expression of the inserted sequences or to process the expressed protein in the desired fashion. Such modifications of the polypeptide include, but are not limited to, acetylation, carboxylation. glycosylation, phosphorylation, lipidation, and acylation. Post-translational processing which cleaves a "prepro" form of the protein may also be used to facilitate correct insertion, folding and/or function. Different host cells such as CHO, COS, HeLa, MDCK, HEK293, and WI38, which have specific cellular machinery and characteristic mechanisms for such post-translational activities, may be chosen to ensure the correct modification and processing of the foreign protein.

For long-term, high-yield production of recombinant proteins, stable expression is generally preferred. For example, cell lines which stably express a polynucleotide of interest may be transformed using expression vectors which may contain viral origins of replication and/or endogenous expression elements and a selectable marker gene on the same or on a separate vector. Following the introduction of the vector, cells may be allowed to grow for 1-2 days in an enriched media before they are switched to selective media. The purpose of the selectable marker is to confer resistance to selection, and its presence allows growth and recovery of cells which

successfully express the introduced sequences. Resistant clones of stably transformed cells may be proliferated using tissue culture techniques appropriate to the cell type.

Any number of selection systems may be used to recover transformed cell lines. These include, but are not limited to, the herpes simplex virus thymidine kinase (Wigler, M. et al. (1977) *Cell 11*:223-32) and adenine phosphoribosyltransferase (Lowy, I. et al. (1990) *Cell 22*:817-23) genes which can be employed in tk.sup.- or aprt.sup.- cells, respectively. Also, antimetabolite, antibiotic or herbicide resistance can be used as the basis for selection; for example, dhfr which confers resistance to methotrexate (Wigler, M. et al. (1980) *Proc. Natl. Acad. Sci. 77*:3567-70); npt, which confers resistance to the aminoglycosides, neomycin and G-418 (Colbere-Garapin, F. et al (1981) *J. Mol. Biol. 150*:1-14); and als or pat, which confer resistance to chlorsulfuron and phosphinotricin acetyltransferase, respectively (Murry, *supra*). Additional selectable genes have been described, for example, trpB, which allows cells to utilize indole in place of tryptophan, or hisD, which allows cells to utilize histinol in place of histidine (Hartman, S. C. and R. C. Mulligan (1988) *Proc. Natl. Acad. Sci. 85*:8047-51). The use of visible markers has gained popularity with such markers as anthocyanins, beta-glucuronidase and its substrate GUS, and luciferase and its substrate luciferin, being widely used not only to identify transformants, but also to quantify the amount of transient or stable protein expression attributable to a specific vector system (Rhodes, C. A. et al. (1995) *Methods Mol. Biol. 55*:121-131).

Although the presence/absence of marker gene expression suggests that the gene of interest is also present, its presence and expression may need to be confirmed. For example, if the sequence encoding a polypeptide is inserted within a marker gene sequence, recombinant cells containing sequences can be identified by the absence of marker gene function. Alternatively, a marker gene can be placed in tandem with a polypeptide-encoding sequence under the control of a single promoter. Expression of the marker gene in response to induction or selection usually indicates expression of the tandem gene as well.

Alternatively, host cells that contain and express a desired polynucleotide sequence may be identified by a variety of procedures known to those of

skill in the art. These procedures include, but are not limited to, DNA-DNA or DNA-RNA hybridizations and protein bioassay or immunoassay techniques which include, for example, membrane, solution, or chip based technologies for the detection and/or quantification of nucleic acid or protein.

A variety of protocols for detecting and measuring the expression of polynucleotide-encoded products, using either polyclonal or monoclonal antibodies specific for the product are known in the art. Examples include enzyme-linked immunosorbent assay (ELISA), radioimmunoassay (RIA), and fluorescence activated cell sorting (FACS). A two-site, monoclonal-based immunoassay utilizing monoclonal antibodies reactive to two non-interfering epitopes on a given polypeptide may be preferred for some applications, but a competitive binding assay may also be employed. These and other assays are described, among other places, in Hampton, R. et al. (1990; Serological Methods, a Laboratory Manual, APS Press, St Paul. Minn.) and Maddox, D. E. et al. (1983; *J. Exp. Med. 158*:1211-1216).

A wide variety of labels and conjugation techniques are known by those skilled in the art and may be used in various nucleic acid and amino acid assays. Means for producing labeled hybridization or PCR probes for detecting sequences related to polynucleotides include oligolabeling, nick translation, end-labeling or PCR amplification using a labeled nucleotide. Alternatively, the sequences, or any portions thereof may be cloned into a vector for the production of an mRNA probe. Such vectors are known in the art, are commercially available, and may be used to synthesize RNA probes in vitro by addition of an appropriate RNA polymerase such as T7, T3, or SP6 and labeled nucleotides. These procedures may be conducted using a variety of commercially available kits. Suitable reporter molecules or labels, which may be used include radionuclides, enzymes, fluorescent, chemiluminescent, or chromogenic agents as well as substrates, cofactors, inhibitors, magnetic particles, and the like.

Host cells transformed with a polynucleotide sequence of interest may be cultured under conditions suitable for the expression and recovery of the protein from cell culture. The protein produced by a recombinant cell may be secreted or contained intracellularly depending on the sequence and/or the vector used. As will be understood

by those of skill in the art, expression vectors containing polynucleotides of the invention may be designed to contain signal sequences which direct secretion of the encoded polypeptide through a prokaryotic or eukaryotic cell membrane. Other recombinant constructions may be used to join sequences encoding a polypeptide of interest to nucleotide sequence encoding a polypeptide domain which will facilitate purification of soluble proteins. Such purification facilitating domains include, but are not limited to, metal chelating peptides such as histidine-tryptophan modules that allow purification on immobilized metals, protein A domains that allow purification on immobilized immunoglobulin, and the domain utilized in the FLAGS extension/affinity purification system (Immunex Corp., Seattle, Wash.). The inclusion of cleavable linker sequences such as those specific for Factor XA or enterokinase (Invitrogen. San Diego, Calif.) between the purification domain and the encoded polypeptide may be used to facilitate purification. One such expression vector provides for expression of a fusion protein containing a polypeptide of interest and a nucleic acid encoding 6 histidine residues preceding a thioredoxin or an enterokinase cleavage site. The histidine residues facilitate purification on IMIAC (immobilized metal ion affinity chromatography) as described in Porath, J. et al. (1992, *Prot. Exp. Purif. 3*:263-281) while the enterokinase cleavage site provides a means for purifying the desired polypeptide from the fusion protein. A discussion of vectors which contain fusion proteins is provided in Kroll, D. J. et al. (1993; *DNA Cell Biol. 12*:441-453).

In addition to recombinant production methods, polypeptides of the invention, and fragments thereof, may be produced by direct peptide synthesis using solid-phase techniques (Merrifield J. (1963) *J. Am. Chem. Soc. 85*:2149-2154). Protein synthesis may be performed using manual techniques or by automation. Automated synthesis may be achieved, for example, using Applied Biosystems 431A Peptide Synthesizer (Perkin Elmer). Alternatively, various fragments may be chemically synthesized separately and combined using chemical methods to produce the full length molecule.

Antibody Compositions, Fragments Thereof and Other Binding Agents

According to another aspect, the present invention further provides binding agents, such as antibodies and antigen-binding fragments thereof, that exhibit immunological binding to a tumor polypeptide disclosed herein, or to a portion, variant or derivative thereof. An antibody, or antigen-binding fragment thereof, is said to "specifically bind," "immunogically bind," and/or is "immunologically reactive" to a polypeptide of the invention if it reacts at a detectable level (within, for example, an ELISA assay) with the polypeptide, and does not react detectably with unrelated polypeptides under similar conditions.

Immunological binding, as used in this context, generally refers to the non-covalent interactions of the type which occur between an immunoglobulin molecule and an antigen for which the immunoglobulin is specific. The strength, or affinity of immunological binding interactions can be expressed in terms of the dissociation constant (K_d) of the interaction, wherein a smaller K_d represents a greater affinity. Immunological binding properties of selected polypeptides can be quantified using methods well known in the art. One such method entails measuring the rates of antigen-binding site/antigen complex formation and dissociation, wherein those rates depend on the concentrations of the complex partners, the affinity of the interaction, and on geometric parameters that equally influence the rate in both directions. Thus, both the "on rate constant" (K_{on}) and the "off rate constant" (K_{off}) can be determined by calculation of the concentrations and the actual rates of association and dissociation. The ratio of K_{off}/K_{on} enables cancellation of all parameters not related to affinity, and is thus equal to the dissociation constant K_d. See, generally, Davies et al. (1990) Annual Rev. Biochem. 59:439-473.

An "antigen-binding site," or "binding portion" of an antibody refers to the part of the immunoglobulin molecule that participates in antigen binding. The antigen binding site is formed by amino acid residues of the N-terminal variable ("V") regions of the heavy ("H") and light ("L") chains. Three highly divergent stretches within the V regions of the heavy and light chains are referred to as "hypervariable regions" which are interposed between more conserved flanking stretches known as

"framework regions," or "FRs". Thus the term "FR" refers to amino acid sequences which are naturally found between and adjacent to hypervariable regions in immunoglobulins. In an antibody molecule, the three hypervariable regions of a light chain and the three hypervariable regions of a heavy chain are disposed relative to each other in three dimensional space to form an antigen-binding surface. The antigen-binding surface is complementary to the three-dimensional surface of a bound antigen, and the three hypervariable regions of each of the heavy and light chains are referred to as "complementarity-determining regions," or "CDRs."

Binding agents may be further capable of differentiating between patients with and without a cancer, such as prostate cancer, using the representative assays provided herein. For example, antibodies or other binding agents that bind to a tumor protein will preferably generate a signal indicating the presence of a cancer in at least about 20% of patients with the disease, more preferably at least about 30% of patients. Alternatively, or in addition, the antibody will generate a negative signal indicating the absence of the disease in at least about 90% of individuals without the cancer. To determine whether a binding agent satisfies this requirement, biological samples (*e.g.*, blood, sera, sputum, urine and/or tumor biopsies) from patients with and without a cancer (as determined using standard clinical tests) may be assayed as described herein for the presence of polypeptides that bind to the binding agent. Preferably, a statistically significant number of samples with and without the disease will be assayed. Each binding agent should satisfy the above criteria; however, those of ordinary skill in the art will recognize that binding agents may be used in combination to improve sensitivity.

Any agent that satisfies the above requirements may be a binding agent. For example, a binding agent may be a ribosome, with or without a peptide component, an RNA molecule or a polypeptide. In a preferred embodiment, a binding agent is an antibody or an antigen-binding fragment thereof. Antibodies may be prepared by any of a variety of techniques known to those of ordinary skill in the art. *See, e.g.,* Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In general, antibodies can be produced by cell culture techniques, including the generation

of monoclonal antibodies as described herein, or via transfection of antibody genes into suitable bacterial or mammalian cell hosts, in order to allow for the production of recombinant antibodies. In one technique, an immunogen comprising the polypeptide is initially injected into any of a wide variety of mammals (*e.g.*, mice, rats, rabbits, sheep or goats). In this step, the polypeptides of this invention may serve as the immunogen without modification. Alternatively, particularly for relatively short polypeptides, a superior immune response may be elicited if the polypeptide is joined to a carrier protein, such as bovine serum albumin or keyhole limpet hemocyanin. The immunogen is injected into the animal host, preferably according to a predetermined schedule incorporating one or more booster immunizations, and the animals are bled periodically. Polyclonal antibodies specific for the polypeptide may then be purified from such antisera by, for example, affinity chromatography using the polypeptide coupled to a suitable solid support.

Monoclonal antibodies specific for an antigenic polypeptide of interest may be prepared, for example, using the technique of Kohler and Milstein, *Eur. J. Immunol. 6*:511-519, 1976, and improvements thereto. Briefly, these methods involve the preparation of immortal cell lines capable of producing antibodies having the desired specificity (*i.e.*, reactivity with the polypeptide of interest). Such cell lines may be produced, for example, from spleen cells obtained from an animal immunized as described above. The spleen cells are then immortalized by, for example, fusion with a myeloma cell fusion partner, preferably one that is syngeneic with the immunized animal. A variety of fusion techniques may be employed. For example, the spleen cells and myeloma cells may be combined with a nonionic detergent for a few minutes and then plated at low density on a selective medium that supports the growth of hybrid cells, but not myeloma cells. A preferred selection technique uses HAT (hypoxanthine, aminopterin, thymidine) selection. After a sufficient time, usually about 1 to 2 weeks, colonies of hybrids are observed. Single colonies are selected and their culture supernatants tested for binding activity against the polypeptide. Hybridomas having high reactivity and specificity are preferred.

Monoclonal antibodies may be isolated from the supernatants of growing hybridoma colonies. In addition, various techniques may be employed to enhance the yield, such as injection of the hybridoma cell line into the peritoneal cavity of a suitable vertebrate host, such as a mouse. Monoclonal antibodies may then be harvested from the ascites fluid or the blood. Contaminants may be removed from the antibodies by conventional techniques, such as chromatography, gel filtration, precipitation, and extraction. The polypeptides of this invention may be used in the purification process in, for example, an affinity chromatography step.

A number of therapeutically useful molecules are known in the art which comprise antigen-binding sites that are capable of exhibiting immunological binding properties of an antibody molecule. The proteolytic enzyme papain preferentially cleaves IgG molecules to yield several fragments, two of which (the "F(ab)" fragments) each comprise a covalent heterodimer that includes an intact antigen-binding site. The enzyme pepsin is able to cleave IgG molecules to provide several fragments, including the "$F(ab')_2$ " fragment which comprises both antigen-binding sites. An "Fv" fragment can be produced by preferential proteolytic cleavage of an IgM, and on rare occasions IgG or IgA immunoglobulin molecule. Fv fragments are, however, more commonly derived using recombinant techniques known in the art. The Fv fragment includes a non-covalent V_H::V_L heterodimer including an antigen-binding site which retains much of the antigen recognition and binding capabilities of the native antibody molecule. Inbar et al. (1972) Proc. Nat. Acad. Sci. USA 69:2659-2662; Hochman et al. (1976) Biochem 15:2706-2710; and Ehrlich et al. (1980) Biochem 19:4091-4096.

A single chain Fv ("sFv") polypeptide is a covalently linked V_H::V_L heterodimer which is expressed from a gene fusion including V_H- and V_L-encoding genes linked by a peptide-encoding linker. Huston et al. (1988) Proc. Nat. Acad. Sci. USA 85(16):5879-5883. A number of methods have been described to discern chemical structures for converting the naturally aggregated--but chemically separated--light and heavy polypeptide chains from an antibody V region into an sFv molecule which will fold into a three dimensional structure substantially similar to the structure of an

antigen-binding site. See, *e.g.*, U.S. Pat. Nos. 5,091,513 and 5,132,405, to Huston et al.; and U.S. Pat. No. 4,946,778, to Ladner et al.

Each of the above-described molecules includes a heavy chain and a light chain CDR set, respectively interposed between a heavy chain and a light chain FR set which provide support to the CDRS and define the spatial relationship of the CDRs relative to each other. As used herein, the term "CDR set" refers to the three hypervariable regions of a heavy or light chain V region. Proceeding from the N-terminus of a heavy or light chain, these regions are denoted as "CDR1," "CDR2," and "CDR3" respectively. An antigen-binding site, therefore, includes six CDRs, comprising the CDR set from each of a heavy and a light chain V region. A polypeptide comprising a single CDR, (*e.g.*, a CDR1, CDR2 or CDR3) is referred to herein as a "molecular recognition unit." Crystallographic analysis of a number of antigen-antibody complexes has demonstrated that the amino acid residues of CDRs form extensive contact with bound antigen, wherein the most extensive antigen contact is with the heavy chain CDR3. Thus, the molecular recognition units are primarily responsible for the specificity of an antigen-binding site.

As used herein, the term "FR set" refers to the four flanking amino acid sequences which frame the CDRs of a CDR set of a heavy or light chain V region. Some FR residues may contact bound antigen; however, FRs are primarily responsible for folding the V region into the antigen-binding site, particularly the FR residues directly adjacent to the CDRS. Within FRs, certain amino residues and certain structural features are very highly conserved. In this regard, all V region sequences contain an internal disulfide loop of around 90 amino acid residues. When the V regions fold into a binding-site, the CDRs are displayed as projecting loop motifs which form an antigen-binding surface. It is generally recognized that there are conserved structural regions of FRs which influence the folded shape of the CDR loops into certain "canonical" structures--regardless of the precise CDR amino acid sequence. Further, certain FR residues are known to participate in non-covalent interdomain contacts which stabilize the interaction of the antibody heavy and light chains.

A number of "humanized" antibody molecules comprising an antigen-binding site derived from a non-human immunoglobulin have been described, including chimeric antibodies having rodent V regions and their associated CDRs fused to human constant domains (Winter et al. (1991) Nature 349:293-299; Lobuglio et al. (1989) Proc. Nat. Acad. Sci. USA 86:4220-4224; Shaw et al. (1987) J Immunol. 138:4534-4538; and Brown et al. (1987) Cancer Res. 47:3577-3583), rodent CDRs grafted into a human supporting FR prior to fusion with an appropriate human antibody constant domain (Riechmann et al. (1988) Nature 332:323-327; Verhoeyen et al. (1988) Science 239:1534-1536; and Jones et al. (1986) Nature 321:522-525), and rodent CDRs supported by recombinantly veneered rodent FRs (European Patent Publication No. 519,596, published Dec. 23, 1992). These "humanized" molecules are designed to minimize unwanted immunological response toward rodent antihuman antibody molecules which limits the duration and effectiveness of therapeutic applications of those moieties in human recipients.

As used herein, the terms "veneered FRs" and "recombinantly veneered FRs" refer to the selective replacement of FR residues from, *e.g.*, a rodent heavy or light chain V region, with human FR residues in order to provide a xenogeneic molecule comprising an antigen-binding site which retains substantially all of the native FR polypeptide folding structure. Veneering techniques are based on the understanding that the ligand binding characteristics of an antigen-binding site are determined primarily by the structure and relative disposition of the heavy and light chain CDR sets within the antigen-binding surface. Davies et al. (1990) Ann. Rev. Biochem. 59:439-473. Thus, antigen binding specificity can be preserved in a humanized antibody only wherein the CDR structures, their interaction with each other, and their interaction with the rest of the V region domains are carefully maintained. By using veneering techniques, exterior (*e.g.*, solvent-accessible) FR residues which are readily encountered by the immune system are selectively replaced with human residues to provide a hybrid molecule that comprises either a weakly immunogenic, or substantially non-immunogenic veneered surface.

The process of veneering makes use of the available sequence data for human antibody variable domains compiled by Kabat et al., in Sequences of Proteins of Immunological Interest, 4th ed., (U.S. Dept. of Health and Human Services, U.S. Government Printing Office, 1987), updates to the Kabat database, and other accessible U.S. and foreign databases (both nucleic acid and protein). Solvent accessibilities of V region amino acids can be deduced from the known three-dimensional structure for human and murine antibody fragments. There are two general steps in veneering a murine antigen-binding site. Initially, the FRs of the variable domains of an antibody molecule of interest are compared with corresponding FR sequences of human variable domains obtained from the above-identified sources. The most homologous human V regions are then compared residue by residue to corresponding murine amino acids. The residues in the murine FR which differ from the human counterpart are replaced by the residues present in the human moiety using recombinant techniques well known in the art. Residue switching is only carried out with moieties which are at least partially exposed (solvent accessible), and care is exercised in the replacement of amino acid residues which may have a significant effect on the tertiary structure of V region domains, such as proline, glycine and charged amino acids.

In this manner, the resultant "veneered" murine antigen-binding sites are thus designed to retain the murine CDR residues, the residues substantially adjacent to the CDRs, the residues identified as buried or mostly buried (solvent inaccessible), the residues believed to participate in non-covalent (*e.g.*, electrostatic and hydrophobic) contacts between heavy and light chain domains, and the residues from conserved structural regions of the FRs which are believed to influence the "canonical" tertiary structures of the CDR loops. These design criteria are then used to prepare recombinant nucleotide sequences which combine the CDRs of both the heavy and light chain of a murine antigen-binding site into human-appearing FRs that can be used to transfect mammalian cells for the expression of recombinant human antibodies which exhibit the antigen specificity of the murine antibody molecule.

In another embodiment of the invention, monoclonal antibodies of the present invention may be coupled to one or more therapeutic agents. Suitable agents in

this regard include radionuclides, differentiation inducers, drugs, toxins, and derivatives thereof. Preferred radionuclides include ^{90}Y, ^{123}I, ^{125}I, ^{131}I, ^{186}Re, ^{188}Re, ^{211}At, and ^{212}Bi. Preferred drugs include methotrexate, and pyrimidine and purine analogs. Preferred differentiation inducers include phorbol esters and butyric acid. Preferred toxins include ricin, abrin, diptheria toxin, cholera toxin, gelonin, Pseudomonas exotoxin, Shigella toxin, and pokeweed antiviral protein.

A therapeutic agent may be coupled (*e.g.*, covalently bonded) to a suitable monoclonal antibody either directly or indirectly (*e.g.*, via a linker group). A direct reaction between an agent and an antibody is possible when each possesses a substituent capable of reacting with the other. For example, a nucleophilic group, such as an amino or sulfhydryl group, on one may be capable of reacting with a carbonyl-containing group, such as an anhydride or an acid halide, or with an alkyl group containing a good leaving group (*e.g.*, a halide) on the other.

Alternatively, it may be desirable to couple a therapeutic agent and an antibody via a linker group. A linker group can function as a spacer to distance an antibody from an agent in order to avoid interference with binding capabilities. A linker group can also serve to increase the chemical reactivity of a substituent on an agent or an antibody, and thus increase the coupling efficiency. An increase in chemical reactivity may also facilitate the use of agents, or functional groups on agents, which otherwise would not be possible.

It will be evident to those skilled in the art that a variety of bifunctional or polyfunctional reagents, both homo- and hetero-functional (such as those described in the catalog of the Pierce Chemical Co., Rockford, IL), may be employed as the linker group. Coupling may be effected, for example, through amino groups, carboxyl groups, sulfhydryl groups or oxidized carbohydrate residues. There are numerous references describing such methodology, *e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.

Where a therapeutic agent is more potent when free from the antibody portion of the immunoconjugates of the present invention, it may be desirable to use a linker group which is cleavable during or upon internalization into a cell. A number of different cleavable linker groups have been described. The mechanisms for the

intracellular release of an agent from these linker groups include cleavage by reduction of a disulfide bond (*e.g.*, U.S. Patent No. 4,489,710, to Spitler), by irradiation of a photolabile bond (*e.g.*, U.S. Patent No. 4,625,014, to Senter et al.), by hydrolysis of derivatized amino acid side chains (*e.g.*, U.S. Patent No. 4,638,045, to Kohn et al.), by serum complement-mediated hydrolysis (*e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.), and acid-catalyzed hydrolysis (*e.g.*, U.S. Patent No. 4,569,789, to Blattler et al.).

It may be desirable to couple more than one agent to an antibody. In one embodiment, multiple molecules of an agent are coupled to one antibody molecule. In another embodiment, more than one type of agent may be coupled to one antibody. Regardless of the particular embodiment, immunoconjugates with more than one agent may be prepared in a variety of ways. For example, more than one agent may be coupled directly to an antibody molecule, or linkers that provide multiple sites for attachment can be used. Alternatively, a carrier can be used.

A carrier may bear the agents in a variety of ways, including covalent bonding either directly or via a linker group. Suitable carriers include proteins such as albumins (*e.g.*, U.S. Patent No. 4,507,234, to Kato et al.), peptides and polysaccharides such as aminodextran (*e.g.*, U.S. Patent No. 4,699,784, to Shih et al.). A carrier may also bear an agent by noncovalent bonding or by encapsulation, such as within a liposome vesicle (*e.g.*, U.S. Patent Nos. 4,429,008 and 4,873,088). Carriers specific for radionuclide agents include radiohalogenated small molecules and chelating compounds. For example, U.S. Patent No. 4,735,792 discloses representative radiohalogenated small molecules and their synthesis. A radionuclide chelate may be formed from chelating compounds that include those containing nitrogen and sulfur atoms as the donor atoms for binding the metal, or metal oxide, radionuclide. For example, U.S. Patent No. 4,673,562, to Davison et al. discloses representative chelating compounds and their synthesis.

T Cell Compositions

The present invention, in another aspect, provides T cells specific for a tumor polypeptide disclosed herein, or for a variant or derivative thereof. Such cells

may generally be prepared *in vitro* or *ex vivo*, using standard procedures. For example, T cells may be isolated from bone marrow, peripheral blood, or a fraction of bone marrow or peripheral blood of a patient, using a commercially available cell separation system, such as the Isolex™ System, available from Nexell Therapeutics, Inc. (Irvine, CA; see also U.S. Patent No. 5,240,856; U.S. Patent No. 5,215,926; WO 89/06280; WO 91/16116 and WO 92/07243). Alternatively, T cells may be derived from related or unrelated humans, non-human mammals, cell lines or cultures.

T cells may be stimulated with a polypeptide, polynucleotide encoding a polypeptide and/or an antigen presenting cell (APC) that expresses such a polypeptide. Such stimulation is performed under conditions and for a time sufficient to permit the generation of T cells that are specific for the polypeptide of interest. Preferably, a tumor polypeptide or polynucleotide of the invention is present within a delivery vehicle, such as a microsphere, to facilitate the generation of specific T cells.

T cells are considered to be specific for a polypeptide of the present invention if the T cells specifically proliferate, secrete cytokines or kill target cells coated with the polypeptide or expressing a gene encoding the polypeptide. T cell specificity may be evaluated using any of a variety of standard techniques. For example, within a chromium release assay or proliferation assay, a stimulation index of more than two fold increase in lysis and/or proliferation, compared to negative controls, indicates T cell specificity. Such assays may be performed, for example, as described in Chen et al., *Cancer Res. 54*:1065-1070, 1994. Alternatively, detection of the proliferation of T cells may be accomplished by a variety of known techniques. For example, T cell proliferation can be detected by measuring an increased rate of DNA synthesis (*e.g.,* by pulse-labeling cultures of T cells with tritiated thymidine and measuring the amount of tritiated thymidine incorporated into DNA). Contact with a tumor polypeptide (100 ng/ml - 100 μg/ml, preferably 200 ng/ml - 25 μg/ml) for 3 - 7 days will typically result in at least a two fold increase in proliferation of the T cells. Contact as described above for 2-3 hours should result in activation of the T cells, as measured using standard cytokine assays in which a two fold increase in the level of cytokine release (*e.g.,* TNF or IFN-γ) is indicative of T cell activation (*see* Coligan et

al., Current Protocols in Immunology, vol. 1, Wiley Interscience (Greene 1998)). T cells that have been activated in response to a tumor polypeptide, polynucleotide or polypeptide-expressing APC may be $CD4^+$ and/or $CD8^+$. Tumor polypeptide-specific T cells may be expanded using standard techniques. Within preferred embodiments, the T cells are derived from a patient, a related donor or an unrelated donor, and are administered to the patient following stimulation and expansion.

For therapeutic purposes, $CD4^+$ or $CD8^+$ T cells that proliferate in response to a tumor polypeptide, polynucleotide or APC can be expanded in number either *in vitro* or *in vivo*. Proliferation of such T cells *in vitro* may be accomplished in a variety of ways. For example, the T cells can be re-exposed to a tumor polypeptide, or a short peptide corresponding to an immunogenic portion of such a polypeptide, with or without the addition of T cell growth factors, such as interleukin-2, and/or stimulator cells that synthesize a tumor polypeptide. Alternatively, one or more T cells that proliferate in the presence of the tumor polypeptide can be expanded in number by cloning. Methods for cloning cells are well known in the art, and include limiting dilution.

Pharmaceutical Compositions

In additional embodiments, the present invention concerns formulation of one or more of the polynucleotide, polypeptide, T-cell and/or antibody compositions disclosed herein in pharmaceutically-acceptable carriers for administration to a cell or an animal, either alone, or in combination with one or more other modalities of therapy.

It will be understood that, if desired, a composition as disclosed herein may be administered in combination with other agents as well, such as, *e.g.*, other proteins or polypeptides or various pharmaceutically-active agents. In fact, there is virtually no limit to other components that may also be included, given that the additional agents do not cause a significant adverse effect upon contact with the target cells or host tissues. The compositions may thus be delivered along with various other agents as required in the particular instance. Such compositions may be purified from host cells or other biological sources, or alternatively may be chemically synthesized as

described herein. Likewise, such compositions may further comprise substituted or derivatized RNA or DNA compositions.

Therefore, in another aspect of the present invention, pharmaceutical compositions are provided comprising one or more of the polynucleotide, polypeptide, antibody, and/or T-cell compositions described herein in combination with a physiologically acceptable carrier. In certain preferred embodiments, the pharmaceutical compositions of the invention comprise immunogenic polynucleotide and/or polypeptide compositions of the invention for use in prophylactic and theraputic vaccine applications. Vaccine preparation is generally described in, for example, M.F. Powell and M.J. Newman, eds., "Vaccine Design (the subunit and adjuvant approach)," Plenum Press (NY, 1995). Generally, such compositions will comprise one or more polynucleotide and/or polypeptide compositions of the present invention in combination with one or more immunostimulants.

It will be apparent that any of the pharmaceutical compositions described herein can contain pharmaceutically acceptable salts of the polynucleotides and polypeptides of the invention. Such salts can be prepared, for example, from pharmaceutically acceptable non-toxic bases, including organic bases (*e.g.*, salts of primary, secondary and tertiary amines and basic amino acids) and inorganic bases (*e.g.*, sodium, potassium, lithium, ammonium, calcium and magnesium salts).

In another embodiment, illustrative immunogenic compositions, *e.g.*, vaccine compositions, of the present invention comprise DNA encoding one or more of the polypeptides as described above, such that the polypeptide is generated *in situ*. As noted above, the polynucleotide may be administered within any of a variety of delivery systems known to those of ordinary skill in the art. Indeed, numerous gene delivery techniques are well known in the art, such as those described by Rolland, *Crit. Rev. Therap. Drug Carrier Systems 15*:143-198, 1998, and references cited therein. Appropriate polynucleotide expression systems will, of course, contain the necessary regulatory DNA regulatory sequences for expression in a patient (such as a suitable promoter and terminating signal). Alternatively, bacterial delivery systems may involve

the administration of a bacterium (such as *Bacillus-Calmette-Guerrin*) that expresses an immunogenic portion of the polypeptide on its cell surface or secretes such an epitope.

Therefore, in certain embodiments, polynucleotides encoding immunogenic polypeptides described herein are introduced into suitable mammalian host cells for expression using any of a number of known viral-based systems. In one illustrative embodiment, retroviruses provide a convenient and effective platform for gene delivery systems. A selected nucleotide sequence encoding a polypeptide of the present invention can be inserted into a vector and packaged in retroviral particles using techniques known in the art. The recombinant virus can then be isolated and delivered to a subject. A number of illustrative retroviral systems have been described (*e.g.*, U.S. Pat. No. 5,219,740; Miller and Rosman (1989) BioTechniques 7:980-990; Miller, A. D. (1990) Human Gene Therapy 1:5-14; Scarpa et al. (1991) Virology 180:849-852; Burns et al. (1993) Proc. Natl. Acad. Sci. USA 90:8033-8037; and Boris-Lawrie and Temin (1993) Cur. Opin. Genet. Develop. 3:102-109.

In addition, a number of illustrative adenovirus-based systems have also been described. Unlike retroviruses which integrate into the host genome, adenoviruses persist extrachromosomally thus minimizing the risks associated with insertional mutagenesis (Haj-Ahmad and Graham (1986) J. Virol. 57:267-274; Bett et al. (1993) J. Virol. 67:5911-5921; Mittereder et al. (1994) Human Gene Therapy 5:717-729; Seth et al. (1994) J. Virol. 68:933-940; Barr et al. (1994) Gene Therapy 1:51-58; Berkner, K. L. (1988) BioTechniques 6:616-629; and Rich et al. (1993) Human Gene Therapy 4:461-476).

Various adeno-associated virus (AAV) vector systems have also been developed for polynucleotide delivery. AAV vectors can be readily constructed using techniques well known in the art. See, *e.g.*, U.S. Pat. Nos. 5,173,414 and 5,139,941; International Publication Nos. WO 92/01070 and WO 93/03769; Lebkowski et al. (1988) Molec. Cell. Biol. 8:3988-3996; Vincent et al. (1990) Vaccines 90 (Cold Spring Harbor Laboratory Press); Carter, B. J. (1992) Current Opinion in Biotechnology 3:533-539; Muzyczka, N. (1992) Current Topics in Microbiol. and Immunol. 158:97-129;

Kotin, R. M. (1994) Human Gene Therapy 5:793-801; Shelling and Smith (1994) Gene Therapy 1:165-169; and Zhou et al. (1994) J. Exp. Med. 179:1867-1875.

Additional viral vectors useful for delivering the polynucleotides encoding polypeptides of the present invention by gene transfer include those derived from the pox family of viruses, such as vaccinia virus and avian poxvirus. By way of example, vaccinia virus recombinants expressing the novel molecules can be constructed as follows. The DNA encoding a polypeptide is first inserted into an appropriate vector so that it is adjacent to a vaccinia promoter and flanking vaccinia DNA sequences, such as the sequence encoding thymidine kinase (TK). This vector is then used to transfect cells which are simultaneously infected with vaccinia. Homologous recombination serves to insert the vaccinia promoter plus the gene encoding the polypeptide of interest into the viral genome. The resulting TK.sup.(-) recombinant can be selected by culturing the cells in the presence of 5-bromodeoxyuridine and picking viral plaques resistant thereto.

A vaccinia-based infection/transfection system can be conveniently used to provide for inducible, transient expression or coexpression of one or more polypeptides described herein in host cells of an organism. In this particular system, cells are first infected in vitro with a vaccinia virus recombinant that encodes the bacteriophage T7 RNA polymerase. This polymerase displays exquisite specificity in that it only transcribes templates bearing T7 promoters. Following infection, cells are transfected with the polynucleotide or polynucleotides of interest, driven by a T7 promoter. The polymerase expressed in the cytoplasm from the vaccinia virus recombinant transcribes the transfected DNA into RNA which is then translated into polypeptide by the host translational machinery. The method provides for high level, transient, cytoplasmic production of large quantities of RNA and its translation products. See, *e.g.*, Elroy-Stein and Moss, Proc. Natl. Acad. Sci. USA (1990) 87:6743-6747; Fuerst et al. Proc. Natl. Acad. Sci. USA (1986) 83:8122-8126.

Alternatively, avipoxviruses, such as the fowlpox and canarypox viruses, can also be used to deliver the coding sequences of interest. Recombinant avipox viruses, expressing immunogens from mammalian pathogens, are known to confer

protective immunity when administered to non-avian species. The use of an Avipox vector is particularly desirable in human and other mammalian species since members of the Avipox genus can only productively replicate in susceptible avian species and therefore are not infective in mammalian cells. Methods for producing recombinant Avipoxviruses are known in the art and employ genetic recombination, as described above with respect to the production of vaccinia viruses. See, *e.g.*, WO 91/12882; WO 89/03429; and WO 92/03545.

Any of a number of alphavirus vectors can also be used for delivery of polynucleotide compositions of the present invention, such as those vectors described in U.S. Patent Nos. 5,843,723; 6,015,686; 6,008,035 and 6,015,694. Certain vectors based on Venezuelan Equine Encephalitis (VEE) can also be used, illustrative examples of which can be found in U.S. Patent Nos. 5,505,947 and 5,643,576.

Moreover, molecular conjugate vectors, such as the adenovirus chimeric vectors described in Michael et al. J. Biol. Chem. (1993) 268:6866-6869 and Wagner et al. Proc. Natl. Acad. Sci. USA (1992) 89:6099-6103, can also be used for gene delivery under the invention.

Additional illustrative information on these and other known viral-based delivery systems can be found, for example, in Fisher-Hoch et al., *Proc. Natl. Acad. Sci. USA 86*:317-321, 1989; Flexner et al., *Ann. N.Y. Acad. Sci. 569*:86-103, 1989; Flexner et al., *Vaccine 8*:17-21, 1990; U.S. Patent Nos. 4,603,112, 4,769,330, and 5,017,487; WO 89/01973; U.S. Patent No. 4,777,127; GB 2,200,651; EP 0,345,242; WO 91/02805; Berkner, *Biotechniques 6*:616-627, 1988; Rosenfeld et al., *Science 252*:431-434, 1991; Kolls et al., *Proc. Natl. Acad. Sci. USA 91*:215-219, 1994; Kass-Eisler et al., *Proc. Natl. Acad. Sci. USA 90*:11498-11502, 1993; Guzman et al., *Circulation 88*:2838-2848, 1993; and Guzman et al., *Cir. Res. 73*:1202-1207, 1993.

In certain embodiments, a polynucleotide may be integrated into the genome of a target cell. This integration may be in a specific location and orientation *via* homologous recombination (gene replacement) or it may be integrated in a random, non-specific location (gene augmentation). In yet further embodiments, the polynucleotide may be stably maintained in the cell as a separate, episomal segment of

DNA. Such polynucleotide segments or "episomes" encode sequences sufficient to permit maintenance and replication independent of or in synchronization with the host cell cycle. The manner in which the expression construct is delivered to a cell and where in the cell the polynucleotide remains is dependent on the type of expression construct employed.

In another embodiment of the invention, a polynucleotide is administered/delivered as "naked" DNA, for example as described in Ulmer et al., *Science 259*:1745-1749, 1993 and reviewed by Cohen, *Science 259*:1691-1692, 1993. The uptake of naked DNA may be increased by coating the DNA onto biodegradable beads, which are efficiently transported into the cells.

In still another embodiment, a composition of the present invention can be delivered via a particle bombardment approach, many of which have been described. In one illustrative example, gas-driven particle acceleration can be achieved with devices such as those manufactured by Powderject Pharmaceuticals PLC (Oxford, UK) and Powderject Vaccines Inc. (Madison, WI), some examples of which are described in U.S. Patent Nos. 5,846,796; 6,010,478; 5,865,796; 5,584,807; and EP Patent No. 0500 799. This approach offers a needle-free delivery approach wherein a dry powder formulation of microscopic particles, such as polynucleotide or polypeptide particles, are accelerated to high speed within a helium gas jet generated by a hand held device, propelling the particles into a target tissue of interest.

In a related embodiment, other devices and methods that may be useful for gas-driven needle-less injection of compositions of the present invention include those provided by Bioject, Inc. (Portland, OR), some examples of which are described in U.S. Patent Nos. 4,790,824; 5,064,413; 5,312,335; 5,383,851; 5,399,163; 5,520,639 and 5,993,412.

According to another embodiment, the pharmaceutical compositions described herein will comprise one or more immunostimulants in addition to the immunogenic polynucleotide, polypeptide, antibody, T-cell and/or APC compositions of this invention. An immunostimulant refers to essentially any substance that enhances or potentiates an immune response (antibody and/or cell-mediated) to an exogenous

antigen. One preferred type of immunostimulant comprises an adjuvant. Many adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune responses, such as lipid A, *Bortadella pertussis* or *Mycobacterium tuberculosis* derived proteins. Certain adjuvants are commercially available as, for example, Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI); Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ); AS-2 (SmithKline Beecham, Philadelphia, PA); aluminum salts such as aluminum hydroxide gel (alum) or aluminum phosphate; salts of calcium, iron or zinc; an insoluble suspension of acylated tyrosine; acylated sugars; cationically or anionically derivatized polysaccharides; polyphosphazenes; biodegradable microspheres; monophosphoryl lipid A and quil A. Cytokines, such as GM-CSF, interleukin-2, -7, -12, and other like growth factors, may also be used as adjuvants.

Within certain embodiments of the invention, the adjuvant composition is preferably one that induces an immune response predominantly of the Th1 type. High levels of Th1-type cytokines (*e.g.*, IFN-γ, TNFα, IL-2 and IL-12) tend to favor the induction of cell mediated immune responses to an administered antigen. In contrast, high levels of Th2-type cytokines (*e.g.*, IL-4, IL-5, IL-6 and IL-10) tend to favor the induction of humoral immune responses. Following application of a vaccine as provided herein, a patient will support an immune response that includes Th1- and Th2-type responses. Within a preferred embodiment, in which a response is predominantly Th1-type, the level of Th1-type cytokines will increase to a greater extent than the level of Th2-type cytokines. The levels of these cytokines may be readily assessed using standard assays. For a review of the families of cytokines, see Mosmann and Coffman, *Ann. Rev. Immunol.* 7:145-173, 1989.

Certain preferred adjuvants for eliciting a predominantly Th1-type response include, for example, a combination of monophosphoryl lipid A, preferably 3-de-O-acylated monophosphoryl lipid A, together with an aluminum salt. MPL® adjuvants are available from Corixa Corporation (Seattle, WA; *see*, for example, US Patent Nos. 4,436,727; 4,877,611; 4,866,034 and 4,912,094). CpG-containing

oligonucleotides (in which the CpG dinucleotide is unmethylated) also induce a predominantly Th1 response. Such oligonucleotides are well known and are described, for example, in WO 96/02555, WO 99/33488 and U.S. Patent Nos. 6,008,200 and 5,856,462. Immunostimulatory DNA sequences are also described, for example, by Sato et al., *Science 273*:352, 1996. Another preferred adjuvant comprises a saponin, such as Quil A, or derivatives thereof, including QS21 and QS7 (Aquila Biopharmaceuticals Inc., Framingham, MA); Escin; Digitonin; or *Gypsophila* or *Chenopodium quinoa* saponins . Other preferred formulations include more than one saponin in the adjuvant combinations of the present invention, for example combinations of at least two of the following group comprising QS21, QS7, Quil A, β-escin, or digitonin.

Alternatively the saponin formulations may be combined with vaccine vehicles composed of chitosan or other polycationic polymers, polylactide and polylactide-co-glycolide particles, poly-N-acetyl glucosamine-based polymer matrix, particles composed of polysaccharides or chemically modified polysaccharides, liposomes and lipid-based particles, particles composed of glycerol monoesters, etc. The saponins may also be formulated in the presence of cholesterol to form particulate structures such as liposomes or ISCOMs. Furthermore, the saponins may be formulated together with a polyoxyethylene ether or ester, in either a non-particulate solution or suspension, or in a particulate structure such as a paucilamelar liposome or ISCOM. The saponins may also be formulated with excipients such as Carbopol[R] to increase viscosity, or may be formulated in a dry powder form with a powder excipient such as lactose.

In one preferred embodiment, the adjuvant system includes the combination of a monophosphoryl lipid A and a saponin derivative, such as the combination of QS21 and 3D-MPL® adjuvant, as described in WO 94/00153, or a less reactogenic composition where the QS21 is quenched with cholesterol, as described in WO 96/33739. Other preferred formulations comprise an oil-in-water emulsion and tocopherol. Another particularly preferred adjuvant formulation employing QS21, 3D-

MPL® adjuvant and tocopherol in an oil-in-water emulsion is described in WO 95/17210.

Another enhanced adjuvant system involves the combination of a CpG-containing oligonucleotide and a saponin derivative particularly the combination of CpG and QS21 is disclosed in WO 00/09159. Preferably the formulation additionally comprises an oil in water emulsion and tocopherol.

Additional illustrative adjuvants for use in the pharmaceutical compositions of the invention include Montanide ISA 720 (Seppic, France), SAF (Chiron, California, United States), ISCOMS (CSL), MF-59 (Chiron), the SBAS series of adjuvants (*e.g.*, SBAS-2 or SBAS-4, available from SmithKline Beecham, Rixensart, Belgium), Detox (Enhanzyn®; Corixa, Hamilton, MT), RC-529 (Corixa, Hamilton, MT) and other aminoalkyl glucosaminide 4-phosphates (AGPs), such as those described in pending U.S. Patent Application Serial Nos. 08/853,826 and 09/074,720, the disclosures of which are incorporated herein by reference in their entireties, and polyoxyethylene ether adjuvants such as those described in WO 99/52549A1.

Other preferred adjuvants include adjuvant molecules of the general formula

(I): $HO(CH_2CH_2O)_n\text{-}A\text{-}R$,

wherein, n is 1-50, A is a bond or –C(O)-, R is C_{1-50} alkyl or Phenyl C_{1-50} alkyl.

One embodiment of the present invention consists of a vaccine formulation comprising a polyoxyethylene ether of general formula (I), wherein *n* is between 1 and 50, preferably 4-24, most preferably 9; the *R* component is C_{1-50}, preferably C_4-C_{20} alkyl and most preferably C_{12} alkyl, and *A* is a bond. The concentration of the polyoxyethylene ethers should be in the range 0.1-20%, preferably from 0.1-10%, and most preferably in the range 0.1-1%. Preferred polyoxyethylene ethers are selected from the following group: polyoxyethylene-9-lauryl ether, polyoxyethylene-9-steoryl ether, polyoxyethylene-8-steoryl ether, polyoxyethylene-4-lauryl ether, polyoxyethylene-35-lauryl ether, and polyoxyethylene-23-lauryl ether. Polyoxyethylene ethers such as polyoxyethylene lauryl ether are described in the Merck index (12th edition: entry 7717). These adjuvant molecules are described in WO

99/52549. The polyoxyethylene ether according to the general formula (I) above may, if desired, be combined with another adjuvant. For example, a preferred adjuvant combination is preferably with CpG as described in the pending UK patent application GB 9820956.2.

According to another embodiment of this invention, an immunogenic composition described herein is delivered to a host via antigen presenting cells (APCs), such as dendritic cells, macrophages, B cells, monocytes and other cells that may be engineered to be efficient APCs. Such cells may, but need not, be genetically modified to increase the capacity for presenting the antigen, to improve activation and/or maintenance of the T cell response, to have anti-tumor effects *per se* and/or to be immunologically compatible with the receiver (*i.e.,* matched HLA haplotype). APCs may generally be isolated from any of a variety of biological fluids and organs, including tumor and peritumoral tissues, and may be autologous, allogeneic, syngeneic or xenogeneic cells.

Certain preferred embodiments of the present invention use dendritic cells or progenitors thereof as antigen-presenting cells. Dendritic cells are highly potent APCs (Banchereau and Steinman, *Nature 392*:245-251, 1998) and have been shown to be effective as a physiological adjuvant for eliciting prophylactic or therapeutic antitumor immunity (*see* Timmerman and Levy, *Ann. Rev. Med. 50*:507-529, 1999). In general, dendritic cells may be identified based on their typical shape (stellate *in situ*, with marked cytoplasmic processes (dendrites) visible *in vitro*), their ability to take up, process and present antigens with high efficiency and their ability to activate naïve T cell responses. Dendritic cells may, of course, be engineered to express specific cell-surface receptors or ligands that are not commonly found on dendritic cells *in vivo* or *ex vivo*, and such modified dendritic cells are contemplated by the present invention. As an alternative to dendritic cells, secreted vesicles antigen-loaded dendritic cells (called exosomes) may be used within a vaccine (*see* Zitvogel et al., *Nature Med. 4*:594-600, 1998).

Dendritic cells and progenitors may be obtained from peripheral blood, bone marrow, tumor-infiltrating cells, peritumoral tissues-infiltrating cells, lymph

nodes, spleen, skin, umbilical cord blood or any other suitable tissue or fluid. For example, dendritic cells may be differentiated *ex vivo* by adding a combination of cytokines such as GM-CSF, IL-4, IL-13 and/or TNFα to cultures of monocytes harvested from peripheral blood. Alternatively, CD34 positive cells harvested from peripheral blood, umbilical cord blood or bone marrow may be differentiated into dendritic cells by adding to the culture medium combinations of GM-CSF, IL-3, TNFα, CD40 ligand, LPS, flt3 ligand and/or other compound(s) that induce differentiation, maturation and proliferation of dendritic cells.

Dendritic cells are conveniently categorized as "immature" and "mature" cells, which allows a simple way to discriminate between two well characterized phenotypes. However, this nomenclature should not be construed to exclude all possible intermediate stages of differentiation. Immature dendritic cells are characterized as APC with a high capacity for antigen uptake and processing, which correlates with the high expression of Fcγ receptor and mannose receptor. The mature phenotype is typically characterized by a lower expression of these markers, but a high expression of cell surface molecules responsible for T cell activation such as class I and class II MHC, adhesion molecules (*e.g.,* CD54 and CD11) and costimulatory molecules (*e.g.,* CD40, CD80, CD86 and 4-1BB).

APCs may generally be transfected with a polynucleotide of the invention (or portion or other variant thereof) such that the encoded polypeptide, or an immunogenic portion thereof, is expressed on the cell surface. Such transfection may take place *ex vivo*, and a pharmaceutical composition comprising such transfected cells may then be used for therapeutic purposes, as described herein. Alternatively, a gene delivery vehicle that targets a dendritic or other antigen presenting cell may be administered to a patient, resulting in transfection that occurs *in vivo*. *In vivo* and *ex vivo* transfection of dendritic cells, for example, may generally be performed using any methods known in the art, such as those described in WO 97/24447, or the gene gun approach described by Mahvi et al., *Immunology and cell Biology* 75:456-460, 1997. Antigen loading of dendritic cells may be achieved by incubating dendritic cells or progenitor cells with the tumor polypeptide, DNA (naked or within a plasmid vector) or

RNA; or with antigen-expressing recombinant bacterium or viruses (*e.g.*, vaccinia, fowlpox, adenovirus or lentivirus vectors). Prior to loading, the polypeptide may be covalently conjugated to an immunological partner that provides T cell help (*e.g.*, a carrier molecule). Alternatively, a dendritic cell may be pulsed with a non-conjugated immunological partner, separately or in the presence of the polypeptide.

While any suitable carrier known to those of ordinary skill in the art may be employed in the pharmaceutical compositions of this invention, the type of carrier will typically vary depending on the mode of administration. Compositions of the present invention may be formulated for any appropriate manner of administration, including for example, topical, oral, nasal, mucosal, intravenous, intracranial, intraperitoneal, subcutaneous and intramuscular administration.

Carriers for use within such pharmaceutical compositions are biocompatible, and may also be biodegradable. In certain embodiments, the formulation preferably provides a relatively constant level of active component release. In other embodiments, however, a more rapid rate of release immediately upon administration may be desired. The formulation of such compositions is well within the level of ordinary skill in the art using known techniques. Illustrative carriers useful in this regard include microparticles of poly(lactide-co-glycolide), polyacrylate, latex, starch, cellulose, dextran and the like. Other illustrative delayed-release carriers include supramolecular biovectors, which comprise a non-liquid hydrophilic core (*e.g.*, a cross-linked polysaccharide or oligosaccharide) and, optionally, an external layer comprising an amphiphilic compound, such as a phospholipid (*see e.g.*, U.S. Patent No. 5,151,254 and PCT applications WO 94/20078, WO/94/23701 and WO 96/06638). The amount of active compound contained within a sustained release formulation depends upon the site of implantation, the rate and expected duration of release and the nature of the condition to be treated or prevented.

In another illustrative embodiment, biodegradable microspheres (*e.g.*, polylactate polyglycolate) are employed as carriers for the compositions of this invention. Suitable biodegradable microspheres are disclosed, for example, in U.S. Patent Nos. 4,897,268; 5,075,109; 5,928,647; 5,811,128; 5,820,883; 5,853,763;

5,814,344, 5,407,609 and 5,942,252. Modified hepatitis B core protein carrier systems. such as described in WO/99 40934, and references cited therein, will also be useful for many applications. Another illustrative carrier/delivery system employs a carrier comprising particulate-protein complexes, such as those described in U.S. Patent No. 5,928,647, which are capable of inducing a class I-restricted cytotoxic T lymphocyte responses in a host.

The pharmaceutical compositions of the invention will often further comprise one or more buffers (*e.g.*, neutral buffered saline or phosphate buffered saline), carbohydrates (*e.g.*, glucose, mannose, sucrose or dextrans), mannitol, proteins, polypeptides or amino acids such as glycine, antioxidants, bacteriostats, chelating agents such as EDTA or glutathione, adjuvants (*e.g.*, aluminum hydroxide), solutes that render the formulation isotonic, hypotonic or weakly hypertonic with the blood of a recipient, suspending agents, thickening agents and/or preservatives. Alternatively, compositions of the present invention may be formulated as a lyophilizate.

The pharmaceutical compositions described herein may be presented in unit-dose or multi-dose containers, such as sealed ampoules or vials. Such containers are typically sealed in such a way to preserve the sterility and stability of the formulation until use. In general, formulations may be stored as suspensions, solutions or emulsions in oily or aqueous vehicles. Alternatively, a pharmaceutical composition may be stored in a freeze-dried condition requiring only the addition of a sterile liquid carrier immediately prior to use.

The development of suitable dosing and treatment regimens for using the particular compositions described herein in a variety of treatment regimens, including *e.g.*, oral, parenteral, intravenous, intranasal, and intramuscular administration and formulation, is well known in the art, some of which are briefly discussed below for general purposes of illustration.

In certain applications, the pharmaceutical compositions disclosed herein may be delivered *via* oral administration to an animal. As such, these compositions may be formulated with an inert diluent or with an assimilable edible carrier, or they

may be enclosed in hard- or soft-shell gelatin capsule, or they may be compressed into tablets, or they may be incorporated directly with the food of the diet.

The active compounds may even be incorporated with excipients and used in the form of ingestible tablets, buccal tables, troches, capsules, elixirs, suspensions, syrups, wafers, and the like (see, for example, Mathiowitz *et al.*, Nature 1997 Mar 27;386(6623):410-4; Hwang *et al.*, Crit Rev Ther Drug Carrier Syst 1998;15(3):243-84; U. S. Patent 5,641,515; U. S. Patent 5,580,579 and U. S. Patent 5,792,451). Tablets, troches, pills, capsules and the like may also contain any of a variety of additional components, for example, a binder, such as gum tragacanth, acacia, cornstarch, or gelatin; excipients, such as dicalcium phosphate; a disintegrating agent, such as corn starch, potato starch, alginic acid and the like; a lubricant, such as magnesium stearate; and a sweetening agent, such as sucrose, lactose or saccharin may be added or a flavoring agent, such as peppermint, oil of wintergreen, or cherry flavoring. When the dosage unit form is a capsule, it may contain, in addition to materials of the above type, a liquid carrier. Various other materials may be present as coatings or to otherwise modify the physical form of the dosage unit. For instance, tablets, pills, or capsules may be coated with shellac, sugar, or both. Of course, any material used in preparing any dosage unit form should be pharmaceutically pure and substantially non-toxic in the amounts employed. In addition, the active compounds may be incorporated into sustained-release preparation and formulations.

Typically, these formulations will contain at least about 0.1% of the active compound or more, although the percentage of the active ingredient(s) may, of course, be varied and may conveniently be between about 1 or 2% and about 60% or 70% or more of the weight or volume of the total formulation. Naturally, the amount of active compound(s) in each therapeutically useful composition may be prepared is such a way that a suitable dosage will be obtained in any given unit dose of the compound. Factors such as solubility, bioavailability, biological half-life, route of administration, product shelf life, as well as other pharmacological considerations will be contemplated by one skilled in the art of preparing such pharmaceutical formulations, and as such, a variety of dosages and treatment regimens may be desirable.

For oral administration, the compositions of the present invention may alternatively be incorporated with one or more excipients in the form of a mouthwash, dentifrice, buccal tablet, oral spray, or sublingual orally-administered formulation. Alternatively, the active ingredient may be incorporated into an oral solution such as one containing sodium borate, glycerin and potassium bicarbonate, or dispersed in a dentifrice, or added in a therapeutically-effective amount to a composition that may include water, binders, abrasives, flavoring agents, foaming agents, and humectants. Alternatively the compositions may be fashioned into a tablet or solution form that may be placed under the tongue or otherwise dissolved in the mouth.

In certain circumstances it will be desirable to deliver the pharmaceutical compositions disclosed herein parenterally, intravenously, intramuscularly, or even intraperitoneally. Such approaches are well known to the skilled artisan, some of which are further described, for example, in U. S. Patent 5,543,158; U. S. Patent 5,641,515 and U. S. Patent 5,399,363. In certain embodiments, solutions of the active compounds as free base or pharmacologically acceptable salts may be prepared in water suitably mixed with a surfactant, such as hydroxypropylcellulose. Dispersions may also be prepared in glycerol, liquid polyethylene glycols, and mixtures thereof and in oils. Under ordinary conditions of storage and use, these preparations generally will contain a preservative to prevent the growth of microorganisms.

Illustrative pharmaceutical forms suitable for injectable use include sterile aqueous solutions or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersions (for example, see U. S. Patent 5,466,468). In all cases the form must be sterile and must be fluid to the extent that easy syringability exists. It must be stable under the conditions of manufacture and storage and must be preserved against the contaminating action of microorganisms, such as bacteria and fungi. The carrier can be a solvent or dispersion medium containing, for example, water, ethanol, polyol (*e.g.*, glycerol, propylene glycol, and liquid polyethylene glycol, and the like), suitable mixtures thereof, and/or vegetable oils. Proper fluidity may be maintained, for example, by the use of a coating, such as lecithin, by the maintenance of the required particle size in the case of dispersion and/or

by the use of surfactants. The prevention of the action of microorganisms can be facilitated by various antibacterial and antifungal agents, for example, parabens, chlorobutanol, phenol, sorbic acid, thimerosal, and the like. In many cases, it will be preferable to include isotonic agents, for example, sugars or sodium chloride. Prolonged absorption of the injectable compositions can be brought about by the use in the compositions of agents delaying absorption, for example, aluminum monostearate and gelatin.

In one embodiment, for parenteral administration in an aqueous solution, the solution should be suitably buffered if necessary and the liquid diluent first rendered isotonic with sufficient saline or glucose. These particular aqueous solutions are especially suitable for intravenous, intramuscular, subcutaneous and intraperitoneal administration. In this connection, a sterile aqueous medium that can be employed will be known to those of skill in the art in light of the present disclosure. For example, one dosage may be dissolved in 1 ml of isotonic NaCl solution and either added to 1000 ml of hypodermoclysis fluid or injected at the proposed site of infusion, (see for example, "Remington's Pharmaceutical Sciences" 15th Edition, pages 1035-1038 and 1570-1580). Some variation in dosage will necessarily occur depending on the condition of the subject being treated. Moreover, for human administration, preparations will of course preferably meet sterility, pyrogenicity, and the general safety and purity standards as required by FDA Office of Biologics standards.

In another embodiment of the invention, the compositions disclosed herein may be formulated in a neutral or salt form. Illustrative pharmaceutically-acceptable salts include the acid addition salts (formed with the free amino groups of the protein) and which are formed with inorganic acids such as, for example, hydrochloric or phosphoric acids, or such organic acids as acetic, oxalic, tartaric, mandelic, and the like. Salts formed with the free carboxyl groups can also be derived from inorganic bases such as, for example, sodium, potassium, ammonium, calcium, or ferric hydroxides, and such organic bases as isopropylamine, trimethylamine, histidine, procaine and the like. Upon formulation, solutions will be

administered in a manner compatible with the dosage formulation and in such amount as is therapeutically effective.

The carriers can further comprise any and all solvents, dispersion media, vehicles, coatings, diluents, antibacterial and antifungal agents, isotonic and absorption delaying agents, buffers, carrier solutions, suspensions, colloids, and the like. The use of such media and agents for pharmaceutical active substances is well known in the art. Except insofar as any conventional media or agent is incompatible with the active ingredient, its use in the therapeutic compositions is contemplated. Supplementary active ingredients can also be incorporated into the compositions. The phrase "pharmaceutically-acceptable" refers to molecular entities and compositions that do not produce an allergic or similar untoward reaction when administered to a human.

In certain embodiments, the pharmaceutical compositions may be delivered by intranasal sprays, inhalation, and/or other aerosol delivery vehicles. Methods for delivering genes, nucleic acids, and peptide compositions directly to the lungs *via* nasal aerosol sprays has been described, *e.g.,* in U. S. Patent 5,756,353 and U. S. Patent 5,804,212. Likewise, the delivery of drugs using intranasal microparticle resins (Takenaga *et al.*, J Controlled Release 1998 Mar 2;52(1-2):81-7) and lysophosphatidyl-glycerol compounds (U. S. Patent 5,725,871) are also well-known in the pharmaceutical arts. Likewise, illustrative transmucosal drug delivery in the form of a polytetrafluoroetheylene support matrix is described in U. S. Patent 5,780,045.

In certain embodiments, liposomes, nanocapsules, microparticles, lipid particles, vesicles, and the like, are used for the introduction of the compositions of the present invention into suitable host cells/organisms. In particular, the compositions of the present invention may be formulated for delivery either encapsulated in a lipid particle, a liposome, a vesicle, a nanosphere, or a nanoparticle or the like. Alternatively, compositions of the present invention can be bound, either covalently or non-covalently, to the surface of such carrier vehicles.

The formation and use of liposome and liposome-like preparations as potential drug carriers is generally known to those of skill in the art (see for example, Lasic, Trends Biotechnol 1998 Jul;16(7):307-21; Takakura, Nippon Rinsho 1998

Mar;56(3):691-5; Chandran *et al.*, Indian J Exp Biol. 1997 Aug;35(8):801-9; Margalit, Crit Rev Ther Drug Carrier Syst. 1995;12(2-3):233-61; U.S. Patent 5,567,434; U.S. Patent 5,552,157; U.S. Patent 5,565,213; U.S. Patent 5,738,868 and U.S. Patent 5,795,587, each specifically incorporated herein by reference in its entirety).

Liposomes have been used successfully with a number of cell types that are normally difficult to transfect by other procedures, including T cell suspensions, primary hepatocyte cultures and PC 12 cells (Renneisen *et al.,* J Biol Chem. 1990 Sep 25;265(27):16337-42; Muller *et al.,* DNA Cell Biol. 1990 Apr;9(3):221-9). In addition, liposomes are free of the DNA length constraints that are typical of viral-based delivery systems. Liposomes have been used effectively to introduce genes, various drugs, radiotherapeutic agents, enzymes, viruses, transcription factors, allosteric effectors and the like, into a variety of cultured cell lines and animals. Furthermore, he use of liposomes does not appear to be associated with autoimmune responses or unacceptable toxicity after systemic delivery.

In certain embodiments, liposomes are formed from phospholipids that are dispersed in an aqueous medium and spontaneously form multilamellar concentric bilayer vesicles (also termed multilamellar vesicles (MLVs).

Alternatively, in other embodiments, the invention provides for pharmaceutically-acceptable nanocapsule formulations of the compositions of the present invention. Nanocapsules can generally entrap compounds in a stable and reproducible way (see, for example, Quintanar-Guerrero *et al.*, Drug Dev Ind Pharm. 1998 Dec;24(12):1113-28). To avoid side effects due to intracellular polymeric overloading, such ultrafine particles (sized around 0.1 μm) may be designed using polymers able to be degraded *in vivo*. Such particles can be made as described, for example, by Couvreur *et al.,* Crit Rev Ther Drug Carrier Syst. 1988;5(1):1-20; zur Muhlen *et al.*, Eur J Pharm Biopharm. 1998 Mar;45(2):149-55; Zambaux *et al.* J Controlled Release. 1998 Jan 2;50(1-3):31-40; and U. S. Patent 5,145,684.

Cancer Therapeutic Methods

In further aspects of the present invention, the pharmaceutical compositions described herein may be used for the treatment of cancer, particularly for the immunotherapy of prostate cancer. Within such methods, the pharmaceutical compositions described herein are administered to a patient, typically a warm-blooded animal, preferably a human. A patient may or may not be afflicted with cancer. Accordingly, the above pharmaceutical compositions may be used to prevent the development of a cancer or to treat a patient afflicted with a cancer. Pharmaceutical compositions and vaccines may be administered either prior to or following surgical removal of primary tumors and/or treatment such as administration of radiotherapy or conventional chemotherapeutic drugs. As discussed above, administration of the pharmaceutical compositions may be by any suitable method, including administration by intravenous, intraperitoneal, intramuscular, subcutaneous, intranasal, intradermal, anal, vaginal, topical and oral routes.

Within certain embodiments, immunotherapy may be active immunotherapy, in which treatment relies on the *in vivo* stimulation of the endogenous host immune system to react against tumors with the administration of immune response-modifying agents (such as polypeptides and polynucleotides as provided herein).

Within other embodiments, immunotherapy may be passive immunotherapy, in which treatment involves the delivery of agents with established tumor-immune reactivity (such as effector cells or antibodies) that can directly or indirectly mediate antitumor effects and does not necessarily depend on an intact host immune system. Examples of effector cells include T cells as discussed above, T lymphocytes (such as $CD8^+$ cytotoxic T lymphocytes and $CD4^+$ T-helper tumor-infiltrating lymphocytes), killer cells (such as Natural Killer cells and lymphokine-activated killer cells), B cells and antigen-presenting cells (such as dendritic cells and macrophages) expressing a polypeptide provided herein. T cell receptors and antibody receptors specific for the polypeptides recited herein may be cloned, expressed and transferred into other vectors or effector cells for adoptive immunotherapy. The

polypeptides provided herein may also be used to generate antibodies or anti-idiotypic antibodies (as described above and in U.S. Patent No. 4,918,164) for passive immunotherapy.

Effector cells may generally be obtained in sufficient quantities for adoptive immunotherapy by growth *in vitro*, as described herein. Culture conditions for expanding single antigen-specific effector cells to several billion in number with retention of antigen recognition *in vivo* are well known in the art. Such *in vitro* culture conditions typically use intermittent stimulation with antigen, often in the presence of cytokines (such as IL-2) and non-dividing feeder cells. As noted above, immunoreactive polypeptides as provided herein may be used to rapidly expand antigen-specific T cell cultures in order to generate a sufficient number of cells for immunotherapy. In particular, antigen-presenting cells, such as dendritic, macrophage, monocyte, fibroblast and/or B cells, may be pulsed with immunoreactive polypeptides or transfected with one or more polynucleotides using standard techniques well known in the art. For example, antigen-presenting cells can be transfected with a polynucleotide having a promoter appropriate for increasing expression in a recombinant virus or other expression system. Cultured effector cells for use in therapy must be able to grow and distribute widely, and to survive long term *in vivo*. Studies have shown that cultured effector cells can be induced to grow in vivo and to survive long term in substantial numbers by repeated stimulation with antigen supplemented with IL-2 (*see*, for example, Cheever et al., *Immunological Reviews 157*:177, 1997).

Alternatively, a vector expressing a polypeptide recited herein may be introduced into antigen presenting cells taken from a patient and clonally propagated *ex vivo* for transplant back into the same patient. Transfected cells may be reintroduced into the patient using any means known in the art, preferably in sterile form by intravenous, intracavitary, intraperitoneal or intratumor administration.

Routes and frequency of administration of the therapeutic compositions described herein, as well as dosage, will vary from individual to individual, and may be readily established using standard techniques. In general, the pharmaceutical compositions and vaccines may be administered by injection (*e.g.*, intracutaneous,

intramuscular, intravenous or subcutaneous), intranasally (*e.g.*, by aspiration) or orally. Preferably, between 1 and 10 doses may be administered over a 52 week period. Preferably, 6 doses are administered, at intervals of 1 month, and booster vaccinations may be given periodically thereafter. Alternate protocols may be appropriate for individual patients. A suitable dose is an amount of a compound that, when administered as described above, is capable of promoting an anti-tumor immune response, and is at least 10-50% above the basal (*i.e.*, untreated) level. Such response can be monitored by measuring the anti-tumor antibodies in a patient or by vaccine-dependent generation of cytolytic effector cells capable of killing the patient's tumor cells *in vitro*. Such vaccines should also be capable of causing an immune response that leads to an improved clinical outcome (*e.g.*, more frequent remissions, complete or partial or longer disease-free survival) in vaccinated patients as compared to non-vaccinated patients. In general, for pharmaceutical compositions and vaccines comprising one or more polypeptides, the amount of each polypeptide present in a dose ranges from about 25 μg to 5 mg per kg of host. Suitable dose sizes will vary with the size of the patient, but will typically range from about 0.1 mL to about 5 mL.

In general, an appropriate dosage and treatment regimen provides the active compound(s) in an amount sufficient to provide therapeutic and/or prophylactic benefit. Such a response can be monitored by establishing an improved clinical outcome (*e.g.*, more frequent remissions, complete or partial, or longer disease-free survival) in treated patients as compared to non-treated patients. Increases in preexisting immune responses to a tumor protein generally correlate with an improved clinical outcome. Such immune responses may generally be evaluated using standard proliferation, cytotoxicity or cytokine assays, which may be performed using samples obtained from a patient before and after treatment.

<u>Cancer Detection and Diagnostic Compositions, Methods and Kits</u>

In general, a cancer may be detected in a patient based on the presence of one or more prostate tumor proteins and/or polynucleotides encoding such proteins in a biological sample (for example, blood, sera, sputum urine and/or tumor biopsies)

obtained from the patient. In other words, such proteins may be used as markers to indicate the presence or absence of a cancer such as prostate cancer. In addition, such proteins may be useful for the detection of other cancers. The binding agents provided herein generally permit detection of the level of antigen that binds to the agent in the biological sample. Polynucleotide primers and probes may be used to detect the level of mRNA encoding a tumor protein, which is also indicative of the presence or absence of a cancer. In general, a prostate tumor sequence should be present at a level that is at least three fold higher in tumor tissue than in normal tissue

There are a variety of assay formats known to those of ordinary skill in the art for using a binding agent to detect polypeptide markers in a sample. *See, e.g.*, Harlow and Lane, *Antibodies: A Laboratory Manual,* Cold Spring Harbor Laboratory, 1988. In general, the presence or absence of a cancer in a patient may be determined by (a) contacting a biological sample obtained from a patient with a binding agent; (b) detecting in the sample a level of polypeptide that binds to the binding agent; and (c) comparing the level of polypeptide with a predetermined cut-off value.

In a preferred embodiment, the assay involves the use of binding agent immobilized on a solid support to bind to and remove the polypeptide from the remainder of the sample. The bound polypeptide may then be detected using a detection reagent that contains a reporter group and specifically binds to the binding agent/polypeptide complex. Such detection reagents may comprise, for example, a binding agent that specifically binds to the polypeptide or an antibody or other agent that specifically binds to the binding agent, such as an anti-immunoglobulin, protein G, protein A or a lectin. Alternatively, a competitive assay may be utilized, in which a polypeptide is labeled with a reporter group and allowed to bind to the immobilized binding agent after incubation of the binding agent with the sample. The extent to which components of the sample inhibit the binding of the labeled polypeptide to the binding agent is indicative of the reactivity of the sample with the immobilized binding agent. Suitable polypeptides for use within such assays include full length prostate tumor proteins and polypeptide portions thereof to which the binding agent binds, as described above.

The solid support may be any material known to those of ordinary skill in the art to which the tumor protein may be attached. For example, the solid support may be a test well in a microtiter plate or a nitrocellulose or other suitable membrane. Alternatively, the support may be a bead or disc, such as glass, fiberglass, latex or a plastic material such as polystyrene or polyvinylchloride. The support may also be a magnetic particle or a fiber optic sensor, such as those disclosed, for example, in U.S. Patent No. 5,359,681. The binding agent may be immobilized on the solid support using a variety of techniques known to those of skill in the art, which are amply described in the patent and scientific literature. In the context of the present invention, the term "immobilization" refers to both noncovalent association, such as adsorption, and covalent attachment (which may be a direct linkage between the agent and functional groups on the support or may be a linkage by way of a cross-linking agent). Immobilization by adsorption to a well in a microtiter plate or to a membrane is preferred. In such cases, adsorption may be achieved by contacting the binding agent, in a suitable buffer, with the solid support for a suitable amount of time. The contact time varies with temperature, but is typically between about 1 hour and about 1 day. In general, contacting a well of a plastic microtiter plate (such as polystyrene or polyvinylchloride) with an amount of binding agent ranging from about 10 ng to about 10 μg, and preferably about 100 ng to about 1 μg, is sufficient to immobilize an adequate amount of binding agent.

Covalent attachment of binding agent to a solid support may generally be achieved by first reacting the support with a bifunctional reagent that will react with both the support and a functional group, such as a hydroxyl or amino group, on the binding agent. For example, the binding agent may be covalently attached to supports having an appropriate polymer coating using benzoquinone or by condensation of an aldehyde group on the support with an amine and an active hydrogen on the binding partner (*see, e.g.*, Pierce Immunotechnology Catalog and Handbook, 1991, at A12-A13).

In certain embodiments, the assay is a two-antibody sandwich assay. This assay may be performed by first contacting an antibody that has been immobilized

on a solid support, commonly the well of a microtiter plate, with the sample, such that polypeptides within the sample are allowed to bind to the immobilized antibody. Unbound sample is then removed from the immobilized polypeptide-antibody complexes and a detection reagent (preferably a second antibody capable of binding to a different site on the polypeptide) containing a reporter group is added. The amount of detection reagent that remains bound to the solid support is then determined using a method appropriate for the specific reporter group.

More specifically, once the antibody is immobilized on the support as described above, the remaining protein binding sites on the support are typically blocked. Any suitable blocking agent known to those of ordinary skill in the art, such as bovine serum albumin or Tween 20™ (Sigma Chemical Co., St. Louis, MO). The immobilized antibody is then incubated with the sample, and polypeptide is allowed to bind to the antibody. The sample may be diluted with a suitable diluent, such as phosphate-buffered saline (PBS) prior to incubation. In general, an appropriate contact time (*i.e.*, incubation time) is a period of time that is sufficient to detect the presence of polypeptide within a sample obtained from an individual with prostate cancer. Preferably, the contact time is sufficient to achieve a level of binding that is at least about 95% of that achieved at equilibrium between bound and unbound polypeptide. Those of ordinary skill in the art will recognize that the time necessary to achieve equilibrium may be readily determined by assaying the level of binding that occurs over a period of time. At room temperature, an incubation time of about 30 minutes is generally sufficient.

Unbound sample may then be removed by washing the solid support with an appropriate buffer, such as PBS containing 0.1% Tween 20™. The second antibody, which contains a reporter group, may then be added to the solid support. Preferred reporter groups include those groups recited above.

The detection reagent is then incubated with the immobilized antibody-polypeptide complex for an amount of time sufficient to detect the bound polypeptide. An appropriate amount of time may generally be determined by assaying the level of binding that occurs over a period of time. Unbound detection reagent is then removed

and bound detection reagent is detected using the reporter group. The method employed for detecting the reporter group depends upon the nature of the reporter group. For radioactive groups, scintillation counting or autoradiographic methods are generally appropriate. Spectroscopic methods may be used to detect dyes, luminescent groups and fluorescent groups. Biotin may be detected using avidin, coupled to a different reporter group (commonly a radioactive or fluorescent group or an enzyme). Enzyme reporter groups may generally be detected by the addition of substrate (generally for a specific period of time), followed by spectroscopic or other analysis of the reaction products.

To determine the presence or absence of a cancer, such as prostate cancer, the signal detected from the reporter group that remains bound to the solid support is generally compared to a signal that corresponds to a predetermined cut-off value. In one preferred embodiment, the cut-off value for the detection of a cancer is the average mean signal obtained when the immobilized antibody is incubated with samples from patients without the cancer. In general, a sample generating a signal that is three standard deviations above the predetermined cut-off value is considered positive for the cancer. In an alternate preferred embodiment, the cut-off value is determined using a Receiver Operator Curve, according to the method of Sackett et al., *Clinical Epidemiology: A Basic Science for Clinical Medicine*, Little Brown and Co., 1985, p. 106-7. Briefly, in this embodiment, the cut-off value may be determined from a plot of pairs of true positive rates (*i.e.*, sensitivity) and false positive rates (100%-specificity) that correspond to each possible cut-off value for the diagnostic test result. The cut-off value on the plot that is the closest to the upper left-hand corner (*i.e.*, the value that encloses the largest area) is the most accurate cut-off value, and a sample generating a signal that is higher than the cut-off value determined by this method may be considered positive. Alternatively, the cut-off value may be shifted to the left along the plot, to minimize the false positive rate, or to the right, to minimize the false negative rate. In general, a sample generating a signal that is higher than the cut-off value determined by this method is considered positive for a cancer.

In a related embodiment, the assay is performed in a flow-through or strip test format, wherein the binding agent is immobilized on a membrane, such as nitrocellulose. In the flow-through test, polypeptides within the sample bind to the immobilized binding agent as the sample passes through the membrane. A second, labeled binding agent then binds to the binding agent-polypeptide complex as a solution containing the second binding agent flows through the membrane. The detection of bound second binding agent may then be performed as described above. In the strip test format, one end of the membrane to which binding agent is bound is immersed in a solution containing the sample. The sample migrates along the membrane through a region containing second binding agent and to the area of immobilized binding agent. Concentration of second binding agent at the area of immobilized antibody indicates the presence of a cancer. Typically, the concentration of second binding agent at that site generates a pattern, such as a line, that can be read visually. The absence of such a pattern indicates a negative result. In general, the amount of binding agent immobilized on the membrane is selected to generate a visually discernible pattern when the biological sample contains a level of polypeptide that would be sufficient to generate a positive signal in the two-antibody sandwich assay, in the format discussed above. Preferred binding agents for use in such assays are antibodies and antigen-binding fragments thereof. Preferably, the amount of antibody immobilized on the membrane ranges from about 25 ng to about 1 μg, and more preferably from about 50 ng to about 500 ng. Such tests can typically be performed with a very small amount of biological sample.

Of course, numerous other assay protocols exist that are suitable for use with the tumor proteins or binding agents of the present invention. The above descriptions are intended to be exemplary only. For example, it will be apparent to those of ordinary skill in the art that the above protocols may be readily modified to use tumor polypeptides to detect antibodies that bind to such polypeptides in a biological sample. The detection of such tumor protein specific antibodies may correlate with the presence of a cancer.

A cancer may also, or alternatively, be detected based on the presence of T cells that specifically react with a tumor protein in a biological sample. Within certain methods, a biological sample comprising $CD4^+$ and/or $CD8^+$ T cells isolated from a patient is incubated with a tumor polypeptide, a polynucleotide encoding such a polypeptide and/or an APC that expresses at least an immunogenic portion of such a polypeptide, and the presence or absence of specific activation of the T cells is detected. Suitable biological samples include, but are not limited to, isolated T cells. For example, T cells may be isolated from a patient by routine techniques (such as by Ficoll/Hypaque density gradient centrifugation of peripheral blood lymphocytes). T cells may be incubated *in vitro* for 2-9 days (typically 4 days) at 37°C with polypeptide (*e.g.*, 5 - 25 μg/ml). It may be desirable to incubate another aliquot of a T cell sample in the absence of tumor polypeptide to serve as a control. For $CD4^+$ T cells, activation is preferably detected by evaluating proliferation of the T cells. For $CD8^+$ T cells, activation is preferably detected by evaluating cytolytic activity. A level of proliferation that is at least two fold greater and/or a level of cytolytic activity that is at least 20% greater than in disease-free patients indicates the presence of a cancer in the patient.

As noted above, a cancer may also, or alternatively, be detected based on the level of mRNA encoding a tumor protein in a biological sample. For example, at least two oligonucleotide primers may be employed in a polymerase chain reaction (PCR) based assay to amplify a portion of a tumor cDNA derived from a biological sample, wherein at least one of the oligonucleotide primers is specific for (*i.e.*, hybridizes to) a polynucleotide encoding the tumor protein. The amplified cDNA is then separated and detected using techniques well known in the art, such as gel electrophoresis. Similarly, oligonucleotide probes that specifically hybridize to a polynucleotide encoding a tumor protein may be used in a hybridization assay to detect the presence of polynucleotide encoding the tumor protein in a biological sample.

To permit hybridization under assay conditions, oligonucleotide primers and probes should comprise an oligonucleotide sequence that has at least about 60%, preferably at least about 75% and more preferably at least about 90%, identity to a portion of a polynucleotide encoding a tumor protein of the invention that is at least 10

nucleotides, and preferably at least 20 nucleotides, in length. Preferably, oligonucleotide primers and/or probes hybridize to a polynucleotide encoding a polypeptide described herein under moderately stringent conditions, as defined above. Oligonucleotide primers and/or probes which may be usefully employed in the diagnostic methods described herein preferably are at least 10-40 nucleotides in length. In a preferred embodiment, the oligonucleotide primers comprise at least 10 contiguous nucleotides, more preferably at least 15 contiguous nucleotides, of a DNA molecule having a sequence as disclosed herein. Techniques for both PCR based assays and hybridization assays are well known in the art (*see*, for example, Mullis et al., *Cold Spring Harbor Symp. Quant. Biol.*, *51*:263, 1987; Erlich ed., *PCR Technology*, Stockton Press, NY, 1989).

One preferred assay employs RT-PCR, in which PCR is applied in conjunction with reverse transcription. Typically, RNA is extracted from a biological sample, such as biopsy tissue, and is reverse transcribed to produce cDNA molecules. PCR amplification using at least one specific primer generates a cDNA molecule, which may be separated and visualized using, for example, gel electrophoresis. Amplification may be performed on biological samples taken from a test patient and from an individual who is not afflicted with a cancer. The amplification reaction may be performed on several dilutions of cDNA spanning two orders of magnitude. A two-fold or greater increase in expression in several dilutions of the test patient sample as compared to the same dilutions of the non-cancerous sample is typically considered positive.

In another embodiment, the compositions described herein may be used as markers for the progression of cancer. In this embodiment, assays as described above for the diagnosis of a cancer may be performed over time, and the change in the level of reactive polypeptide(s) or polynucleotide(s) evaluated. For example, the assays may be performed every 24-72 hours for a period of 6 months to 1 year, and thereafter performed as needed. In general, a cancer is progressing in those patients in whom the level of polypeptide or polynucleotide detected increases over time. In contrast, the

cancer is not progressing when the level of reactive polypeptide or polynucleotide either remains constant or decreases with time.

Certain *in vivo* diagnostic assays may be performed directly on a tumor. One such assay involves contacting tumor cells with a binding agent. The bound binding agent may then be detected directly or indirectly via a reporter group. Such binding agents may also be used in histological applications. Alternatively, polynucleotide probes may be used within such applications.

As noted above, to improve sensitivity, multiple tumor protein markers may be assayed within a given sample. It will be apparent that binding agents specific for different proteins provided herein may be combined within a single assay. Further, multiple primers or probes may be used concurrently. The selection of tumor protein markers may be based on routine experiments to determine combinations that results in optimal sensitivity. In addition, or alternatively, assays for tumor proteins provided herein may be combined with assays for other known tumor antigens.

The present invention further provides kits for use within any of the above diagnostic methods. Such kits typically comprise two or more components necessary for performing a diagnostic assay. Components may be compounds, reagents, containers and/or equipment. For example, one container within a kit may contain a monoclonal antibody or fragment thereof that specifically binds to a tumor protein. Such antibodies or fragments may be provided attached to a support material, as described above. One or more additional containers may enclose elements, such as reagents or buffers, to be used in the assay. Such kits may also, or alternatively, contain a detection reagent as described above that contains a reporter group suitable for direct or indirect detection of antibody binding.

Alternatively, a kit may be designed to detect the level of mRNA encoding a tumor protein in a biological sample. Such kits generally comprise at least one oligonucleotide probe or primer, as described above, that hybridizes to a polynucleotide encoding a tumor protein. Such an oligonucleotide may be used, for example, within a PCR or hybridization assay. Additional components that may be

present within such kits include a second oligonucleotide and/or a diagnostic reagent or container to facilitate the detection of a polynucleotide encoding a tumor protein.

The following Examples are offered by way of illustration and not by way of limitation.

EXAMPLES

EXAMPLE 1

ISOLATION AND CHARACTERIZATION OF PROSTATE-SPECIFIC POLYPEPTIDES

This Example describes the isolation of certain prostate-specific polypeptides from a prostate tumor cDNA library.

A human prostate tumor cDNA expression library was constructed from prostate tumor poly A^+ RNA using a Superscript Plasmid System for cDNA Synthesis and Plasmid Cloning kit (BRL Life Technologies, Gaithersburg, MD 20897) following the manufacturer's protocol. Specifically, prostate tumor tissues were homogenized with polytron (Kinematica, Switzerland) and total RNA was extracted using Trizol reagent (BRL Life Technologies) as directed by the manufacturer. The poly A^+ RNA was then purified using a Qiagen oligotex spin column mRNA purification kit (Qiagen, Santa Clarita, CA 91355) according to the manufacturer's protocol. First-strand cDNA was synthesized using the NotI/Oligo-dT18 primer. Double-stranded cDNA was synthesized, ligated with EcoRI/BAXI adaptors (Invitrogen, San Diego, CA) and digested with NotI. Following size fractionation with Chroma Spin-1000 columns (Clontech, Palo Alto, CA), the cDNA was ligated into the EcoRI/NotI site of pCDNA3.1 (Invitrogen) and transformed into ElectroMax *E. coli* DH10B cells (BRL Life Technologies) by electroporation.

Using the same procedure, a normal human pancreas cDNA expression library was prepared from a pool of six tissue specimens (Clontech). The cDNA libraries were characterized by determining the number of independent colonies, the percentage of clones that carried insert, the average insert size and by sequence analysis. The prostate tumor library contained 1.64 x 10^7 independent colonies, with 70% of clones having an insert and the average insert size being 1745 base pairs. The normal pancreas cDNA library contained 3.3 x 10^6 independent colonies, with 69% of clones having inserts and the average insert size being 1120 base pairs. For both libraries,

sequence analysis showed that the majority of clones had a full length cDNA sequence and were synthesized from mRNA, with minimal rRNA and mitochondrial DNA contamination.

cDNA library subtraction was performed using the above prostate tumor and normal pancreas cDNA libraries, as described by Hara *et al.* (*Blood*, *84*:189-199, 1994) with some modifications. Specifically, a prostate tumor-specific subtracted cDNA library was generated as follows. Normal pancreas cDNA library (70 μg) was digested with EcoRI, NotI, and SfuI, followed by a filling-in reaction with DNA polymerase Klenow fragment. After phenol-chloroform extraction and ethanol precipitation, the DNA was dissolved in 100 μl of H_2O, heat-denatured and mixed with 100 μl (100 μg) of Photoprobe biotin (Vector Laboratories, Burlingame, CA). As recommended by the manufacturer, the resulting mixture was irradiated with a 270 W sunlamp on ice for 20 minutes. Additional Photoprobe biotin (50 μl) was added and the biotinylation reaction was repeated. After extraction with butanol five times, the DNA was ethanol-precipitated and dissolved in 23 μl H_2O to form the driver DNA.

To form the tracer DNA, 10 μg prostate tumor cDNA library was digested with BamHI and XhoI, phenol chloroform extracted and passed through Chroma spin-400 columns (Clontech). Following ethanol precipitation, the tracer DNA was dissolved in 5 μl H_2O. Tracer DNA was mixed with 15 μl driver DNA and 20 μl of 2 x hybridization buffer (1.5 M NaCl/10 mM EDTA/50 mM HEPES pH 7.5/0.2% sodium dodecyl sulfate), overlaid with mineral oil, and heat-denatured completely. The sample was immediately transferred into a 68 ^{0}C water bath and incubated for 20 hours (long hybridization [LH]). The reaction mixture was then subjected to a streptavidin treatment followed by phenol/chloroform extraction. This process was repeated three more times. Subtracted DNA was precipitated, dissolved in 12 μl H_2O, mixed with 8 μl driver DNA and 20 μl of 2 x hybridization buffer, and subjected to a hybridization at 68 ^{0}C for 2 hours (short hybridization [SH]). After removal of biotinylated double-stranded DNA, subtracted cDNA was ligated into BamHI/XhoI site of chloramphenicol resistant pBCSK$^+$ (Stratagene, La Jolla, CA 92037) and transformed into ElectroMax *E.*

coli DH10B cells by electroporation to generate a prostate tumor specific subtracted cDNA library (referred to as "prostate subtraction 1").

To analyze the subtracted cDNA library, plasmid DNA was prepared from 100 independent clones, randomly picked from the subtracted prostate tumor specific library and grouped based on insert size. Representative cDNA clones were further characterized by DNA sequencing with a Perkin Elmer/Applied Biosystems Division Automated Sequencer Model 373A (Foster City, CA). Six cDNA clones, hereinafter referred to as F1-13, F1-12, F1-16, H1-1, H1-9 and H1-4, were shown to be abundant in the subtracted prostate-specific cDNA library. The determined 3' and 5' cDNA sequences for F1-12 are provided in SEQ ID NO: 2 and 3, respectively, with determined 3' cDNA sequences for F1-13, F1-16, H1-1, H1-9 and H1-4 being provided in SEQ ID NO: 1 and 4-7, respectively.

The cDNA sequences for the isolated clones were compared to known sequences in the gene bank using the EMBL and GenBank databases (release 96). Four of the prostate tumor cDNA clones, F1-13, F1-16, H1-1, and H1-4, were determined to encode the following previously identified proteins: prostate specific antigen (PSA), human glandular kallikrein, human tumor expression enhanced gene, and mitochondria cytochrome C oxidase subunit II. H1-9 was found to be identical to a previously identified human autonomously replicating sequence. No significant homologies to the cDNA sequence for F1-12 were found.

Subsequent studies led to the isolation of a full-length cDNA sequence for F1-12 (also referred to as P504S). This sequence is provided in SEQ ID NO: 107, with the corresponding predicted amino acid sequence being provided in SEQ ID NO: 108. cDNA splice variants of P504S are provided in SEQ ID NO: 600-605.

To clone less abundant prostate tumor specific genes, cDNA library subtraction was performed by subtracting the prostate tumor cDNA library described above with the normal pancreas cDNA library and with the three most abundant genes in the previously subtracted prostate tumor specific cDNA library: human glandular kallikrein, prostate specific antigen (PSA), and mitochondria cytochrome C oxidase subunit II. Specifically, 1 μg each of human glandular kallikrein, PSA and

mitochondria cytochrome C oxidase subunit II cDNAs in pCDNA3.1 were added to the driver DNA and subtraction was performed as described above to provide a second subtracted cDNA library hereinafter referred to as the "subtracted prostate tumor specific cDNA library with spike".

Twenty-two cDNA clones were isolated from the subtracted prostate tumor specific cDNA library with spike. The determined 3' and 5' cDNA sequences for the clones referred to as J1-17, L1-12, N1-1862, J1-13, J1-19, J1-25, J1-24, K1-58, K1-63, L1-4 and L1-14 are provided in SEQ ID NOS: 8-9, 10-11, 12-13, 14-15, 16-17, 18-19, 20-21, 22-23, 24-25, 26-27 and 28-29, respectively. The determined 3' cDNA sequences for the clones referred to as J1-12, J1-16, J1-21, K1-48, K1-55, L1-2, L1-6, N1-1858, N1-1860, N1-1861, N1-1864 are provided in SEQ ID NOS: 30-40, respectively. Comparison of these sequences with those in the gene bank as described above, revealed no significant homologies to three of the five most abundant DNA species, (J1-17, L1-12 and N1-1862; SEQ ID NOS: 8-9, 10-11 and 12-13, respectively). Of the remaining two most abundant species, one (J1-12; SEQ ID NO:30) was found to be identical to the previously identified human pulmonary surfactant-associated protein, and the other (K1-48; SEQ ID NO:33) was determined to have some homology to *R. norvegicus* mRNA for 2-arylpropionyl-CoA epimerase. Of the 17 less abundant cDNA clones isolated from the subtracted prostate tumor specific cDNA library with spike, four (J1-16, K1-55, L1-6 and N1-1864; SEQ ID NOS:31, 34, 36 and 40, respectively) were found to be identical to previously identified sequences, two (J1-21 and N1-1860; SEQ ID NOS: 32 and 38, respectively) were found to show some homology to non-human sequences, and two (L1-2 and N1-1861; SEQ ID NOS: 35 and 39, respectively) were found to show some homology to known human sequences. No significant homologies were found to the polypeptides J1-13, J1-19, J1-24, J1-25, K1-58, K1-63, L1-4, L1-14 (SEQ ID NOS: 14-15, 16-17, 20-21, 18-19, 22-23, 24-25, 26-27, 28-29, respectively).

Subsequent studies led to the isolation of full length cDNA sequences for J1-17, L1-12 and N1-1862 (SEQ ID NOS: 109-111, respectively). The corresponding

predicted amino acid sequences are provided in SEQ ID NOS: 112-114. L1-12 is also referred to as P501S. A cDNA splice variant of P501S is provided in SEQ ID NO: 606.

In a further experiment, four additional clones were identified by subtracting a prostate tumor cDNA library with normal prostate cDNA prepared from a pool of three normal prostate poly A+ RNA (referred to as "prostate subtraction 2"). The determined cDNA sequences for these clones, hereinafter referred to as U1-3064, U1-3065, V1-3692 and 1A-3905, are provided in SEQ ID NO: 69-72, respectively. Comparison of the determined sequences with those in the gene bank revealed no significant homologies to U1-3065.

A second subtraction with spike (referred to as "prostate subtraction spike 2") was performed by subtracting a prostate tumor specific cDNA library with spike with normal pancreas cDNA library and further spiked with PSA, J1-17, pulmonary surfactant-associated protein, mitochondrial DNA, cytochrome c oxidase subunit II, N1-1862, autonomously replicating sequence, L1-12 and tumor expression enhanced gene. Four additional clones, hereinafter referred to as V1-3686, R1-2330, 1B-3976 and V1-3679, were isolated. The determined cDNA sequences for these clones are provided in SEQ ID NO:73-76, respectively. Comparison of these sequences with those in the gene bank revealed no significant homologies to V1-3686 and R1-2330.

Further analysis of the three prostate subtractions described above (prostate subtraction 2, subtracted prostate tumor specific cDNA library with spike, and prostate subtraction spike 2) resulted in the identification of sixteen additional clones, referred to as 1G-4736, 1G-4738, 1G-4741, 1G-4744, 1G-4734, 1H-4774, 1H-4781, 1H-4785, 1H-4787, 1H-4796, 1I-4810, 1I-4811, 1J-4876, 1K-4884 and 1K-4896. The determined cDNA sequences for these clones are provided in SEQ ID NOS: 77-92, respectively. Comparison of these sequences with those in the gene bank as described above, revealed no significant homologies to 1G-4741, 1G-4734, 1I-4807, 1J-4876 and 1K-4896 (SEQ ID NOS: 79, 81, 87, 90 and 92, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1G-4736, 1G-4738, 1G-4741, 1G-4744, 1H-4774, 1H-4781, 1H-4785, 1H-4787, 1H-4796, 1I-4807,

1J-4876, 1K-4884 and 1K-4896, provided in SEQ ID NOS: 179-188 and 191-193, respectively, and to the determination of additional partial cDNA sequences for 1I-4810 and 1I-4811, provided in SEQ ID NOS: 189 and 190, respectively.

Additional studies with prostate subtraction spike 2 resulted in the isolation of three more clones. Their sequences were determined as described above and compared to the most recent GenBank. All three clones were found to have homology to known genes, which are Cysteine-rich protein, KIAA0242, and KIAA0280 (SEQ ID NO: 317, 319, and 320, respectively). Further analysis of these clones by Synteni microarray (Synteni, Palo Alto, CA) demonstrated that all three clones were over-expressed in most prostate tumors and prostate BPH, as well as in the majority of normal prostate tissues tested, but low expression in all other normal tissues.

An additional subtraction was performed by subtracting a normal prostate cDNA library with normal pancreas cDNA (referred to as "prostate subtraction 3"). This led to the identification of six additional clones referred to as 1G-4761, 1G-4762, 1H-4766, 1H-4770, 1H-4771 and 1H-4772 (SEQ ID NOS: 93-98). Comparison of these sequences with those in the gene bank revealed no significant homologies to 1G-4761 and 1H-4771 (SEQ ID NOS: 93 and 97, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1G-4761, 1G-4762, 1H-4766 and 1H-4772 provided in SEQ ID NOS: 194-196 and 199, respectively, and to the determination of additional partial cDNA sequences for 1H-4770 and 1H-4771, provided in SEQ ID NOS: 197 and 198, respectively.

Subtraction of a prostate tumor cDNA library, prepared from a pool of polyA+ RNA from three prostate cancer patients, with a normal pancreas cDNA library (prostate subtraction 4) led to the identification of eight clones, referred to as 1D-4297, 1D-4309, 1D.1-4278, 1D-4288, 1D-4283, 1D-4304, 1D-4296 and 1D-4280 (SEQ ID NOS: 99-107). These sequences were compared to those in the gene bank as described above. No significant homologies were found to 1D-4283 and 1D-4304 (SEQ ID NOS: 103 and 104, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1D-4309, 1D.1-4278, 1D-4288, 1D-

4283, 1D-4304, 1D-4296 and 1D-4280, provided in SEQ ID NOS: 200-206, respectively.

cDNA clones isolated in prostate subtraction 1 and prostate subtraction 2, described above, were colony PCR amplified and their mRNA expression levels in prostate tumor, normal prostate and in various other normal tissues were determined using microarray technology (Synteni, Palo Alto, CA). Briefly, the PCR amplification products were dotted onto slides in an array format, with each product occupying a unique location in the array. mRNA was extracted from the tissue sample to be tested, reverse transcribed, and fluorescent-labeled cDNA probes were generated. The microarrays were probed with the labeled cDNA probes, the slides scanned and fluorescence intensity was measured. This intensity correlates with the hybridization intensity. Two clones (referred to as P509S and P510S) were found to be over-expressed in prostate tumor and normal prostate and expressed at low levels in all other normal tissues tested (liver, pancreas, skin, bone marrow, brain, breast, adrenal gland, bladder, testes, salivary gland, large intestine, kidney, ovary, lung, spinal cord, skeletal muscle and colon). The determined cDNA sequences for P509S and P510S are provided in SEQ ID NO: 223 and 224, respectively. Comparison of these sequences with those in the gene bank as described above, revealed some homology to previously identified ESTs.

Additional, studies led to the isolation of the full-length cDNA sequence for P509S. This sequence is provided in SEQ ID NO: 332, with the corresponding predicted amino acid sequence being provided in SEQ ID NO: 339. Two variant full-length cDNA sequences for P510S are provided in SEQ ID NO: 535 and 536, with the corresponding predicted amino acid sequences being provided in SEQ ID NO: 537 and 538, respectively. Additional splice variants of P510S are provided in SEQ ID NO: 598 and 599.

The determined cDNA sequences for additional prostate-specific clones isolated during characterization of prostate specific cDNA libraries are provided in SEQ ID NO: 618-689, 691-697 and 709-772. Comparison of these sequences with those in the public databases revealed no significant homologies to any of these sequences.

EXAMPLE 2

DETERMINATION OF TISSUE SPECIFICITY OF PROSTATE-SPECIFIC POLYPEPTIDES

Using gene specific primers, mRNA expression levels for the representative prostate-specific polypeptides F1-16, H1-1, J1-17 (also referred to as P502S), L1-12 (also referred to as P501S), F1-12 (also referred to as P504S) and N1-1862 (also referred to as P503S) were examined in a variety of normal and tumor tissues using RT-PCR.

Briefly, total RNA was extracted from a variety of normal and tumor tissues using Trizol reagent as described above. First strand synthesis was carried out using 1-2 μg of total RNA with SuperScript II reverse transcriptase (BRL Life Technologies) at 42 ^{0}C for one hour. The cDNA was then amplified by PCR with gene-specific primers. To ensure the semi-quantitative nature of the RT-PCR, β-actin was used as an internal control for each of the tissues examined. First, serial dilutions of the first strand cDNAs were prepared and RT-PCR assays were performed using β-actin specific primers. A dilution was then chosen that enabled the linear range amplification of the β-actin template and which was sensitive enough to reflect the differences in the initial copy numbers. Using these conditions, the β-actin levels were determined for each reverse transcription reaction from each tissue. DNA contamination was minimized by DNase treatment and by assuring a negative PCR result when using first strand cDNA that was prepared without adding reverse transcriptase.

mRNA Expression levels were examined in four different types of tumor tissue (prostate tumor from 2 patients, breast tumor from 3 patients, colon tumor, lung tumor), and sixteen different normal tissues, including prostate, colon, kidney, liver, lung, ovary, pancreas, skeletal muscle, skin, stomach, testes, bone marrow and brain. F1-16 was found to be expressed at high levels in prostate tumor tissue, colon tumor and normal prostate, and at lower levels in normal liver, skin and testes, with expression being undetectable in the other tissues examined. H1-1 was found to be expressed at high levels in prostate tumor, lung tumor, breast tumor, normal prostate, normal colon

and normal brain, at much lower levels in normal lung, pancreas, skeletal muscle, skin, small intestine, bone marrow, and was not detected in the other tissues tested. J1-17 (P502S) and L1-12 (P501S) appear to be specifically over-expressed in prostate, with both genes being expressed at high levels in prostate tumor and normal prostate but at low to undetectable levels in all the other tissues examined. N1-1862 (P503S) was found to be over-expressed in 60% of prostate tumors and detectable in normal colon and kidney. The RT-PCR results thus indicate that F1-16, H1-1, J1-17 (P502S), N1-1862 (P503S) and L1-12 (P501S) are either prostate specific or are expressed at significantly elevated levels in prostate.

Further RT-PCR studies showed that F1-12 (P504S) is over-expressed in 60% of prostate tumors, detectable in normal kidney but not detectable in all other tissues tested. Similarly, R1-2330 was shown to be over-expressed in 40% of prostate tumors, detectable in normal kidney and liver, but not detectable in all other tissues tested. U1-3064 was found to be over-expressed in 60% of prostate tumors, and also expressed in breast and colon tumors, but was not detectable in normal tissues.

RT-PCR characterization of R1-2330, U1-3064 and 1D-4279 showed that these three antigens are over-expressed in prostate and/or prostate tumors.

Northern analysis with four prostate tumors, two normal prostate samples, two BPH prostates, and normal colon, kidney, liver, lung, pancrease, skeletal muscle, brain, stomach, testes, small intestine and bone marrow, showed that L1-12 (P501S) is over-expressed in prostate tumors and normal prostate, while being undetectable in other normal tissues tested. J1-17 (P502S) was detected in two prostate tumors and not in the other tissues tested. N1-1862 (P503S) was found to be over-expressed in three prostate tumors and to be expressed in normal prostate, colon and kidney, but not in other tissues tested. F1-12 (P504S) was found to be highly expressed in two prostate tumors and to be undetectable in all other tissues tested.

The microarray technology described above was used to determine the expression levels of representative antigens described herein in prostate tumor, breast tumor and the following normal tissues: prostate, liver, pancreas, skin, bone marrow, brain, breast, adrenal gland, bladder, testes, salivary gland, large intestine, kidney,

ovary, lung, spinal cord, skeletal muscle and colon. L1-12 (P501S) was found to be over-expressed in normal prostate and prostate tumor, with some expression being detected in normal skeletal muscle. Both J1-12 and F1-12 (P504S) were found to be over-expressed in prostate tumor, with expression being lower or undetectable in all other tissues tested. N1-1862 (P503S) was found to be expressed at high levels in prostate tumor and normal prostate, and at low levels in normal large intestine and normal colon, with expression being undetectable in all other tissues tested. R1-2330 was found to be over-expressed in prostate tumor and normal prostate, and to be expressed at lower levels in all other tissues tested. 1D-4279 was found to be over-expressed in prostate tumor and normal prostate, expressed at lower levels in normal spinal cord, and to be undetectable in all other tissues tested.

Further microarray analysis to specifically address the extent to which P501S (SEQ ID NO: 110) was expressed in breast tumor revealed moderate over-expression not only in breast tumor, but also in metastatic breast tumor (2/31), with negligible to low expression in normal tissues. This data suggests that P501S may be over-expressed in various breast tumors as well as in prostate tumors.

The expression levels of 32 ESTs (expressed sequence tags) described by Vasmatzis *et al.* (*Proc. Natl. Acad. Sci. USA 95*:300-304, 1998) in a variety of tumor and normal tissues were examined by microarray technology as described above. Two of these clones (referred to as P1000C and P1001C) were found to be over-expressed in prostate tumor and normal prostate, and expressed at low to undetectable levels in all other tissues tested (normal aorta, thymus, resting and activated PBMC, epithelial cells, spinal cord, adrenal gland, fetal tissues, skin, salivary gland, large intestine, bone marrow, liver, lung, dendritic cells, stomach, lymph nodes, brain, heart, small intestine, skeletal muscle, colon and kidney. The determined cDNA sequences for P1000C and P1001C are provided in SEQ ID NO: 384 and 472, respectively. The sequence of P1001C was found to show some homology to the previously isolated Human mRNA for JM27 protein. Subsequent comparison of the sequence of SEQ ID NO: 384 with sequences in the public databases, led to the identification of a full-length cDNA sequence of P1000C (SEQ ID NO: 929), which encodes a 492 amino acid sequence.

Analysis of the amino acid sequence using the PSORT II program led to the identification of a putative transmembrane domain from amino acids 84-100. The cDNA sequence of the open reading frame of P1000C, including the stop codon, is provided in SEQ ID NO: 930, with the open reading frame without the stop codon being provided in SEQ ID NO: 931. The full-length amino acid sequence of P1000C is provided in SEQ ID NO: 932. SEQ ID NO: 933 and 934 represent amino acids 1-100 and 100-492 of P1000C, respectively.

The expression of the polypeptide encoded by the full length cDNA sequence for F1-12 (also referred to as P504S; SEQ ID NO: 108) was investigated by immunohistochemical analysis. Rabbit-anti-P504S polyclonal antibodies were generated against the full length P504S protein by standard techniques. Subsequent isolation and characterization of the polyclonal antibodies were also performed by techniques well known in the art. Immunohistochemical analysis showed that the P504S polypeptide was expressed in 100% of prostate carcinoma samples tested (n=5).

The rabbit-anti-P504S polyclonal antibody did not appear to label benign prostate cells with the same cytoplasmic granular staining, but rather with light nuclear staining. Analysis of normal tissues revealed that the encoded polypeptide was found to be expressed in some, but not all normal human tissues. Positive cytoplasmic staining with rabbit-anti-P504S polyclonal antibody was found in normal human kidney, liver, brain, colon and lung-associated macrophages, whereas heart and bone marrow were negative.

This data indicates that the P504S polypeptide is present in prostate cancer tissues, and that there are qualitative and quantitative differences in the staining between benign prostatic hyperplasia tissues and prostate cancer tissues, suggesting that this polypeptide may be detected selectively in prostate tumors and therefore be useful in the diagnosis of prostate cancer.

EXAMPLE 3

ISOLATION AND CHARACTERIZATION OF PROSTATE-SPECIFIC POLYPEPTIDES BY PCR-BASED SUBTRACTION

A cDNA subtraction library, containing cDNA from normal prostate subtracted with ten other normal tissue cDNAs (brain, heart, kidney, liver, lung, ovary, placenta, skeletal muscle, spleen and thymus) and then submitted to a first round of PCR amplification, was purchased from Clontech. This library was subjected to a second round of PCR amplification, following the manufacturer's protocol. The resulting cDNA fragments were subcloned into the vector pT7 Blue T-vector (Novagen, Madison, WI) and transformed into XL-1 Blue MRF' *E. coli* (Stratagene). DNA was isolated from independent clones and sequenced using a Perkin Elmer/Applied Biosystems Division Automated Sequencer Model 373A.

Fifty-nine positive clones were sequenced. Comparison of the DNA sequences of these clones with those in the gene bank, as described above, revealed no significant homologies to 25 of these clones, hereinafter referred to as P5, P8, P9, P18, P20, P30, P34, P36, P38, P39, P42, P49, P50, P53, P55, P60, P64, P65, P73, P75, P76, P79 and P84. The determined cDNA sequences for these clones are provided in SEQ ID NO: 41-45, 47-52 and 54-65, respectively. P29, P47, P68, P80 and P82 (SEQ ID NO: 46, 53 and 66-68, respectively) were found to show some degree of homology to previously identified DNA sequences. To the best of the inventors' knowledge, none of these sequences have been previously shown to be present in prostate.

Further studies employing the sequence of SEQ ID NO: 67 as a probe in standard full-length cloning methods, resulted in the isolation of three cDNA sequences which appear to be splice variants of P80 (also known as P704P). These sequences are provided in SEQ ID NO: 699-701.

Further studies using the PCR-based methodology described above resulted in the isolation of more than 180 additional clones, of which 23 clones were found to show no significant homologies to known sequences. The determined cDNA sequences for these clones are provided in SEQ ID NO: 115-123, 127, 131, 137, 145,

147-151, 153, 156-158 and 160. Twenty-three clones (SEQ ID NO: 124-126, 128-130, 132-136, 138-144, 146, 152, 154, 155 and 159) were found to show some homology to previously identified ESTs. An additional ten clones (SEQ ID NO: 161-170) were found to have some degree of homology to known genes. Larger cDNA clones containing the P20 sequence represent splice variants of a gene referred to as P703P. The determined DNA sequence for the variants referred to as DE1, DE13 and DE14 are provided in SEQ ID NOS: 171, 175 and 177, respectively, with the corresponding predicted amino acid sequences being provided in SEQ ID NO: 172, 176 and 178, respectively. The determined cDNA sequence for an extended spliced form of P703 is provided in SEQ ID NO: 225. The DNA sequences for the splice variants referred to as DE2 and DE6 are provided in SEQ ID NOS: 173 and 174, respectively.

mRNA Expression levels for representative clones in tumor tissues (prostate (n=5), breast (n=2), colon and lung) normal tissues (prostate (n=5), colon, kidney, liver, lung (n=2), ovary (n=2), skeletal muscle, skin, stomach, small intestine and brain), and activated and non-activated PBMC was determined by RT-PCR as described above. Expression was examined in one sample of each tissue type unless otherwise indicated.

P9 was found to be highly expressed in normal prostate and prostate tumor compared to all normal tissues tested except for normal colon which showed comparable expression. P20, a portion of the P703P gene, was found to be highly expressed in normal prostate and prostate tumor, compared to all twelve normal tissues tested. A modest increase in expression of P20 in breast tumor (n=2), colon tumor and lung tumor was seen compared to all normal tissues except lung (1 of 2). Increased expression of P18 was found in normal prostate, prostate tumor and breast tumor compared to other normal tissues except lung and stomach. A modest increase in expression of P5 was observed in normal prostate compared to most other normal tissues. However, some elevated expression was seen in normal lung and PBMC. Elevated expression of P5 was also observed in prostate tumors (2 of 5), breast tumor and one lung tumor sample. For P30, similar expression levels were seen in normal prostate and prostate tumor, compared to six of twelve other normal tissues tested.

Increased expression was seen in breast tumors, one lung tumor sample and one colon tumor sample, and also in normal PBMC. P29 was found to be over-expressed in prostate tumor (5 of 5) and normal prostate (5 of 5) compared to the majority of normal tissues. However, substantial expression of P29 was observed in normal colon and normal lung (2 of 2). P80 was found to be over-expressed in prostate tumor (5 of 5) and normal prostate (5 of 5) compared to all other normal tissues tested, with increased expression also being seen in colon tumor.

Further studies resulted in the isolation of twelve additional clones, hereinafter referred to as 10-d8, 10-h10, 11-c8, 7-g6, 8-b5, 8-b6, 8-d4, 8-d9, 8-g3, 8-h11, 9-f12 and 9-f3. The determined DNA sequences for 10-d8, 10-h10, 11-c8, 8-d4, 8-d9, 8-h11, 9-f12 and 9-f3 are provided in SEQ ID NO: 207, 208, 209, 216, 217, 220, 221 and 222, respectively. The determined forward and reverse DNA sequences for 7-g6, 8-b5, 8-b6 and 8-g3 are provided in SEQ ID NO: 210 and 211; 212 and 213; 214 and 215; and 218 and 219, respectively. Comparison of these sequences with those in the gene bank revealed no significant homologies to the sequence of 9-f3. The clones 10-d8, 11-c8 and 8-h11 were found to show some homology to previously isolated ESTs, while 10-h10, 8-b5, 8-b6, 8-d4, 8-d9, 8-g3 and 9-f12 were found to show some homology to previously identified genes. Further characterization of 7-G6 and 8-G3 showed identity to the known genes PAP and PSA, respectively.

mRNA expression levels for these clones were determined using the micro-array technology described above. The clones 7-G6, 8-G3, 8-B5, 8-B6, 8-D4, 8-D9, 9-F3, 9-F12, 9-H3, 10-A2, 10-A4, 11-C9 and 11-F2 were found to be over-expressed in prostate tumor and normal prostate, with expression in other tissues tested being low or undetectable. Increased expression of 8-F11 was seen in prostate tumor and normal prostate, bladder, skeletal muscle and colon. Increased expression of 10-H10 was seen in prostate tumor and normal prostate, bladder, lung, colon, brain and large intestine. Increased expression of 9-B1 was seen in prostate tumor, breast tumor, and normal prostate, salivary gland, large intestine and skin, with increased expression of 11-C8 being seen in prostate tumor, and normal prostate and large intestine.

An additional cDNA fragment derived from the PCR-based normal prostate subtraction, described above, was found to be prostate specific by both micro-array technology and RT-PCR. The determined cDNA sequence of this clone (referred to as 9-A11) is provided in SEQ ID NO: 226. Comparison of this sequence with those in the public databases revealed 99% identity to the known gene HOXB13.

Further studies led to the isolation of the clones 8-C6 and 8-H7. The determined cDNA sequences for these clones are provided in SEQ ID NO: 227 and 228, respectively. These sequences were found to show some homology to previously isolated ESTs.

PCR and hybridization-based methodologies were employed to obtain longer cDNA sequences for clone P20 (also referred to as P703P), yielding three additional cDNA fragments that progressively extend the 5' end of the gene. These fragments, referred to as P703PDE5, P703P6.26, and P703PX-23 (SEQ ID NO: 326, 328 and 330, with the predicted corresponding amino acid sequences being provided in SEQ ID NO: 327, 329 and 331, respectively) contain additional 5' sequence. P703PDE5 was recovered by screening of a cDNA library (#141-26) with a portion of P703P as a probe. P703P6.26 was recovered from a mixture of three prostate tumor cDNAs and P703PX_23 was recovered from cDNA library (#438-48). Together, the additional sequences include all of the putative mature serine protease along with part of the putative signal sequence. The full-length cDNA sequence for P703P is provided in SEQ ID NO: 524, with the corresponding amino acid sequence being provided in SEQ ID NO: 525.

Using computer algorithms, the following regions of P703P were predicted to represent potential HLA A2-binding CTL epitopes: amino acids 164-172 of SEQ ID NO: 525 (SEQ ID NO: 866); amino acids 160-168 of SEQ ID NO: 525 (SEQ ID NO: 867); amino acids 239-247 of SEQ ID NO: 525 (SEQ ID NO: 868); amino acids 118-126 of SEQ ID NO: 525 (SEQ ID NO: 869); amino acids 112-120 of SEQ ID NO: 525 (SEQ ID NO: 870); amino acids 155-164 of SEQ ID NO: 525 (SEQ ID NO: 871); amino acids 117-126 of SEQ ID NO: 525 (SEQ ID NO: 872); amino acids 164-173 of SEQ ID NO: 525 (SEQ ID NO: 873); amino acids 154-163 of SEQ ID NO:

525 (SEQ ID NO: 874); amino acids 163-172 of SEQ ID NO: 525 (SEQ ID NO: 875); amino acids 58-66 of SEQ ID NO: 525 (SEQ ID NO: 876); and amino acids 59-67 of SEQ ID NO: 525 (SEQ ID NO: 877).

P703P was found to show some homology to previously identified proteases, such as thrombin. The thrombin receptor has been shown to be preferentially expressed in highly metastatic breast carcinoma cells and breast carcinoma biopsy samples. Introduction of thrombin receptor antisense cDNA has been shown to inhibit the invasion of metastatic breast carcinoma cells in culture. Antibodies against thrombin receptor inhibit thrombin receptor activation and thrombin-induced platelet activation. Furthermore, peptides that resemble the receptor's tethered ligand domain inhibit platelet aggregation by thrombin. P703P may play a role in prostate cancer through a protease-activated receptor on the cancer cell or on stromal cells. The potential trypsin-like protease activity of P703P may either activate a protease-activated receptor on the cancer cell membrane to promote tumorgenesis or activate a protease-activated receptor on the adjacent cells (such as stromal cells) to secrete growth factors and/or proteases (such as matrix metalloproteinases) that could promote tumor angiogenesis, invasion and metastasis. P703P may thus promote tumor progression and/or metastasis through the activation of protease-activated receptor. Polypeptides and antibodies that block the P703P-receptor interaction may therefore be usefully employed in the treatment of prostate cancer.

To determine whether P703P expression increases with increased severity of Gleason grade, an indicator of tumor stage, quantitative PCR analysis was performed on prostate tumor samples with a range of Gleason scores from 5 to > 8. The mean level of P703P expression increased with increasing Gleason score, indicating that P703P expression may correlate with increased disease severity.

Further studies using a PCR-based subtraction library of a prostate tumor pool subtracted against a pool of normal tissues (referred to as JP: PCR subtraction) resulted in the isolation of thirteen additional clones, seven of which did not share any significant homology to known GenBank sequences. The determined cDNA sequences for these seven clones (P711P, P712P, novel 23, P774P, P775P, P710P and P768P) are

provided in SEQ ID NO: 307-311, 313 and 315, respectively. The remaining six clones (SEQ ID NO: 316 and 321-325) were shown to share some homology to known genes. By microarray analysis, all thirteen clones showed three or more fold over-expression in prostate tissues, including prostate tumors, BPH and normal prostate as compared to normal non-prostate tissues. Clones P711P, P712P, novel 23 and P768P showed over-expression in most prostate tumors and BPH tissues tested (n=29), and in the majority of normal prostate tissues (n=4), but background to low expression levels in all normal tissues. Clones P774P, P775P and P710P showed comparatively lower expression and expression in fewer prostate tumors and BPH samples, with negative to low expression in normal prostate.

Further studies led to the isolation of an extended cDNA sequence for P712P (SEQ ID NO: 552). The amino acid sequences encoded by 16 predicted open reading frames present within the sequence of SEQ ID NO: 552 are provided in SEQ ID NO: 553-568.

The full-length cDNA for P711P was obtained by employing the partial sequence of SEQ ID NO: 307 to screen a prostate cDNA library. Specifically, a directionally cloned prostate cDNA library was prepared using standard techniques. One million colonies of this library were plated onto LB/Amp plates. Nylon membrane filters were used to lift these colonies, and the cDNAs which were picked up by these filters were denatured and cross-linked to the filters by UV light. The P711P cDNA fragment of SEQ ID NO: 307 was radio-labeled and used to hybridize with these filters. Positive clones were selected, and cDNAs were prepared and sequenced using an automatic Perkin Elmer/Applied Biosystems sequencer. The determined full-length sequence of P711P is provided in SEQ ID NO: 382, with the corresponding predicted amino acid sequence being provided in SEQ ID NO: 383.

Using PCR and hybridization-based methodologies, additional cDNA sequence information was derived for two clones described above, 11-C9 and 9-F3, herein after referred to as P707P and P714P, respectively (SEQ ID NO: 333 and 334). After comparison with the most recent GenBank, P707P was found to be a splice variant of the known gene HoxB13. In contrast, no significant homologies to P714P

were found. Further studies employing the sequence of SEQ ID NO: 334 as a probe in standard full-length cloning methods, resulted in an extended cDNA sequence for P714P. This sequence is provided in SEQ ID NO: 698. This sequence was found to show some homology to the gene that encodes human ribosomal L23A protein.

Clones 8-B3, P89, P98, P130 and P201 (as disclosed in U.S. Patent Application No. 09/020,956, filed February 9, 1998) were found to be contained within one contiguous sequence, referred to as P705P (SEQ ID NO: 335, with the predicted amino acid sequence provided in SEQ ID NO: 336), which was determined to be a splice variant of the known gene NKX 3.1.

Further studies on P775P resulted in the isolation of four additional sequences (SEQ ID NO: 473-476) which are all splice variants of the P775P gene. The sequence of SEQ ID NO: 474 was found to contain two open reading frames (ORFs). The predicted amino acid sequences encoded by these ORFs are provided in SEQ ID NO: 477 and 478. The cDNA sequence of SEQ ID NO: 475 was found to contain an ORF which encodes the amino acid sequence of SEQ ID NO: 479. The cDNA sequence of SEQ ID NO: 473 was found to contain four ORFs. The predicted amino acid sequences encoded by these ORFs are provided in SEQ ID NO: 480-483. Additional splice variants of P775P are provided in SEQ ID NO: 593-597.

Subsequent studies led to the identification of a genomic region on chromosome 22q11.2, known as the Cat Eye Syndrome region, that contains the five prostate genes P704P, P712P, P774P, P775P and B305D. The relative location of each of these five genes within the genomic region is shown in Fig. 10. This region may therefore be associated with malignant tumors, and other potential tumor genes may be contained within this region. These studies also led to the identification of a potential open reading frame (ORF) for P775P (provided in SEQ ID NO: 533), which encodes the amino acid sequence of SEQ ID NO: 534.

Comparison of the clone of SEQ ID NO: 325 (referred to as P558S) with sequences in the GenBank and GeneSeq DNA databases showed that P558S is identical to the prostate-specific transglutaminase gene, which is known to have two forms. The full-length sequences for the two forms are provided in SEQ ID NO: 773 and 774, with

the corresponding amino acid sequences being provided in SEQ ID NO: 775 and 776, respectively. The cDNA sequence of SEQ ID NO: 774 has a 15 pair base insert, resulting in a 5 amino acid insert in the corresponding amino acid sequence (SEQ ID NO: 776). This insert is not present in the sequence of SEQ ID NO: 773.

Further studies on P768P (SEQ ID NO: 315) led to the identification of the putative full-length open reading frame (ORF). The cDNA sequence of the ORF with stop codon is provided in SEQ ID NO: 907. The cDNA sequence of the ORF without stop codon is provided in SEQ ID NO: 908, with the corresponding amino acid sequence being provided in SEQ ID NO: 909. This sequence was found to show 86% identity to a rat calcium transporter protein, indicating that P768P may represent a human calcium transporter protein. The locations of transmembrane domains within P768P were predicted using the PSORT II computer algorithm. Six transmembrane domains were predicted at amino acid positions 118-134, 172-188, 211-227, 230-246, 282-298 and 348-364. The amino acid sequences of SEQ ID NO: 910-915 represent amino acids 1-134, 135-188, 189-227, 228-246, 247-298 and 299-511 of P768P, respectively.

EXAMPLE 4

SYNTHESIS OF POLYPEPTIDES

Polypeptides may be synthesized on a Perkin Elmer/Applied Biosystems 430A peptide synthesizer using FMOC chemistry with HPTU (O-Benzotriazole-N,N,N',N'-tetramethyluronium hexafluorophosphate) activation. A Gly-Cys-Gly sequence may be attached to the amino terminus of the peptide to provide a method of conjugation, binding to an immobilized surface, or labeling of the peptide. Cleavage of the peptides from the solid support may be carried out using the following cleavage mixture: trifluoroacetic acid:ethanedithiol:thioanisole:water:phenol (40:1:2:2:3). After cleaving for 2 hours, the peptides may be precipitated in cold methyl-t-butyl-ether. The peptide pellets may then be dissolved in water containing 0.1% trifluoroacetic acid (TFA) and lyophilized prior to purification by C18 reverse phase HPLC. A gradient of

0%-60% acetonitrile (containing 0.1% TFA) in water (containing 0.1% TFA) may be used to elute the peptides. Following lyophilization of the pure fractions, the peptides may be characterized using electrospray or other types of mass spectrometry and by amino acid analysis.

EXAMPLE 5

FURTHER ISOLATION AND CHARACTERIZATION OF PROSTATE-SPECIFIC POLYPEPTIDES BY PCR-BASED SUBTRACTION

A cDNA library generated from prostate primary tumor mRNA as described above was subtracted with cDNA from normal prostate. The subtraction was performed using a PCR-based protocol (Clontech), which was modified to generate larger fragments. Within this protocol, tester and driver double stranded cDNA were separately digested with five restriction enzymes that recognize six-nucleotide restriction sites (MluI, MscI, PvuII, SalI and StuI). This digestion resulted in an average cDNA size of 600 bp, rather than the average size of 300 bp that results from digestion with RsaI according to the Clontech protocol. This modification did not affect the subtraction efficiency. Two tester populations were then created with different adapters, and the driver library remained without adapters.

The tester and driver libraries were then hybridized using excess driver cDNA. In the first hybridization step, driver was separately hybridized with each of the two tester cDNA populations. This resulted in populations of (a) unhybridized tester cDNAs, (b) tester cDNAs hybridized to other tester cDNAs, (c) tester cDNAs hybridized to driver cDNAs and (d) unhybridized driver cDNAs. The two separate hybridization reactions were then combined, and rehybridized in the presence of additional denatured driver cDNA. Following this second hybridization, in addition to populations (a) through (d), a fifth population (e) was generated in which tester cDNA with one adapter hybridized to tester cDNA with the second adapter. Accordingly, the second hybridization step resulted in enrichment of differentially expressed sequences which could be used as templates for PCR amplification with adaptor-specific primers.

The ends were then filled in, and PCR amplification was performed using adaptor-specific primers. Only population (e), which contained tester cDNA that did not hybridize to driver cDNA, was amplified exponentially. A second PCR amplification step was then performed, to reduce background and further enrich differentially expressed sequences.

This PCR-based subtraction technique normalizes differentially expressed cDNAs so that rare transcripts that are overexpressed in prostate tumor tissue may be recoverable. Such transcripts would be difficult to recover by traditional subtraction methods.

In addition to genes known to be overexpressed in prostate tumor, seventy-seven further clones were identified. Sequences of these partial cDNAs are provided in SEQ ID NO: 29 to 305. Most of these clones had no significant homology to database sequences. Exceptions were JPTPN23 (SEQ ID NO: 231; similarity to pig valosin-containing protein), JPTPN30 (SEQ ID NO: 234; similarity to rat mRNA for proteasome subunit), JPTPN45 (SEQ ID NO: 243; similarity to rat *norvegicus* cytosolic NADP-dependent isocitrate dehydrogenase), JPTPN46 (SEQ ID NO: 244; similarity to human subclone H8 4 d4 DNA sequence), JP1D6 (SEQ ID NO: 265; similarity to *G. gallus* dynein light chain-A), JP8D6 (SEQ ID NO: 288; similarity to human BAC clone RG016J04), JP8F5 (SEQ ID NO: 289; similarity to human subclone H8 3 b5 DNA sequence), and JP8E9 (SEQ ID NO: 299; similarity to human Alu sequence).

Additional studies using the PCR-based subtraction library consisting of a prostate tumor pool subtracted against a normal prostate pool (referred to as PT-PN PCR subtraction) yielded three additional clones. Comparison of the cDNA sequences of these clones with the most recent release of GenBank revealed no significant homologies to the two clones referred to as P715P and P767P (SEQ ID NO: 312 and 314). The remaining clone was found to show some homology to the known gene KIAA0056 (SEQ ID NO: 318). Using microarray analysis to measure mRNA expression levels in various tissues, all three clones were found to be over-expressed in prostate tumors and BPH tissues. Specifically, clone P715P was over-expressed in most prostate tumors and BPH tissues by a factor of three or greater, with elevated expression

seen in the majority of normal prostate samples and in fetal tissue, but negative to low expression in all other normal tissues. Clone P767P was over-expressed in several prostate tumors and BPH tissues, with moderate expression levels in half of the normal prostate samples, and background to low expression in all other normal tissues tested.

Further analysis, by microarray as described above, of the PT-PN PCR subtraction library and of a DNA subtraction library containing cDNA from prostate tumor subtracted with a pool of normal tissue cDNAs, led to the isolation of 27 additional clones (SEQ ID NO: 340-365 and 381) which were determined to be over-expressed in prostate tumor. The clones of SEQ ID NO: 341, 342, 345, 347, 348, 349, 351, 355-359, 361, 362 and 364 were also found to be expressed in normal prostate. Expression of all 26 clones in a variety of normal tissues was found to be low or undetectable, with the exception of P544S (SEQ ID NO: 356) which was found to be expressed in small intestine. Of the 26 clones, 11 (SEQ ID NO: 340-349 and 362) were found to show some homology to previously identified sequences. No significant homologies were found to the clones of SEQ ID NO: 350, 351, 353-361, and 363-365.

Comparison of the sequence of SEQ ID NO: 362 with sequences in the GenBank and GeneSeq DNA databases showed that this clone (referred to as P788P) is identical to GeneSeq Accession No. X27262, which encodes a protein found in the GeneSeq protein Accession No. Y00931. The full length cDNA sequence of P788P is shown in Figure 12A (SEQ ID NO: 777), with the corresponding predicted amino acid being shown in Figure 12B (SEQ ID NO: 778). Subsequently, a full-length cDNA sequence for P788P that contains polymorphisms not found in the sequence of SEQ ID NO: 779, was cloned multiple times by PCR amplification from cDNA prepared from several RNA templates from three individuals. This determined cDNA sequence of this polymorphic variant of P788P is provided in SEQ ID NO: 779, with the corresponding amino acid sequence being provided in SEQ ID NO: 780. The sequence of SEQ ID NO: 780 differs from that of SEQ ID NO: 778 by six amino acid residues. The P788P protein has 7 potential transmembrane domains at the C-terminal portion and is predicted to be a plasma membrane protein with an extracellular N-terminal region.

Further studies on the clone of SEQ ID NO: 352 (referred to as P790P) led to the isolation of the full-length cDNA sequence of SEQ ID NO: 526. The corresponding predicted amino acid is provided in SEQ ID NO: 527. Data from two quantitative PCR experiments indicated that P790P is over-expressed in 11/15 tested prostate tumor samples and is expressed at low levels in spinal cord, with no expression being seen in all other normal samples tested. Data from further PCR experiments and microarray experiments showed over-expression in normal prostate and prostate tumor with little or no expression in other tissues tested. P790P was subsequently found to show significant homology to a previously identified G-protein coupled prostate tissue receptor.

Additional studies on the clone of SEQ ID NO: 354 (referred to as P776P) led to the isolation of an extended cDNA sequence, provided in SEQ ID NO: 569. The determined cDNA sequences of three additional splice variants of P776P are provided in SEQ ID NO: 570-572. The amino acid sequences encoded by two predicted open reading frames (ORFs) contained within SEQ ID NO: 570, one predicted ORF contained within SEQ ID NO: 571, and 11 predicted ORFs contained within SEQ ID NO: 569, are provided in SEQ ID NO: 573-586, respectively. Further studies led to the isolation of the full-length sequence for the clone of SEQ ID NO: 570 (provided in SEQ ID NO: 880). Full-length cloning efforts on the clone of SEQ ID NO: 571 led to the isolation of two sequences (provided in SEQ ID NO: 881 and 882), representing a single clone, that are identical with the exception of a polymorphic insertion/deletion at position 1293. Specifically, the clone of SEQ ID NO: 882 (referred to as clone F1) has a C at position 1293. The clone of SEQ ID NO: 881 (referred to as clone F2) has a single base pair deletion at position 1293. The predicted amino acid sequences encoded by 5 open reading frames located within SEQ ID NO: 880 are provided in SEQ ID NO: 883-887, with the predicted amino acid sequences encoded by the clone of SEQ ID NO: 881 and 882 being provided in SEQ ID NO: 888-893.

Comparison of the cDNA sequences for the clones P767P (SEQ ID NO: 314) and P777P (SEQ ID NO: 350) with sequences in the GenBank human EST database showed that the two clones matched many EST sequences in common,

suggesting that P767P and P777P may represent the same gene. A DNA consensus sequence derived from a DNA sequence alignment of P767P, P777P and multiple EST clones is provided in SEQ ID NO: 587. The amino acid sequences encoded by three putative ORFs located within SEQ ID NO: 587 are provided in SEQ ID NO: 588-590.

The clone of SEQ ID NO: 342 (referred to as P789P) was found to show homology to a previously identified gene. The full length cDNA sequence for P789P and the corresponding amino acid sequence are provided in SEQ ID NO: 878 and 879, respectively.

EXAMPLE 6

PEPTIDE PRIMING OF MICE AND PROPAGATION OF CTL LINES

6.1. This Example illustrates the preparation of a CTL cell line specific for cells expressing the P502S gene.

Mice expressing the transgene for human HLA A2Kb (provided by Dr L. Sherman, The Scripps Research Institute, La Jolla, CA) were immunized with P2S#12 peptide (VLGWVAEL; SEQ ID NO: 306), which is derived from the P502S gene (also referred to herein as J1-17, SEQ ID NO: 8), as described by Theobald et al., *Proc. Natl. Acad. Sci. USA 92*:11993-11997, 1995 with the following modifications. Mice were immunized with 100μg of P2S#12 and 120μg of an I-A^b binding peptide derived from hepatitis B Virus protein emulsified in incomplete Freund's adjuvant. Three weeks later these mice were sacrificed and using a nylon mesh single cell suspensions prepared. Cells were then resuspended at 6 x 10^6 cells/ml in complete media (RPMI-1640; Gibco BRL, Gaithersburg, MD) containing 10% FCS, 2mM Glutamine (Gibco BRL), sodium pyruvate (Gibco BRL), non-essential amino acids (Gibco BRL), 2 x 10^{-5} M 2-mercaptoethanol, 50U/ml penicillin and streptomycin, and cultured in the presence of irradiated (3000 rads) P2S#12-pulsed (5mg/ml P2S#12 and 10mg/ml β2-microglobulin) LPS blasts (A2 transgenic spleens cells cultured in the presence of 7μg/ml dextran sulfate and 25μg/ml LPS for 3 days). Six days later, cells (5 x 10^5/ml) were restimulated with 2.5 x 10^6/ml peptide pulsed irradiated (20,000 rads) EL4A2Kb cells

(Sherman et al, *Science 258*:815-818, 1992) and 3 x 10^6/ml A2 transgenic spleen feeder cells. Cells were cultured in the presence of 20U/ml IL-2. Cells continued to be restimulated on a weekly basis as described, in preparation for cloning the line.

P2S#12 line was cloned by limiting dilution analysis with peptide pulsed EL4 A2Kb tumor cells (1 x 10^4 cells/ well) as stimulators and A2 transgenic spleen cells as feeders (5 x 10^5 cells/ well) grown in the presence of 30U/ml IL-2. On day 14, cells were restimulated as before. On day 21, clones that were growing were isolated and maintained in culture. Several of these clones demonstrated significantly higher reactivity (lysis) against human fibroblasts (HLA A2Kb expressing) transduced with P502S than against control fibroblasts. An example is presented in Figure 1.

This data indicates that P2S #12 represents a naturally processed epitope of the P502S protein that is expressed in the context of the human HLA A2Kb molecule.

6.2. This Example illustrates the preparation of murine CTL lines and CTL clones specific for cells expressing the P501S gene.

This series of experiments were performed similarly to that described above. Mice were immunized with the P1S#10 peptide (SEQ ID NO: 337), which is derived from the P501S gene (also referred to herein as L1-12, SEQ ID NO: 110). The P1S#10 peptide was derived by analysis of the predicted polypeptide sequence for P501S for potential HLA-A2 binding sequences as defined by published HLA-A2 binding motifs (Parker, KC, *et al*, *J. Immunol.*, 152:163, 1994). P1S#10 peptide was synthesized as described in Example 4, and empirically tested for HLA-A2 binding using a T cell based competition assay. Predicted A2 binding peptides were tested for their ability to compete HLA-A2 specific peptide presentation to an HLA-A2 restricted CTL clone (D150M58), which is specific for the HLA-A2 binding influenza matrix peptide fluM58. D150M58 CTL secretes TNF in response to self-presentation of peptide fluM58. In the competition assay, test peptides at 100-200 μg/ml were added to cultures of D150M58 CTL in order to bind HLA-A2 on the CTL. After thirty minutes,

CTL cultured with test peptides, or control peptides, were tested for their antigen dose response to the fluM58 peptide in a standard TNF bioassay. As shown in Figure 3, peptide P1S#10 competes HLA-A2 restricted presentation of fluM58, demonstrating that peptide P1S#10 binds HLA-A2.

Mice expressing the transgene for human HLA A2Kb were immunized as described by Theobald et al. (*Proc. Natl. Acad. Sci. USA 92*:11993-11997, 1995) with the following modifications. Mice were immunized with 62.5μg of P1S #10 and 120μg of an I-A^b binding peptide derived from Hepatitis B Virus protein emulsified in incomplete Freund's adjuvant. Three weeks later these mice were sacrificed and single cell suspensions prepared using a nylon mesh. Cells were then resuspended at 6 x 10^6 cells/ml in complete media (as described above) and cultured in the presence of irradiated (3000 rads) P1S#10-pulsed (2μg/ml P1S#10 and 10mg/ml β2-microglobulin) LPS blasts (A2 transgenic spleens cells cultured in the presence of 7μg/ml dextran sulfate and 25μg/ml LPS for 3 days). Six days later cells (5 x 10^5/ml) were restimulated with 2.5 x 10^6/ml peptide-pulsed irradiated (20,000 rads) EL4A2Kb cells, as described above, and 3 x 10^6/ml A2 transgenic spleen feeder cells. Cells were cultured in the presence of 20 U/ml IL-2. Cells were restimulated on a weekly basis in preparation for cloning. After three rounds of *in vitro* stimulations, one line was generated that recognized P1S#10-pulsed Jurkat A2Kb targets and P501S-transduced Jurkat targets as shown in Figure 4.

A P1S#10-specific CTL line was cloned by limiting dilution analysis with peptide pulsed EL4 A2Kb tumor cells (1 x 10^4 cells/ well) as stimulators and A2 transgenic spleen cells as feeders (5 x 10^5 cells/ well) grown in the presence of 30U/ml IL-2. On day 14, cells were restimulated as before. On day 21, viable clones were isolated and maintained in culture. As shown in Figure 5, five of these clones demonstrated specific cytolytic reactivity against P501S-transduced Jurkat A2Kb targets. This data indicates that P1S#10 represents a naturally processed epitope of the P501S protein that is expressed in the context of the human HLA-A2.1 molecule.

EXAMPLE 7

PRIMING OF CTL *IN VIVO* USING NAKED DNA IMMUNIZATION WITH A PROSTATE ANTIGEN

The prostate-specific antigen L1-12, as described above, is also referred to as P501S. HLA A2Kb Tg mice (provided by Dr L. Sherman, The Scripps Research Institute, La Jolla, CA) were immunized with 100 μg P501S in the vector VR1012 either intramuscularly or intradermally. The mice were immunized three times, with a two week interval between immunizations. Two weeks after the last immunization, immune spleen cells were cultured with Jurkat A2Kb-P501S transduced stimulator cells. CTL lines were stimulated weekly. After two weeks of *in vitro* stimulation, CTL activity was assessed against P501S transduced targets. Two out of 8 mice developed strong anti-P501S CTL responses. These results demonstrate that P501S contains at least one naturally processed HLA-A2-restricted CTL epitope.

EXAMPLE 8

ABILITY OF HUMAN T CELLS TO RECOGNIZE PROSTATE-SPECIFIC POLYPEPTIDES

This Example illustrates the ability of T cells specific for a prostate tumor polypeptide to recognize human tumor.

Human $CD8^+$ T cells were primed *in vitro* to the P2S-12 peptide (SEQ ID NO: 306) derived from P502S (also referred to as J1-17) using dendritic cells according to the protocol of Van Tsai et al. (*Critical Reviews in Immunology 18*:65-75, 1998). The resulting $CD8^+$ T cell microcultures were tested for their ability to recognize the P2S-12 peptide presented by autologous fibroblasts or fibroblasts which were transduced to express the P502S gene in a γ-interferon ELISPOT assay (*see* Lalvani et al., *J. Exp. Med. 186*:859-865, 1997). Briefly, titrating numbers of T cells were assayed in duplicate on 10^4 fibroblasts in the presence of 3 μg/ml human β_2-microglobulin and 1 μg/ml P2S-12 peptide or control E75 peptide. In addition, T cells were simultaneously assayed on autologous fibroblasts transduced with the P502S gene or as a control, fibroblasts transduced with HER-2/*neu*. Prior to the assay, the

fibroblasts were treated with 10 ng/ml γ-interferon for 48 hours to upregulate class I MHC expression. One of the microcultures (#5) demonstrated strong recognition of both peptide pulsed fibroblasts as well as transduced fibroblasts in a γ-interferon ELISPOT assay. Figure 2A demonstrates that there was a strong increase in the number of γ-interferon spots with increasing numbers of T cells on fibroblasts pulsed with the P2S-12 peptide (solid bars) but not with the control E75 peptide (open bars). This shows the ability of these T cells to specifically recognize the P2S-12 peptide. As shown in Figure 2B, this microculture also demonstrated an increase in the number of γ-interferon spots with increasing numbers of T cells on fibroblasts transduced to express the P502S gene but not the HER-2/*neu* gene. These results provide additional confirmatory evidence that the P2S-12 peptide is a naturally processed epitope of the P502S protein. Furthermore, this also demonstrates that there exists in the human T cell repertoire, high affinity T cells which are capable of recognizing this epitope. These T cells should also be capable of recognizing human tumors which express the P502S gene.

EXAMPLE 9

ELICITATION OF PROSTATE ANTIGEN-SPECIFIC CTL RESPONSES IN HUMAN BLOOD

This Example illustrates the ability of a prostate-specific antigen to elicit a CTL response in blood of normal humans.

Autologous dendritic cells (DC) were differentiated from monocyte cultures derived from PBMC of normal donors by growth for five days in RPMI medium containing 10% human serum, 50 ng/ml GMCSF and 30 ng/ml IL-4. Following culture, DC were infected overnight with recombinant P501S-expressing vaccinia virus at an M.O.I. of 5 and matured for 8 hours by the addition of 2 micrograms/ml CD40 ligand. Virus was inactivated by UV irradiation, $CD8^+$ cells were isolated by positive selection using magnetic beads, and priming cultures were initiated in 24-well plates. Following five stimulation cycles using autologous fibroblasts

retrovirally transduced to express P501S and CD80, CD8+ lines were identified that specifically produced interferon-gamma when stimulated with autologous P501S-transduced fibroblasts. The P501S-specific activity of cell line 3A-1 could be maintained following additional stimulation cycles on autologous B-LCL transduced with P501S. Line 3A-1 was shown to specifically recognize autologous B-LCL transduced to express P501S, but not EGFP-transduced autologous B-LCL, as measured by cytotoxicity assays (^{51}Cr release) and interferon-gamma production (Interferon-gamma Elispot; *see* above and Lalvani et al., *J. Exp. Med. 186*:859-865, 1997). The results of these assays are presented in Figures 6A and 6B.

EXAMPLE 10

IDENTIFICATION OF A NATURALLY PROCESSED CTL EPITOPE CONTAINED WITHIN THE PROSTATE-SPECIFIC ANTIGEN P703P

The 9-mer peptide p5 (SEQ ID NO: 338) was derived from the P703P antigen (also referred to as P20). The p5 peptide is immunogenic in human HLA-A2 donors and is a naturally processed epitope. Antigen specific human CD8+ T cells can be primed following repeated *in vitro* stimulations with monocytes pulsed with p5 peptide. These CTL specifically recognize p5-pulsed and P703P-transduced target cells in both ELISPOT (as described above) and chromium release assays. Additionally, immunization of HLA-A2Kb transgenic mice with p5 leads to the generation of CTL lines which recognize a variety of HLA-A2Kb or HLA-A2 transduced target cells expressing P703P.

Initial studies demonstrating that p5 is a naturally processed epitope were done using HLA-A2Kb transgenic mice. HLA-A2Kb transgenic mice were immunized subcutaneously in the footpad with 100 μg of p5 peptide together with 140 μg of hepatitis B virus core peptide (a Th peptide) in Freund's incomplete adjuvant. Three weeks post immunization, spleen cells from immunized mice were stimulated *in vitro* with peptide-pulsed LPS blasts. CTL activity was assessed by chromium release assay five days after primary *in vitro* stimulation. Retrovirally transduced cells expressing the

control antigen P703P and HLA-A2Kb were used as targets. CTL lines that specifically recognized both p5-pulsed targets as well as P703P-expressing targets were identified.

Human *in vitro* priming experiments demonstrated that the p5 peptide is immunogenic in humans. Dendritic cells (DC) were differentiated from monocyte cultures derived from PBMC of normal human donors by culturing for five days in RPMI medium containing 10% human serum, 50 ng/ml human GM-CSF and 30 ng/ml human IL-4. Following culture, the DC were pulsed with 1 ug/ml p5 peptide and cultured with CD8+ T cell enriched PBMC. CTL lines were restimulated on a weekly basis with p5-pulsed monocytes. Five to six weeks after initiation of the CTL cultures, CTL recognition of p5-pulsed target cells was demonstrated. CTL were additionally shown to recognize human cells transduced to express P703P, demonstrating that p5 is a naturally processed epitope.

Studies identifying a further peptide epitope (referred to as peptide 4) derived from the prostate tumor-specific antigen P703P that is capable of being recognized by CD4 T cells on the surface of cells in the context of HLA class II molecules were carried out as follows. The amino acid sequence for peptide 4 is provided in SEQ ID NO: 781, with the corresponding cDNA sequence being provided in SEQ ID NO: 782.

Twenty 15-mer peptides overlapping by 10 amino acids and derived from the carboxy-terminal fragment of P703P were generated using standard procedures. Dendritic cells (DC) were derived from PBMC of a normal female donor using GM-CSF and IL-4 by standard protocols. CD4 T cells were generated from the same donor as the DC using MACS beads and negative selection. DC were pulsed overnight with pools of the 15-mer peptides, with each peptide at a final concentration of 0.25 microgram/ml. Pulsed DC were washed and plated at 1 x 10^4 cells/well of 96-well V-bottom plates and purified CD4 T cells were added at 1 x 10^5/well. Cultures were supplemented with 60 ng/ml IL-6 and 10 ng/ml IL-12 and incubated at 37 °C. Cultures were restimulated as above on a weekly basis using DC generated and pulsed as above as antigen presenting cells, supplemented with 5 ng/ml IL-7 and 10 u/ml IL-2. Following 4 *in vitro* stimulation cycles, 96 lines (each line corresponding to one well) were tested for specific proliferation and cytokine production in response to the

stimulating pools with an irrelevant pool of peptides derived from mammaglobin being used as a control.

One line (referred to as 1-F9) was identified from pool #1 that demonstrated specific proliferation (measured by 3H proliferation assays) and cytokine production (measured by interferon-gamma ELISA assays) in response to pool #1 of P703P peptides. This line was further tested for specific recognition of the peptide pool, specific recognition of individual peptides in the pool, and in HLA mismatch analyses to identify the relevant restricting allele. Line 1-F9 was found to specifically proliferate and produce interferon-gamma in response to peptide pool #1, and also to peptide 4 (SEQ ID NO: 781). Peptide 4 corresponds to amino acids 126-140 of SEQ ID NO: 327. Peptide titration experiments were conducted to assess the sensitivity of line 1-F9 for the specific peptide. The line was found to specifically respond to peptide 4 at concentrations as low as 0.25 ng/ml, indicating that the T cells are very sensitive and therefore likely to have high affinity for the epitope.

To determine the HLA restriction of the P703P response, a panel of antigen presenting cells (APC) was generated that was partially matched with the donor used to generate the T cells. The APC were pulsed with the peptide and used in proliferation and cytokine assays together with line 1-F9. APC matched with the donor at HLA-DRB0701 and HLA-DQB02 alleles were able to present the peptide to the T cells, indicating that the P703P-specific response is restricted to one of these alleles.

Antibody blocking assays were utilized to determine if the restricting allele was HLA-DR0701 or HLA-DQ02. The anti-HLA-DR blocking antibody L243 or an irrelevant isotype matched IgG2a were added to T cells and APC cultures pulsed with the peptide RMPTVLQCVNVSVVS (SEQ ID NO: 781) at 250 ng/ml. Standard interferon-gamma and proliferation assays were performed. Whereas the control antibody had no effect on the ability of the T cells to recognize peptide-pulsed APC, in both assays the anti-HLA-DR antibody completely blocked the ability of the T cells to specifically recognize peptide-pulsed APC.

To determine if the peptide epitope RMPTVLQCVNVSVVS (SEQ ID NO: 781) was naturally processed, the ability of line 1-F9 to recognize APC pulsed with recombinant P703P protein was examined. For these experiments a number of

recombinant P703P sources were utilized; *E. coli*-derived P703P, Pichia-derived P703P and baculovirus-derived P703P. Irrelevant protein controls used were *E. coli*-derived L3E a lung-specific antigen) and baculovirus-derived mammaglobin. In interferon-gamma ELISA assays, line 1-F9 was able to efficiently recognize both *E. coli* forms of P703P as well as Pichia-derived recombinant P703P, while baculovirus-derived P703P was recognized less efficiently. Subsequent Western blot analysis revealed that the *E coli* and Pichia P703P protein preparations were intact while the baculovirus P703P preparation was approximately 75% degraded. Thus, peptide RMPTVLQCVNVSVVS (SEQ ID NO: 781) from P703P is a naturally processed peptide epitope derived from P703P and presented to T cells in the context of HLA-DRB-0701

In further studies, twenty-four 15-mer peptides overlapping by 10 amino acids and derived from the N-terminal fragment of P703P (corresponding to amino acids 27-154 of SEQ ID NO: 525) were generated by standard procedures and their ability to be recognized by CD4 cells was determined essentially as described above. DC were pulsed overnight with pools of the peptides with each peptide at a final concentration of 10 microgram/ml. A large number of individual CD4 T cell lines (65/480) demonstrated significant proliferation and cytokine release (IFN-gamma) in response to the P703P peptide pools but not to a control peptide pool. The CD4 T cell lines which demonstrated specific activity were restimulated on the appropriate pool of P703P peptides and reassayed on the individual peptides of each pool as well as a peptide dose titration of the pool of peptides in a IFN-gamma release assay and in a proliferation assay.

Sixteen immunogenic peptides were recognized by the T cells from the entire set of peptide antigens tested. The amino acid sequences of these peptides are provided in SEQ ID NO: 799-814, with the corresponding cDNA sequences being provided in SEQ ID NO: 783-798, respectively. In some cases the peptide reactivity of the T cell line could be mapped to a single peptide, however some could be mapped to more than one peptide in each pool. Those CD4 T cell lines that displayed a representative pattern of recognition from each peptide pool with a reasonable affinity for peptide were chosen for further analysis (I-1A, -6A; II-4C, -5E; III-6E, IV-4B, -3F, -9B, -10F, V-5B, -4D, and -10F). These CD4 T cells lines were restimulated on the

appropriate individual peptide and reassayed on autologous DC pulsed with a truncated form of recombinant P703P protein made in *E. coli* (a.a. 96 - 254 of SEQ ID NO: 525), full-length P703P made in the baculovirus expression system, and a fusion between influenza virus NS1 and P703P made in *E. coli*. Of the T cell lines tested, line I-1A recognized specifically the truncated form of P703P (*E. coli*) but no other recombinant form of P703P. This line also recognized the peptide used to elicit the T cells. Line 2-4C recognized the truncated form of P703P (*E. coli*) and the full length form of P703P made in baculovirus, as well as peptide. The remaining T cell lines tested were either peptide-specific only (II-5E, II-6F, IV-4B, IV-3F, IV-9B, IV-10F, V-5B and V-4D) or were non-responsive to any antigen tested (V-10F). These results demonstrate that the peptide sequence RPLLANDLMLIKLDE (SEQ ID NO: 814; corresponding to a.a. 110-124 of SEQ ID NO: 525) recognized by the T cell line I-1A, and the peptide sequences SVSESDTIRSISIAS (SEQ ID NO: 811; corresponding to a.a. 125-139 of SEQ ID NO: 525) and ISIASQCPTAGNSCL (SEQ ID NO: 810; corresponding to a.a. 135-149 of SEQ ID NO: 525) recognized by the T cell line II-4C may be naturally processed epitopes of the P703P protein.

In further studies, forty 15-mer peptides overlapping by 10 amino acids and derived spanning amino acids 47 to 254 of P703P (SEQ ID NO: 525) were generated by standard procedures and their ability to be recognized by CD4 cells was determined essentially as described above. DC were prepared from PBMC of a donor having distinct HLA DR and DQ alleles from that used in previous experiments. DC were pulsed overnight with pools of the peptides with each peptide at a final concentration of 0.25 microgram/ml, and each pool containing 10 peptides. Twelve lines were identified that demonstrated specific proliferation and cytokine production (measured in gamma-interferon ELISA assays) in response to the stimulating peptide pool. These lines were further tested for specific recognition of the peptide pool, specific recognition of individual peptides in the pool, and specific recognition of recombinant P703P protein. Lines 3A5H and 3A9H specifically proliferated and produced gamma-interferon in response to recombinant protein and one individual peptide as well as the peptide pool. Following re-stimulation on targets loaded with the specific peptide, only 3A9H responded specifically to targets exposed to lysates of

fibroblasts infected adenovirus expressing full-length P703P. These results indicates that the line 3A9H can respond to antigenic peptide derived from protein synthesized in mammalian cells. The peptide to which the specific CD4 line responded correspond to amino acids 155-170 of P703P (SEQ ID NO: 943). The DNA sequence for this peptide is provided in SEQ ID NO: 942.

EXAMPLE 11

EXPRESSION OF A BREAST TUMOR-DERIVED ANTIGEN IN PROSTATE

Isolation of the antigen B305D from breast tumor by differential display is described in US Patent Application No. 08/700,014, filed August 20, 1996. Several different splice forms of this antigen were isolated. The determined cDNA sequences for these splice forms are provided in SEQ ID NO: 366-375, with the predicted amino acid sequences corresponding to the sequences of SEQ ID NO: 292, 298 and 301-303 being provided in SEQ ID NO: 299-306, respectively. In further studies, a splice variant of the cDNA sequence of SEQ ID NO: 366 was isolated which was found to contain an additional guanine residue at position 884 (SEQ ID NO: 530), leading to a frameshift in the open reading frame. The determined DNA sequence of this ORF is provided in SEQ ID NO: 531. This frameshift generates a protein sequence (provided in SEQ ID NO: 532) of 293 amino acids that contains the C-terminal domain common to the other isoforms of B305D but that differs in the N-terminal region.

The expression levels of B305D in a variety of tumor and normal tissues were examined by real time PCR and by Northern analysis. The results indicated that B305D is highly expressed in breast tumor, prostate tumor, normal prostate and normal testes, with expression being low or undetectable in all other tissues examined (colon tumor, lung tumor, ovary tumor, and normal bone marrow, colon, kidney, liver, lung, ovary, skin, small intestine, stomach). Using real-time PCR on a panel of prostate tumors, expression of B305D in prostate tumors was shown to increase with increasing

Gleason grade, demonstrating that expression of B305D increases as prostate cancer progresses.

EXAMPLE 12

GENERATION OF HUMAN CTL *IN VITRO* USING WHOLE GENE PRIMING AND STIMULATION TECHNIQUES WITH THE PROSTATE-SPECIFIC ANTIGEN P501S

Using *in vitro* whole-gene priming with P501S-vaccinia infected DC (see, for example, Yee et al, *The Journal of Immunology*, 157(9):4079-86, 1996), human CTL lines were derived that specifically recognize autologous fibroblasts transduced with P501S (also known as L1-12), as determined by interferon-γ ELISPOT analysis as described above. Using a panel of HLA-mismatched B-LCL lines transduced with P501S, these CTL lines were shown to be likely restricted to HLAB class I allele. Specifically, dendritic cells (DC) were differentiated from monocyte cultures derived from PBMC of normal human donors by growing for five days in RPMI medium containing 10% human serum, 50 ng/ml human GM-CSF and 30 ng/ml human IL-4. Following culture, DC were infected overnight with recombinant P501S vaccinia virus at a multiplicity of infection (M.O.I) of five, and matured overnight by the addition of 3 μg/ml CD40 ligand. Virus was inactivated by UV irradiation. CD8+ T cells were isolated using a magnetic bead system, and priming cultures were initiated using standard culture techniques. Cultures were restimulated every 7-10 days using autologous primary fibroblasts retrovirally transduced with P501S and CD80. Following four stimulation cycles, CD8+ T cell lines were identified that specifically produced interferon-γ when stimulated with P501S and CD80-transduced autologous fibroblasts. A panel of HLA-mismatched B-LCL lines transduced with P501S were generated to define the restriction allele of the response. By measuring interferon-γ in an ELISPOT assay, the P501S specific response was shown to be likely restricted by HLA B alleles. These results demonstrate that a CD8+ CTL response to P501S can be elicited.

To identify the epitope(s) recognized, cDNA encoding P501S was fragmented by various restriction digests, and sub-cloned into the retroviral expression vector pBIB-KS. Retroviral supernatants were generated by transfection of the helper packaging line Phoenix-Ampho. Supernatants were then used to transduce Jurkat/A2Kb cells for CTL screening. CTL were screened in IFN-gamma ELISPOT assays against these A2Kb targets transduced with the "library" of P501S fragments. Initial positive fragments P501S/H3 and P501S/F2 were sequenced and found to encode amino acids 106-553 and amino acids 136-547, respectively, of SEQ ID NO: 113. A truncation of H3 was made to encode amino acid residues 106-351 of SEQ ID NO: 113, which was unable to stimulate the CTL, thus localizing the epitope to amino acid residues 351-547. Additional fragments encoding amino acids 1-472 (Fragment A) and amino acids 1-351 (Fragment B) were also constructed. Fragment A but not Fragment B stimulated the CTL thus localizing the epitope to amino acid residues 351-472. Overlapping 20-mer and 18-mer peptides representing this region were tested by pulsing Jurkat/A2Kb cells versus CTL in an IFN-gamma assay. Only peptides P501S-369(20) and P501S-369(18) stimulated the CTL. Nine-mer and 10-mer peptides representing this region were synthesized and similarly tested. Peptide P501S-370 (SEQ ID NO: 539) was the minimal 9-mer giving a strong response. Peptide P501S-376 (SEQ ID NO: 540) also gave a weak response, suggesting that it might represent a cross-reactive epitope.

In subsequent studies, the ability of primary human B cells transduced with P501S to prime MHC class I-restricted, P501S-specific, autologous CD8 T cells was examined. Primary B cells were derived from PBMC of a homozygous HLA-A2 donor by culture in CD40 ligand and IL-4, transduced at high frequency with recombinant P501S in the vector pBIB, and selected with blastocidin-S. For *in vitro* priming, purified CD8+ T cells were cultured with autologous CD40 ligand + IL-4 derived, P501S-transduced B cells in a 96-well microculture format. These CTL microcultures were re-stimulated with P501S-transduced B cells and then assayed for specificity. Following this initial screen, microcultures with significant signal above background were cloned on autologous EBV-transformed B cells (BLCL), also

transduced with P501S. Using IFN-gamma ELISPOT for detection, several of these CD8 T cell clones were found to be specific for P501S, as demonstrated by reactivity to BLCL/P501S but not BLCL transduced with control antigen. It was further demonstrated that the anti-P501S CD8 T cell specificity is HLA-A2-restricted. First, antibody blocking experiments with anti-HLA-A,B,C monoclonal antibody (W6.32), anti-HLA-B,C monoclonal antibody (B1.23.2) and a control monoclonal antibody showed that only the anti-HLA-A,B,C antibody blocked recognition of P501S-expressing autologous BLCL. Secondly, the anti-P501S CTL also recognized an HLA-A2 matched, heterologous BLCL transduced with P501S, but not the corresponding EGFP transduced control BLCL.

A naturally processed, CD8, class I-restricted peptide epitope of P501S was identified as follows. Dendritic Cells (DC) were isolated by Percol gradient followed by differential adherence, and cultured for 5 days in the presence of RPMI medium containing 1% human serum, 50ng/ml GM-CSF and 30ng/ml IL-4. Following culture, DC were infected for 24 hours with P501S-expressing adenovirus at an MOI of 10 and matured for an additional 24 hours by the addition of 2ug/ml CD40 ligand. CD8 cells were enriched for by the subtraction of CD4+, CD14+ and CD16+ populations from PBMC with magnetic beads. Priming cultures containing 10,000 P501S-expressing DC and 100,000 CD8+ T cells per well were set up in 96-well V-bottom plates with RPMI containing 10% human serum, 5ng/ml IL-12 and 10ng/ml IL-6. Cultures were stimulated every 7 days using autologous fibroblasts retrovirally transduced to express P501S and CD80, and were treated with IFN-gamma for 48-72 hours to upregulate MHC Class I expression. 10u/ml IL-2 was added at the time of stimulation and on days 2 and 5 following stimulation. Following 4 stimulation cycles, one P501S-specific CD8+ T cell line (referred to as 2A2) was identified that produced IFN-gamma in response to IFN-gamma-treated P501S/CD80 expressing autologous fibroblasts, but not in response to IFN-gamma-treated P703P/CD80 expressing autologous fibroblasts in a γ-IFN Elispot assay. Line 2A2 was cloned in 96-well plates with 0.5 cell/well or 2 cells/well in the presence of 75,000 PBMC/well, 10,000 B-LCL/well, 30ng/ml OKT3 and 50u/ml IL-2. Twelve clones were isolated that showed strong P501S specificity in response to transduced fibroblasts.

Fluorescence activated cell sorting (FACS) analysis was performed on P501S-specific clones using CD3-, CD4- and CD8-specific antibodies conjugated to PercP, FITC and PE respectively. Consistent with the use of CD8 enriched T cells in the priming cultures, P5401S-specific clones were determined to be CD3+, CD8+ and CD4-.

To identify the relevant P501S epitope recognized by P501S specific CTL, pools of 18-20 mer or 30-mer peptides that spanned the majority of the amino acid sequence of P501S were loaded onto autologous B-LCL and tested in γ-IFN Elispot assays for the ability to stimulate two P501S-specific CTL clones, referred to as 4E5 and 4E7. One pool, composed of five 18-20 mer peptides that spanned amino acids 411-486 of P501S (SEQ ID NO: 113), was found to be recognized by both P501S-specific clones. To identify the specific 18-20 mer peptide recognized by the clones, each of the 18-20 mer peptides that comprised the positive pool were tested individually in γ-IFN Elispot assays for the ability to stimulate the two P501S-specific CTL clones, 4E5 and 4E7. Both 4E5 and 4E7 specifically recognized one 20-mer peptide (SEQ ID NO: 853; cDNA sequence provided in SEQ ID NO: 854) that spanned amino acids 453-472 of P501S. Since the minimal epitope recognized by CD8+ T cells is almost always either a 9 or 10-mer peptide sequence, 10-mer peptides that spanned the entire sequence of SEQ ID NO: 853 were synthesized that differed by 1 amino acid. Each of these 10-mer peptides was tested for the ability to stimulate two P501S-specific clones, (referred to as 1D5 and 1E12). One 10-mer peptide (SEQ ID NO: 855; cDNA sequence provided in SEQ ID NO: 856) was identified that specifically stimulated the P501S-specific clones. This epitope spans amino acids 463-472 of P501S. This sequence defines a minimal 10-mer epitope from P501S that can be naturally processed and to which CTL responses can be identified in normal PBMC. Thus, this epitope is a candidate for use as a vaccine moiety, and as a therapeutic and/or diagnostic reagent for prostate cancer.

To identify the class I restriction element for the P501S-derived sequence of SEQ ID NO: 855, HLA blocking and mismatch analyses were performed. In γ-IFN Elispot assays, the specific response of clones 4A7 and 4E5 to P501S-transduced autologous fibroblasts was blocked by pre-incubation with 25ug/ml W6/32 (pan-Class I blocking antibody) and B1.23.2 (HLA-B/C blocking antibody). These results

demonstrate that the SEQ ID NO: 855-specific response is restricted to an HLA-B or HLA-C allele.

For the HLA mismatch analysis, autologous B-LCL (HLA-A1,A2,B8,B51, Cwl, Cw7) and heterologous B-LCL (HLA-A2,A3,B18,B51,Cw5,Cw14) that share the HLAB51 allele were pulsed for one hour with 20ug/ml of peptide of SEQ ID NO: 855, washed, and tested in γ-IFN Elispot assays for the ability to stimulate clones 4A7 and 4E5. Antibody blocking assays with the B1.23.2 (HLA-B/C blocking antibody) were also performed. SEQ ID NO: 855-specific response was detected using both the autologous (D326) and heterologous (D107) B-LCL, and furthermore the responses were blocked by pre-incubation with 25ug/ml of B1.23.2 HLA-B/C blocking antibody. Together these results demonstrate that the P501S-specific response to the peptide of SEQ ID NO: 855 is restricted to the HLA-B51 class I allele. Molecular cloning and sequence analysis of the HLA-B51 allele from D3326 revealed that the HLA-B51 subtype of D326 is HLA-B51011.

Based on the 10-mer P501S-derived epitope of SEQ ID NO: 855, two 9-mers with the sequences of SEQ ID NO: 857 and 858 were synthesized and tested in Elispot assays for the ability to stimulate two P501S-specific CTL clones derived from line 2A2. The 10-mer peptide of SEQ ID NO: 855, as well as the 9-mer peptide of SEQ ID NO: 858, but not the 9-mer peptide of SEQ ID NO: 857, were capable of stimulating the P501S-specific CTL to produce IFN-gamma. These results demonstrate that the peptide of SEQ ID NO: 858 is a 9-mer P501S-derived epitope recognized by P501S-specific CTL. The DNA sequence encoding the epitope of SEQ ID NO: 858 is provided in SEQ ID NO: 859.

To identify the class I restricting allele for the P501S-derived peptide of SEQ ID NO: 855 and 858 specific response, each of the HLA B and C alleles were cloned from the donor used in the *in vitro* priming experiment. Sequence analysis indicated that the relevant alleles were HLA-B8, HLA-B51, HLA-Cw01 and HLA-Cw07. Each of these alleles were subcloned into an expression vector and co-transfected together with the P501S gene into VA-13 cells. Transfected VA-13 cells were then tested for the ability to specifically stimulate the P501S-specific CTL in ELISPOT assays. VA-13 cells transfected with P501S and HLA-B51 were capable of

stimulating the P501S-specific CTL to secrete gamma-IFN. VA-13 cells transfected with HLA-B51 alone or P501S + the other HLA-alleles were not capable of stimulating the P501S-specific CTL. These results demonstrate that the restricting allele for the P501S-specific response is the HLAB51 allele. Sequence analysis revealed that the subtype of the relevant restricting allele is HLA-B51011.

To determine if the P501S-specific CTL could recognize prostate tumor cells that express P501S, the P501S-positive lines LnCAP and CRL2422 (both expressing "moderate" amounts of P501S mRNA and protein), and PC-3 (expressing low amounts of P501S mRNA and protein), plus the P501S-negative cell line DU-145 were retrovirally transduced with the HLA-B51011 allele that was cloned from the donor used to generate the P501S-specific CTL. HLA-B51011- or EGFP-transduced and selected tumor cells were treated with gamma-interferon and androgen (to upregulate stimulatory functions and P501S, respectively) and used in gamma-interferon Elispot assays with the P501S-specific CTL clones 4E5 and 4E7. Untreated cells were used as a control.

Both 4E5 and 4E7 efficiently and specifically recognized LnCAP and CRL2422 cells that were transduced with the HLA-B51011 allele, but not the same cell lines transduced with EGFP. Additionally, both CTL clones specifically recognized PC-3 cells transduced with HLA-B51011, but not the P501S-negative tumor cell line DU-145. Treatment with gamma-interferon or androgen did not enhance the ability of CTL to recognize tumor cells. These results demonstrate that P501S-specific CTL, generated by *in vitro* whole gene priming, specifically and efficiently recognize prostate tumor cell lines that express P501S.

A naturally processed CD4 epitope of P501S was identified as follows.

CD4 cells specific for P501S were prepared as described above. A series of 16 overlapping peptides were synthesized that spanned approximately 50% of the amino terminal portion of the P501S gene (amino acids 1- 325 of SEQ ID NO: 113). For priming, peptides were combined into pools of 4 peptides, pulsed at 4 µg/ml onto dendritic cells (DC) for 24 hours, with TNF-alpha. DC were then washed and mixed with negatively selected CD4+ T cells in 96 well U-bottom plates. Cultures were re-stimulated weekly on fresh DC loaded with peptide pools. Following a total of 4

stimulation cycles, cells were rested for an additional week and tested for specificity to APC pulsed with peptide pools using γ-IFN ELISA and proliferation assays. For these assays, adherent monocytes loaded with either the relevant peptide pool at 4ug/ml or an irrelevant peptide at μg/ml were used as APC. T cell lines that demonstrated either specific cytokine secretion or proliferation were then tested for recognition of individual peptides that were present in the pool. T cell lines could be identified from pools A and B that recognized individual peptides from these pools.

From pool A, lines AD9 and AE10 specifically recognized peptide 1 (SEQ ID NO: 862), and line AF5 recognized peptide 39 (SEQ ID NO: 861). From pool B, line BC6 could be identified that recognized peptide 58 (SEQ ID NO: 860). Each of these lines were stimulated on the specific peptide and tested for specific recognition of the peptide in a titration assay as well as cell lysates generated by infection of HEK 293 cells with adenovirus expressing either P501S or an irrelevant antigen. For these assays, APC-adherent monocytes were pulsed with either 10, 1, or 0.1 μg/ml individual P501S peptides, and DC were pulsed overnight with a 1:5 dilution of adenovirally infected cell lysates. Lines AD9, AE10 and AF5 retained significant recognition of the relevant P501S-derived peptides even at 0.1 mg/ml. Furthermore, line AD9 demonstrated significant (8.1 fold stimulation index) specific activity for lysates from adenovirus-P501S infected cells. These results demonstrate that high affinity CD4 T cell lines can be generated toward P501S-derived epitopes, and that at least a subset of these T cells specific for the P501S derived sequence of SEQ ID NO: 862 are specific for an epitope that is naturally processed by human cells. The DNA sequences encoding the amino acid sequences of SEQ ID NO: 860-862 are provided in SEQ ID NO: 863-865, respectively.

To further characterize the P501S-specific activity of AD9, the line was cloned using anti-CD3. Three clones, referred to as 1A1, 1A9 and 1F5, were identified that were specific for the P501S-1 peptide (SEQ ID NO: 862). To determine the HLA restriction allele for the P501S-specific response, each of these clones was tested in class II antibody blocking and HLA mismatch assays using proliferation and gamma-interferon assays. In antibody blocking assays and measuring gamma-interferon production using ELISA assays, the ability of all three clones to recognize peptide

pulsed APC was specifically blocked by co-incubation with either a pan-class II blocking antibody or a HLA-DR blocking antibody, but not with a HLA-DQ or an irrelevant antibody. Proliferation assays performed simultaneously with the same cells confirmed these results. These data indicate that the P501S-specific response of the clones is restricted by an HLA-DR allele. Further studies demonstrated that the restricting allele for the P501S-specific response is HLA-DRB1501.

EXAMPLE 13

IDENTIFICATION OF PROSTATE-SPECIFIC ANTIGENS BY MICROARRAY ANALYSIS

This Example describes the isolation of certain prostate-specific polypeptides from a prostate tumor cDNA library.

A human prostate tumor cDNA expression library as described above was screened using microarray analysis to identify clones that display at least a three fold over-expression in prostate tumor and/or normal prostate tissue, as compared to non-prostate normal tissues (not including testis). 372 clones were identified, and 319 were successfully sequenced. Table I presents a summary of these clones, which are shown in SEQ ID NOs:385-400. Of these sequences SEQ ID NOs:386, 389, 390 and 392 correspond to novel genes, and SEQ ID NOs: 393 and 396 correspond to previously identified sequences. The others (SEQ ID NOs:385, 387, 388, 391, 394, 395 and 397-400) correspond to known sequences, as shown in Table I.

Table I

Summary of Prostate Tumor Antigens

Known Genes	Previously Identified Genes	Novel Genes
T-cell gamma chain	P504S	23379 (SEQ ID NO:389)
Kallikrein	P1000C	23399 (SEQ ID NO:392)
Vector	P501S	23320 (SEQ ID NO:386)
CGI-82 protein mRNA (23319; SEQ ID NO:385)	P503S	23381 (SEQ ID NO:390)
PSA	P510S	
Ald. 6 Dehyd.	P784P	
L-iditol-2 dehydrogenase (23376; SEQ ID NO:388)	P502S	
Ets transcription factor PDEF (22672; SEQ ID NO:398)	P706P	
hTGR (22678; SEQ ID NO:399)	19142.2, bangur.seq (22621; SEQ ID NO:396)	
KIAA0295(22685; SEQ ID NO:400)	5566.1 Wang (23404; SEQ ID NO:393)	
Prostatic Acid Phosphatase(22655; SEQ ID NO:397)	P712P	
transglutaminase (22611; SEQ ID NO:395)	P778P	
HDLBP (23508; SEQ ID NO:394)		
CGI-69 Protein(23367; SEQ ID NO:387)		
KIAA0122(23383; SEQ ID NO:391)		
TEEG		

CGI-82 showed 4.06 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 43% of prostate tumors, 25% normal prostate, not detected in other normal tissues tested. L-iditol-2 dehydrogenase showed 4.94 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 90% of prostate tumors, 100% of normal prostate, and not detected in other normal tissues tested. Ets transcription factor PDEF showed 5.55 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 47% prostate tumors, 25% normal prostate and not detected in other normal tissues tested. hTGR1 showed 9.11 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 63% of prostate tumors and is not detected in normal tissues tested including normal prostate. KIAA0295 showed 5.59 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 47% of prostate tumors, low to undetectable in normal tissues tested including normal prostate tissues. Prostatic acid phosphatase showed 9.14 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 67% of prostate tumors, 50% of normal prostate, and not detected in other normal tissues tested. Transglutaminase showed 14.84 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 30% of prostate tumors, 50% of normal prostate, and is not detected in other normal tissues tested. High density lipoprotein binding protein (HDLBP) showed 28.06 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 97% of prostate tumors, 75% of normal prostate, and is undetectable in all other normal tissues tested. CGI-69 showed 3.56 fold over-expression in prostate tissues as compared to other normal tissues tested. It is a low abundant gene, detected in more than 90% of prostate tumors, and in 75% normal prostate tissues. The expression of this gene in normal tissues was very low. KIAA0122 showed 4.24 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 57% of prostate tumors, it was undetectable in all normal tissues tested including normal prostate tissues. 19142.2 bangur showed 23.25 fold over-expression in prostate tissues as compared to other

normal tissues tested. It was over-expressed in 97% of prostate tumors and 100% of normal prostate. It was undetectable in other normal tissues tested. 5566.1 Wang showed 3.31 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 97% of prostate tumors, 75% normal prostate and was also over-expressed in normal bone marrow, pancreas, and activated PBMC. Novel clone 23379 (also referred to as P553S) showed 4.86 fold over-expression in prostate tissues as compared to other normal tissues tested. It was detectable in 97% of prostate tumors and 75% normal prostate and is undetectable in all other normal tissues tested. Novel clone 23399 showed 4.09 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 27% of prostate tumors and was undetectable in all normal tissues tested including normal prostate tissues. Novel clone 23320 showed 3.15 fold over-expression in prostate tissues as compared to other normal tissues tested. It was detectable in all prostate tumors and 50% of normal prostate tissues. It was also expressed in normal colon and trachea. Other normal tissues do not express this gene at high level.

Subsequent full-length cloning studies on P553S, using standard techniques, revealed that this clone is an incomplete spliced form of P501S. The determined cDNA sequences for four splice variants of P553S are provided in SEQ ID NO: 702-705. An amino acid sequence encoded by SEQ ID NO: 705 is provided in SEQ ID NO: 706. The cDNA sequence of SEQ ID NO: 702 was found to contain two open reading frames (ORFs). The amino acid sequences encoded by these two ORFs are provided in SEQ ID NO: 707 and 708.

EXAMPLE 14

IDENTIFICATION OF PROSTATE-SPECIFIC ANTIGENS BY ELECTRONIC SUBTRACTION

This Example describes the use of an electronic subtraction technique to identify prostate-specific antigens.

Potential prostate-specific genes present in the GenBank human EST database were identified by electronic subtraction (similar to that described by Vasmatizis et al., *Proc. Natl. Acad. Sci. USA 95*:300-304, 1998). The sequences of EST clones (43,482) derived from various prostate libraries were obtained from the GenBank public human EST database. Each prostate EST sequence was used as a query sequence in a BLASTN (National Center for Biotechnology Information) search against the human EST database. All matches considered identical (length of matching sequence >100 base pairs, density of identical matches over this region > 70%) were grouped (aligned) together in a cluster. Clusters containing more than 200 ESTs were discarded since they probably represented repetitive elements or highly expressed genes such as those for ribosomal proteins. If two or more clusters shared common ESTs, those clusters were grouped together into a "supercluster," resulting in 4,345 prostate superclusters.

Records for the 479 human cDNA libraries represented in the GenBank release were downloaded to create a database of these cDNA library records. These 479 cDNA libraries were grouped into three groups: Plus (normal prostate and prostate tumor libraries, and breast cell line libraries, in which expression was desired), Minus (libraries from other normal adult tissues, in which expression was not desirable), and Other (libraries from fetal tissue, infant tissue, tissues found only in women, non-prostate tumors and cell lines other than prostate cell lines, in which expression was considered to be irrelevant). A summary of these library groups is presented in Table II.

Table II

Prostate cDNA Libraries and ESTs

Library	# of Libraries	# of ESTs
Plus	25	43,482
Normal	11	18,875
Tumor	11	21,769
Cell lines	3	2,838
Minus	166	
Other	287	

Each supercluster was analyzed in terms of the ESTs within the supercluster. The tissue source of each EST clone was noted and used to classify the superclusters into four groups: Type 1- EST clones found in the Plus group libraries only; no expression detected in Minus or Other group libraries; Type 2- EST clones derived from the Plus and Other group libraries only; no expression detected in the Minus group; Type 3- EST clones derived from the Plus, Minus and Other group libraries, but the number of ESTs derived from the Plus group is higher than in either the Minus or Other groups; and Type 4- EST clones derived from Plus, Minus and Other group libraries, but the number derived from the Plus group is higher than the number derived from the Minus group. This analysis identified 4,345 breast clusters (*see* Table III). From these clusters, 3,172 EST clones were ordered from Research Genetics, Inc., and were received as frozen glycerol stocks in 96-well plates.

Table III

Prostate Cluster Summary

Type	# of Superclusters	# of ESTs Ordered
1	688	677
2	2899	2484
3	85	11
4	673	0
Total	4345	3172

The EST clone inserts were PCR-amplified using amino-linked PCR primers for Synteni microarray analysis. When more than one PCR product was obtained for a particular clone, that PCR product was not used for expression analysis. In total, 2,528 clones from the electronic subtraction method were analyzed by microarray analysis to identify electronic subtraction breast clones that had high levels of tumor vs. normal tissue mRNA. Such screens were performed using a Synteni (Palo Alto, CA) microarray, according to the manufacturer's instructions (and essentially as described by Schena et al., *Proc. Natl. Acad. Sci. USA 93*:10614-10619, 1996 and Heller et al., *Proc. Natl. Acad. Sci. USA 94*:2150-2155, 1997). Within these analyses, the clones were arrayed on the chip, which was then probed with fluorescent probes generated from normal and tumor prostate cDNA, as well as various other normal tissues. The slides were scanned and the fluorescence intensity was measured.

Clones with an expression ratio greater than 3 (*i.e.,* the level in prostate tumor and normal prostate mRNA was at least three times the level in other normal tissue mRNA) were identified as prostate tumor-specific sequences (Table IV). The sequences of these clones are provided in SEQ ID NO: 401-453, with certain novel sequences shown in SEQ ID NO: 407, 413, 416-419, 422, 426, 427 and 450.

Table IV

Prostate-tumor Specific Clones

SEQ ID NO.	Sequence Designation	Comments
401	22545	previously identified P1000C
402	22547	previously identified P704P
403	22548	known
404	22550	known
405	22551	PSA
406	22552	prostate secretory protein 94
407	22553	novel
408	22558	previously identified P509S
409	22562	glandular kallikrein
410	22565	previously identified P1000C
411	22567	PAP
412	22568	B1006C (breast tumor antigen)
413	22570	novel
414	22571	PSA
415	22572	previously identified P706P
416	22573	novel
417	22574	novel
418	22575	novel
419	22580	novel
420	22581	PAP
421	22582	prostatic secretory protein 94
422	22583	novel
423	22584	prostatic secretory protein 94
424	22585	prostatic secretory protein 94
425	22586	known
426	22587	novel
427	22588	novel
428	22589	PAP
429	22590	known
430	22591	PSA
431	22592	known
432	22593	Previously identified P777P
433	22594	T cell receptor gamma chain
434	22595	Previously identified P705P
435	22596	Previously identified P707P
436	22847	PAP
437	22848	known
438	22849	prostatic secretory protein 57

439	22851	PAP
440	22852	PAP
441	22853	PAP
442	22854	previously identified P509S
443	22855	previously identified P705P
444	22856	previously identified P774P
445	22857	PSA
446	23601	previously identified P777P
447	23602	PSA
448	23605	PSA
449	23606	PSA
450	23612	novel
451	23614	PSA
452	23618	previously identified P1000C
453	23622	previously identified P705P

Further studies on the clone of SEQ ID NO: 407 (also referred to as P1020C) led to the isolation of an extended cDNA sequence provided in SEQ ID NO: 591. This extended cDNA sequence was found to contain an open reading frame that encodes the predicted amino acid sequence of SEQ ID NO: 592. The P1020C cDNA and amino acid sequences were found to show some similarity to the human endogenous retroviral HERV-K pol gene and protein.

EXAMPLE 15

FURTHER IDENTIFICATION OF PROSTATE-SPECIFIC ANTIGENS BY MICROARRAY ANALYSIS

This Example describes the isolation of additional prostate-specific polypeptides from a prostate tumor cDNA library.

A human prostate tumor cDNA expression library as described above was screened using microarray analysis to identify clones that display at least a three fold over-expression in prostate tumor and/or normal prostate tissue, as compared to non-prostate normal tissues (not including testis). 142 clones were identified and sequenced. Certain of these clones are shown in SEQ ID NO: 454-467. Of these sequences, SEQ ID NO: 459-460 represent novel genes. The others (SEQ ID NO: 454-458 and 461-467) correspond to known sequences. Comparison of the determined

cDNA sequence of SEQ ID NO: 461 with sequences in the Genbank database using the BLAST program revealed homology to the previously identified transmembrane protease serine 2 (TMPRSS2). The full-length cDNA sequence for this clone is provided in SEQ ID NO: 894, with the corresponding amino acid sequence being provided in SEQ ID NO: 895. The cDNA sequence encoding the first 209 amino acids of TMPRSS2 is provided in SEQ ID NO: 896, with the first 209 amino acids being provided in SEQ ID NO: 897.

The sequence of SEQ ID NO: 462 (referred to as P835P) was found to correspond to the previously identified clone FLJ13518 (Accession AK023643; SEQ ID NO: 917), which had no associated open reading frame (ORF). This clone was used to search the Geneseq DNA database and matched a clone previously identified as a G protein-coupled receptor protein (DNA Geneseq Accession A09351; amino acid Geneseq Accession Y92365), that is characterized by the presence of seven transmembrane domains. The sequences of fragments between these domains are provided in SEQ ID NO: 921-928, with SEQ ID NO: 921, 923, 925 and 927 representing extracellular domains and SEQ ID NO: 922, 924, 926 and 928 representing intracellular domains. SEQ ID NO: 921-928 represent amino acids 1-28, 53-61, 83-103, 124-143, 165-201, 226-238, 263-272 and 297-381, respectively, of P835P. The full-length cDNA sequence for P835P is provided in SEQ ID NO: 916. The cDNA sequence of the open reading frame for P835P, including stop codon, is provided in SEQ ID NO: 918, with the open reading frame without stop codon being provided in SEQ ID NO: 919 and the corresponding amino acid sequence being provided in SEQ ID NO: 920.

EXAMPLE 16

FURTHER CHARACTERIZATION OF PROSTATE-SPECIFIC ANTIGEN P710P

This Example describes the full length cloning of P710P.

The prostate cDNA library described above was screened with the P710P fragment described above. One million colonies were plated on LB/Ampicillin plates.

Nylon membrane filters were used to lift these colonies, and the cDNAs picked up by these filters were then denatured and cross-linked to the filters by UV light. The P710P fragment was radiolabeled and used to hybridize with the filters. Positive cDNA clones were selected and their cDNAs recovered and sequenced by an automatic Perkin Elmer/Applied Biosystems Division Sequencer. Four sequences were obtained, and are presented in SEQ ID NO: 468-471. These sequences appear to represent different splice variants of the P710P gene. Subsequent comparison of the cDNA sequences of P710P with those in Genbank releaved homology to the DD3 gene (Genbank accession numbers AF103907 & AF103908). The cDNA sequence of DD3 is provided in SEQ ID NO: 690.

EXAMPLE 17

PROTEIN EXPRESSION OF PROSTATE-SPECIFIC ANTIGENS

This example describes the expression and purification of prostate-specific antigens in *E. coli*, baculovirus and mammalian cells.

a) Expression of P501S in *E. coli*

Expression of the full-length form of P501S was attempted by first cloning P501S without the leader sequence (amino acids 36-553 of SEQ ID NO: 113) downstream of the first 30 amino acids of the *M. tuberculosis* antigen Ra12 (SEQ ID NO: 484) in pET17b. Specifically, P501S DNA was used to perform PCR using the primers AW025 (SEQ ID NO: 485) and AW003 (SEQ ID NO: 486). AW025 is a sense cloning primer that contains a HindIII site. AW003 is an antisense cloning primer that contains an EcoRI site. DNA amplification was performed using 5 μl 10X Pfu buffer, 1 μl 20 mM dNTPs, 1 μl each of the PCR primers at 10 μM concentration, 40 μl water, 1 μl Pfu DNA polymerase (Stratagene, La Jolla, CA) and 1 μl DNA at 100 ng/μl. Denaturation at 95°C was performed for 30 sec, followed by 10 cycles of 95°C for 30 sec, 60°C for 1 min and by 72°C for 3 min. 20 cycles of 95°C for 30 sec, 65°C for 1 min and by 72°C for 3 min, and lastly by 1 cycle of 72°C for 10 min. The PCR product was

cloned to Ra12m/pET17b using HindIII and EcoRI. The sequence of the resulting fusion construct (referred to as Ra12-P501S-F) was confirmed by DNA sequencing.

The fusion construct was transformed into BL21(DE3)pLysE, pLysS and CodonPlus *E. coli* (Stratagene) and grown overnight in LB broth with kanamycin. The resulting culture was induced with IPTG. Protein was transferred to PVDF membrane and blocked with 5% non-fat milk (in PBS-Tween buffer), washed three times and incubated with mouse anti-His tag antibody (Clontech) for 1 hour. The membrane was washed 3 times and probed with HRP-Protein A (Zymed) for 30 min. Finally, the membrane was washed 3 times and developed with ECL (Amersham). No expression was detected by Western blot. Similarly, no expression was detected by Western blot when the Ra12-P501S-F fusion was used for expression in BL21CodonPlus by CE6 phage (Invitrogen).

An N-terminal fragment of P501S (amino acids 36-325 of SEQ ID NO: 113) was cloned down-stream of the first 30 amino acids of the *M. tuberculosis* antigen Ra12 in pET17b as follows. P501S DNA was used to perform PCR using the primers AW025 (SEQ ID NO: 485) and AW027 (SEQ ID NO: 487). AW027 is an antisense cloning primer that contains an EcoRI site and a stop codon. DNA amplification was performed essentially as described above. The resulting PCR product was cloned to Ra12 in pET17b at the HindIII and EcoRI sites. The fusion construct (referred to as Ra12-P501S-N) was confirmed by DNA sequencing.

The Ra12-P501S-N fusion construct was used for expression in BL21(DE3)pLysE, pLysS and CodonPlus, essentially as described above. Using Western blot analysis, protein bands were observed at the expected molecular weight of 36 kDa. Some high molecular weight bands were also observed, probably due to aggregation of the recombinant protein. No expression was detected by Western blot when the Ra12-P501S-F fusion was used for expression in BL21CodonPlus by CE6 phage.

A fusion construct comprising a C-terminal portion of P501S (amino acids 257-553 of SEQ ID NO: 113) located down-stream of the first 30 amino acids of the *M. tuberculosis* antigen Ra12 (SEQ ID NO: 484) was prepared as follows. P501S

DNA was used to perform PCR using the primers AW026 (SEQ ID NO: 488) and AW003 (SEQ ID NO: 486). AW026 is a sense cloning primer that contains a HindIII site. DNA amplification was performed essentially as described above. The resulting PCR product was cloned to Ra12 in pET17b at the HindIII and EcoRI sites. The sequence for the fusion construct (referred to as Ra12-P501S-C) was confirmed.

The Ra12-P501S-C fusion construct was used for expression in BL21(DE3)pLysE, pLysS and CodonPlus, as described above. A small amount of protein was detected by Western blot, with some molecular weight aggregates also being observed. Expression was also detected by Western blot when the Ra12-P501S-C fusion was used for expression in BL21CodonPlus induced by CE6 phage.

A fusion construct comprising a fragment of P501S (amino acids 36-298 of SEQ ID NO: 113) located down-stream of the *M. tuberculosis* antigen Ra12 (SEQ ID NO: 848) was prepared as follows. P501S DNA was used to perform PCR using the primers AW042 (SEQ ID NO: 849) and AW053 (SEQ ID NO: 850). AW042 is a sense cloning primer that contains a EcoRI site. AW053 is an antisense primer with stop and Xho I sites. DNA amplification was performed essentially as described above. The resulting PCR product was cloned to Ra12 in pET17b at the EcoRI and Xho I sites. The resulting fusion construct (referred to as Ra12-P501S-E2) was expressed in B834 (DE3) pLys S *E. coli* host cells in TB media for 2 h at room temperature. Expressed protein was purified by washing the inclusion bodies and running on a Ni-NTA column. The purified protein stayed soluble in buffer containing 20 mM Tris-HCl (pH 8), 100 mM NaCl, 10 mM β-Me and 5% glycerol. The determined cDNA and amino acid sequences for the expressed fusion protein are provided in SEQ ID NO: 851 and 852, respectfully.

b) Expression of P501S in Baculovirus

The Bac-to-Bac baculovirus expression system (BRL Life Technologies, Inc.) was used to express P501S protein in insect cells. Full-length P501S (SEQ ID NO: 113) was amplified by PCR and cloned into the XbaI site of the donor plasmid pFastBacI. The recombinant bacmid and baculovirus were prepared according to the

manufacturer's instructions. The recombinant baculovirus was amplified in Sf9 cells and the high titer viral stocks were utilized to infect High Five cells (Invitrogen) to make the recombinant protein. The identity of the full-length protein was confirmed by N-terminal sequencing of the recombinant protein and by Western blot analysis (Figure 7). Specifically, 0.6 million High Five cells in 6-well plates were infected with either the unrelated control virus BV/ECD_PD (lane 2), with recombinant baculovirus for P501S at different amounts or MOIs (lanes 4-8), or were uninfected (lane 3). Cell lysates were run on SDS-PAGE under reducing conditions and analyzed by Western blot with the anti-P501S monoclonal antibody P501S-10E3-G4D3 (prepared as described below). Lane 1 is the biotinylated protein molecular weight marker (BioLabs).

The localization of recombinant P501S in the insect cells was investigated as follows. The insect cells overexpressing P501S were fractionated into fractions of nucleus, mitochondria, membrane and cytosol. Equal amounts of protein from each fraction were analyzed by Western blot with a monoclonal antibody against P501S. Due to the scheme of fractionation, both nucleus and mitochondria fractions contain some plasma membrane components. However, the membrane fraction is basically free from mitochondria and nucleus. P501S was found to be present in all fractions that contain the membrane component, suggesting that P501S may be associated with plasma membrane of the insect cells expressing the recombinant protein.

c) Expression of P501S in mammalian cells

Full-length P501S (553 amino acids; SEQ ID NO: 113) was cloned into various mammalian expression vectors, including pCEP4 (Invitrogen), pVR1012 (Vical, San Diego, CA) and a modified form of the retroviral vector pBMN, referred to as pBIB. Transfection of P501S/pCEP4 and P501S/pVR1012 into HEK293 fibroblasts was carried out using the Fugene transfection reagent (Boehringer Mannheim). Briefly, 2 ul of Fugene reagent was diluted into 100 ul of serum-free media and incubated at room temperature for 5-10 min. This mixture was added to 1 ug of P501S plasmid DNA, mixed briefly and incubated for 30 minutes at room temperature. The

Fugene/DNA mixture was added to cells and incubated for 24-48 hours. Expression of recombinant P501S in transfected HEK293 fibroblasts was detected by means of Western blot employing a monoclonal antibody to P501S.

Transfection of p501S/pCEP4 into CHO-K cells (American Type Culture Collection, Rockville, MD) was carried out using GenePorter transfection reagent (Gene Therapy Systems, San Diego, CA). Briefly, 15 µl of GenePorter was diluted in 500 µl of serum-free media and incubated at room temperature for 10 min. The GenePorter/media mixture was added to 2 µg of plasmid DNA that was diluted in 500 µl of serum-free media, mixed briefly and incubated for 30 min at room temperature. CHO-K cells were rinsed in PBS to remove serum proteins, and the GenePorter/DNA mix was added and incubated for 5 hours. The transfected cells were then fed an equal volume of 2x media and incubated for 24-48 hours.

FACS analysis of P501S transiently infected CHO-K cells, demonstrated surface expression of P501S. Expression was detected using rabbit polyclonal antisera raised against a P501S peptide, as described below. Flow cytometric analysis was performed using a FaCScan (Becton Dickinson), and the data were analyzed using the Cell Quest program.

d) Expression of P703P in Baculovirus

The cDNA for full-length P703P-DE5 (SEQ ID NO: 326), together with several flanking restriction sites, was obtained by digesting the plasmid pCDNA703 with restriction endonucleases Xba I and Hind III. The resulting restriction fragment (approx. 800 base pairs) was ligated into the transfer plasmid pFastBacI which was digested with the same restriction enzymes. The sequence of the insert was confirmed by DNA sequencing. The recombinant transfer plasmid pFBP703 was used to make recombinant bacmid DNA and baculovirus using the Bac-To-Bac Baculovirus expression system (BRL Life Technologies). High Five cells were infected with the recombinant virus BVP703, as described above, to obtain recombinant P703P protein.

e) Expression of P788P in *E. Coli*

A truncated, N-terminal portion, of P788P (residues 1-644 of SEQ ID NO: 777; referred to as P788P-N) fused with a C-terminal 6xHis Tag was expressed in *E. coli* as follows. P788P cDNA was amplified using the primers AW080 and AW081 (SEQ ID NO: 815 and 816). AW080 is a sense cloning primer with an NdeI site. AW081 is an antisense cloning primer with a XhoI site. The PCR-amplified P788P, as well as the vector pCRX1, were digested with NdeI and XhoI. Vector and insert were ligated and transformed into NovaBlue cells. Colonies were randomly screened for insert and then sequenced. P788P-N clone #6 was confirmed to be identical to the designed construct. The expression construct P788P-N #6/pCRX1 was transformed into *E. coli* BL21 CodonPlus-RIL competent cells. After induction, most of the cells grew well, achieving OD600 of greater than 2.0 after 3 hr. Coomassie stained SDS-PAGE showed an over-expressed band at about 75 kD. Western blot analysis using a 6xHisTag antibody confirmed the band was P788P-N. The determined cDNA sequence for P788P-N is provided in SEQ ID NO: 817, with the corresponding amino acid sequence being provided in SEQ ID NO: 818.

f) Expression of P510S in *E. coli*

The P510S protein has 9 potential transmembrane domains and is predicted to be located at the plasma membrane. The C-terminal protein of this protein, as well as the predicted third extracellular domain of P510S were expressed in *E. coli* as follows.

The expression construct referred to as Ra12-P501S-C was designed to have a 6 HisTag at the N-terminal enc, followed by the *M. tuberculosis* antigen Ra12 (SEQ ID NO: 819) and then the C-terminal portion of P510S (amino residues 1176-1261 of SEQ ID NO: 538). Full-length P510S was used to amplify the P510S-C fragment by PCR using the primers AW056 and AW057 (SEQ ID NO: 820 and 821, respectively). AW056 is a sense cloning primer with an EcoRI site. AW057 is an antisense primer with stop and XhoI sites. The amplified P501S fragment and Ra12/pCRX1 were digested with EcoRI and XhoI and then purified. The insert and

vector were ligated together and transformed into NovaBlue. Colonies were randomly screened for insert and sequences. For protein expression, the expression construct was transformed into *E. coli* BL21 (DE3) CodonPlus-RIL competent cells. A mini-induction screen was performed to optimize the expression conditions. After induction the cells grew well, achieving OD 600 nm greater than 2.0 after 3 hours. Coomassie stain SDS-PAGE showed a highly over-expressed band at approx. 30 kD. Though this is higher than the expected molecular weight, western blot analysis was positive, showing this band to be the His tag-containing protein. The optimized culture conditions are as follows. Dilute overnight culture/daytime culture (LB + kanamycin + chloramphenicol) into 2xYT (with kanamycin and chloramphenicol) at a ratio of 25 ml culture to 1 liter 2xYT. Allow to grow at 37 °C until OD600 = 0.6. Take an aliquot out as T0 sample. Add 1 mM IPTG and allow to grow at 30 °C for 3 hours. Take out a T3 sample, spin down cells and store at -80 °C. The determined cDNA and amino acid sequences for the Ra12-P510S-C construct are provided in SEQ ID NO: 822 and 825, respectively.

The expression construct P510S-C was designed to have a 5' added start codon and a glycine (GGA) codon and then the P510S C terminal fragment followed by the in frame 6x histidine tag and stop codon from the pET28b vector. The cloning strategy is similar to that used for Ra12-P510S-C, except that the PCR primers employed were those shown in SEQ ID NO: 828 and 829, respectively and the NcoI/XhoI cut in pET28b was used. The primer of SEQ ID NO: 828 created a 5' NcoI site and added a start codon. The antisense primer of SEQ ID NO: 829 creates a XhoI site on P510S C terminal fragment. Clones were confirmed by sequencing. For protein expression, the expression construct was transformed into *E. coli* BL21 (DE3) CodonPlus-RIL competent cells. An OD600 of greater than 2.0 was obtained 30 hours after induction. Coomassie stained SDS-PAGE showed an over-expressed band at about 11 kD. Western blot analysis confirmed that the band was P510S-C, as did N-terminal protein sequencing. The optimized culture conditions are as follows: dilute overnight culture/daytime culture (LB + kanamycin + chloramphenicol) into 2x YT (+ kanamycin and chloramphenicol) at a ratio of 25 mL culture to 1 liter 2x YT, and allow

to grow at 37 °C until an OD 600 of about 0.5 is reached. Take out an aliquot as T0 sample. Add 1 mM IPTG and allow to grow at 30 °C for 3 hours. Spin down the cells and store at -80 °C until purification. The determined cDNA and amino acid sequences for the P510S-C construct are shown in SEQ ID NO: 823 and 826, respectively.

The predicted third extracellular domain of P510S (P510S-E3; residues 328-676 of SEQ ID NO: 538) was expressed in *E. coli* as follows. The P510S fragment was amplified by PCR using the primers shown in SEQ ID NO: 830 and 831. The primer of SEQ ID NO: 830 is a sense primer with an NdeI site for use in ligating into pPDM. The primer of SEQ ID NO: 831 is an antisense primer with an added XhoI site for use in ligating into pPDM. The resulting fragment was cloned to pPDM at the NdeI and XhoI sites. Clones were confirmed by sequencing. For protein expression, the clone ws transformed into E. coli BL21 (DE3) CodonPlus-RIL competent cells. After induction, an OD600 of greater than 2.0 was achieved after 3 hours. Coomassie stained SDS-PAGE showed an over-expressed band at about 39 kD, and N-terminal sequencing confirmed the N-terminal to be that of P510S-E3. Optimized culture conditions are as follows: dilute overnight culture/daytime culture (LB + kanamycin + chloramphenicol) into 2x YT (kanamycin and chloramphenicol) at a ratio of 25 ml culture to 1 liter 2x YT. Allow to grow at 37 °C until OD 600 equals 0.6. Take out an aliquot as T0 sample. Add 1 mM IPTG and allow to grow at 30 °C for 3 hours. Take out a T3 sample, spin down the cells and store at -80 °C until purification. The determined cDNA and amino acid sequences for the P501S-E3 construct are provided in SEQ ID NO: 824 and 827, respectively.

g) Expression of P775S in *E. Coli*

The antigen P775P contains multiple open reading frames (ORF). The third ORF, encoding the protein of SEQ ID NO: 483, has the best emotif score. An expression fusion construct containing the *M. tuberculosis* antigen Ra12 (SEQ ID NO: 819) and P775P-ORF3 with an N-terminal 6x HisTag was prepared as follows. P775P-ORF3 was amplified using the sense PCR primers of SEQ ID NO: 832 and the anti-sense PCR primer of SEQ ID NO: 833. The PCR amplified fragment of P775P and

Ra12/pCRX1 were digested with the restriction enzymes EcoRI and XhoI. Vector and insert were ligated and then transformed into NovaBlue cells. Colonies were randomly screened for insert and then sequenced. A clone having the desired sequence was transformed into E. coli BL21 (DE3) CodonPlus-RIL competent cells. Two hours after induction, the cell density peaked at OD600 of approximately 1.8. Coomassie stained SDS-PAGE showed an over-expressed band at about 31 kD. Western blot using 6x HisTag antibody confirmed that the band was Ra12-P775P-ORF3. The determined cDNA and amino acid sequences for the fusion construct are provided in SEQ ID NO: 834 and 835, respectively.

H) <u>Expression of a P703P His tag fusion protein in *E. coli*</u>

The cDNA for the coding region of P703P was prepared by PCR using the primers of SEQ ID NO: 836 and 837. The PCR product was digested with EcoRI restriction enzyme, gel purified and cloned into a modified pET28 vector with a His tag in frame, which had been digested with Eco72I and EcoRI restriction enzymes. The correct construct was confirmed by DNA sequence analysis and then transformed into *E. coli* BL21 (DE3) pLys S expression host cells. The determined amino acid and cDNA sequences for the expressed recombinant P703P are provided in SEQ ID NO: 838 and 839, respectively.

I) <u>Expression of a P705P His tag fusion protein in *E. coli*</u>

The cDNA for the coding region of P705P was prepared by PCR using the primers of SEQ ID NO: 840 and 841. The PCR product was digested with EcoRI restriction enzyme, gel purified and cloned into a modified pET28 vector with a His tag in frame, which had been digested with Eco72I and EcoRI restriction enzymes. The correct construct was confirmed by DNA sequence analysis and then transformed into *E. coli* BL21 (DE3) pLys S and BL21 (DE3) CodonPlus expression host cells. The determined amino acid and cDNA sequences for the expressed recombinant P705P are provided in SEQ ID NO: 842 and 843, respectively.

J) Expression of a P711P His tag fusion protein in *E. coli*

The cDNA for the coding region of P711P was prepared by PCR using the primers of SEQ ID NO: 844 and 845. The PCR product was digested with EcoRI restriction enzyme, gel purified and cloned into a modified pET28 vector with a His tag in frame, which had been digested with Eco72I and EcoRI restriction enzymes. The correct construct was confirmed by DNA sequence analysis and then transformed into *E. coli* BL21 (DE3) pLys S and BL21 (DE3) CodonPlus expression host cells. The determined amino acid and cDNA sequences for the expressed recombinant P711P are provided in SEQ ID NO: 846 and 847, respectively.

K) Expression of P767P in *E. coli*

The full-length coding region of P767P (amino acids 2-374 of SEQ ID NO: 590) was amplified by PCR using the primers PDM-468 and PDM-469 (SEQ ID NO: 935 and 936, respectively). DNA amplification was performed using 10 μl 10X Pfu buffer, 1 μl 10 mM dNTPs, 2 μl each of the PCR primers at 10 μM concentration, 83 μl water, 1.5 μl Pfu DNA polymerase (Stratagene, La Jolla, CA) and 1 μl DNA at 100 ng/μl. Denaturation at 96°C was performed for 2 min, followed by 40 cycles of 96°C for 20 sec, 66°C for 15 sec and by 72°C for 2 min., and lastly by 1 cycle of 72°C for 4 min. The PCR product was digested with XhoI and cloned into a modified pET28 vector with a histidine tag in frame on the 5' end that was digested with Eco72I and XhoI. The construct was confirmed to be correct through sequence analysis and transformed into *E. coli* BL21 pLysS and BL21 CodonPlus RP cells. The cDNA coding region for the recombinant B767P protein is provided in SEQ ID NO: 938, with the corresponding amino acid sequence being provided in SEQ ID NO: 941. The full-length P767P did not express at high enough levels for detection or purification.

A truncated coding region of P767P (referred to as B767P-B; amino acids 47-374 of SEQ ID NO: 590) was amplified by PCR using the primers PDM-573 and PDM-469 (SEQ ID NO: 937 and 936, respectively) and the PCR conditions described above for full-length P767P. The PCR product was digested with XhoI and cloned into the modified pET28 vector that was digested with Eco72I and XhoI. The

construct was confirmed to be correct through sequence analysis and transformed into *E. coli* BL21 pLysS and BL21 CodonPlus RP cells. The protein was found to be expressed in the inclusion body pellet. The coding region for the expressed B767P-B protein is provided in SEQ ID NO: 939, with the corresponding amino acid sequence being provided in SEQ ID NO: 940.

EXAMPLE 18

PREPARATION AND CHARACTERIZATION OF ANTIBODIES AGAINST PROSTATE-SPECIFIC POLYPEPTIDES

a) Preparation and Characterization of Polyclonal Antibodies against P703P, P504S and P509S

Polyclonal antibodies against P703P, P504S and P509S were prepared as follows.

Each prostate tumor antigen expressed in an *E. coli* recombinant expression system was grown overnight in LB broth with the appropriate antibiotics at 37°C in a shaking incubator. The next morning, 10 ml of the overnight culture was added to 500 ml to 2x YT plus appropriate antibiotics in a 2L-baffled Erlenmeyer flask. When the Optical Density (at 560 nm) of the culture reached 0.4-0.6, the cells were induced with IPTG (1 mM). Four hours after induction with IPTG, the cells were harvested by centrifugation. The cells were then washed with phosphate buffered saline and centrifuged again. The supernatant was discarded and the cells were either frozen for future use or immediately processed. Twenty ml of lysis buffer was added to the cell pellets and vortexed. To break open the *E. coli* cells, this mixture was then run through the French Press at a pressure of 16,000 psi. The cells were then centrifuged again and the supernatant and pellet were checked by SDS-PAGE for the partitioning of the recombinant protein. For proteins that localized to the cell pellet, the pellet was resuspended in 10 mM Tris pH 8.0, 1% CHAPS and the inclusion body pellet was washed and centrifuged again. This procedure was repeated twice more. The washed

inclusion body pellet was solubilized with either 8 M urea or 6 M guanidine HCl containing 10 mM Tris pH 8.0 plus 10 mM imidazole. The solubilized protein was added to 5 ml of nickel-chelate resin (Qiagen) and incubated for 45 min to 1 hour at room temperature with continuous agitation. After incubation, the resin and protein mixture were poured through a disposable column and the flow through was collected. The column was then washed with 10-20 column volumes of the solubilization buffer. The antigen was then eluted from the column using 8M urea, 10 mM Tris pH 8.0 and 300 mM imidazole and collected in 3 ml fractions. A SDS-PAGE gel was run to determine which fractions to pool for further purification.

As a final purification step, a strong anion exchange resin such as HiPrepQ (Biorad) was equilibrated with the appropriate buffer and the pooled fractions from above were loaded onto the column. Each antigen was eluted off the column with a increasing salt gradient. Fractions were collected as the column was run and another SDS-PAGE gel was run to determine which fractions from the column to pool. The pooled fractions were dialyzed against 10 mM Tris pH 8.0. The proteins were then vialed after filtration through a 0.22 micron filter and the antigens were frozen until needed for immunization.

Four hundred micrograms of each prostate antigen was combined with 100 micrograms of muramyldipeptide (MDP). Every four weeks rabbits were boosted with 100 micrograms mixed with an equal volume of Incomplete Freund's Adjuvant (IFA). Seven days following each boost, the animal was bled. Sera was generated by incubating the blood at 4°C for 12-4 hours followed by centrifugation.

Ninety-six well plates were coated with antigen by incubating with 50 microliters (typically 1 microgram) of recombinant protein at 4 °C for 20 hours. 250 microliters of BSA blocking buffer was added to the wells and incubated at room temperature for 2 hours. Plates were washed 6 times with PBS/0.01% Tween. Rabbit sera was diluted in PBS. Fifty microliters of diluted sera was added to each well and incubated at room temperature for 30 min. Plates were washed as described above before 50 microliters of goat anti-rabbit horse radish peroxidase (HRP) at a 1:10000 dilution was added and incubated at room temperature for 30 min. Plates were again

washed as described above and 100 microliters of TMB microwell peroxidase substrate was added to each well. Following a 15 min incubation in the dark at room temperature, the colorimetric reaction was stopped with 100 microliters of 1N H_2SO_4 and read immediately at 450 nm. All polyclonal antibodies showed immunoreactivity to the appropriate antigen.

b) Preparation and Characterization of Antibodies against P501S

A murine monoclonal antibody directed against the carboxy-terminus of the prostate-specific antigen P501S was prepared as follows.

A truncated fragment of P501S (amino acids 355-526 of SEQ ID NO: 113) was generated and cloned into the pET28b vector (Novagen) and expressed in *E. coli* as a thioredoxin fusion protein with a histidine tag. The trx-P501S fusion protein was purified by nickel chromatography, digested with thrombin to remove the trx fragment and further purified by an acid precipitation procedure followed by reverse phase HPLC.

Mice were immunized with truncated P501S protein. Serum bleeds from mice that potentially contained anti-P501S polyclonal sera were tested for P501S-specific reactivity using ELISA assays with purified P501S and trx-P501S proteins. Serum bleeds that appeared to react specifically with P501S were then screened for P501S reactivity by Western analysis. Mice that contained a P501S-specific antibody component were sacrificed and spleen cells were used to generate anti-P501S antibody producing hybridomas using standard techniques. Hybridoma supernatants were tested for P501S-specific reactivity initially by ELISA, and subsequently by FACS analysis of reactivity with P501S transduced cells. Based on these results, a monoclonal hybridoma referred to as 10E3 was chosen for further subcloning. A number of subclones were generated, tested for specific reactivity to P501S using ELISA and typed for IgG isotype. The results of this analysis are shown below in Table V. Of the 16 subclones tested, the monoclonal antibody 10E3-G4-D3 was selected for further study.

Table V

Isotype analysis of murine anti-P501S monoclonal antibodies

Hybridoma clone	Isotype	Estimated [Ig] in supernatant (μg/ml)
4D11	IgG1	14.6
1G1	IgG1	0.6
4F6	IgG1	72
4H5	IgG1	13.8
4H5-E12	IgG1	10.7
4H5-EH2	IgG1	9.2
4H5-H2-A10	IgG1	10
4H5-H2-A3	IgG1	12.8
4H5-H2-A10-G6	IgG1	13.6
4H5-H2-B11	IgG1	12.3
10E3	IgG2a	3.4
10E3-D4	IgG2a	3.8
10E3-D4-G3	IgG2a	9.5
10E3-D4-G6	IgG2a	10.4
10E3-E7	IgG2a	6.5
8H12	IgG2a	0.6

The specificity of 10E3-G4-D3 for P501S was examined by FACS analysis. Specifically, cells were fixed (2% formaldehyde, 10 minutes), permeabilized (0.1% saponin, 10 minutes) and stained with 10E3-G4-D3 at 0.5 – 1 μg/ml, followed by incubation with a secondary, FITC-conjugated goat anti-mouse Ig antibody (Pharmingen, San Diego, CA). Cells were then analyzed for FITC fluorescence using an Excalibur fluorescence activated cell sorter. For FACS analysis of transduced cells, B-LCL were retrovirally transduced with P501S. For analysis of infected cells, B-LCL were infected with a vaccinia vector that expresses P501S. To demonstrate specificity in these assays, B-LCL transduced with a different antigen (P703P) and uninfected B-LCL vectors were utilized. 10E3-G4-D3 was shown to bind with P501S-transduced B-LCL and also with P501S-infected B-LCL, but not with either uninfected cells or P703P-transduced cells.

To determine whether the epitope recognized by 10E3-G4-D3 was found on the surface or in an intracellular compartment of cells, B-LCL were transduced with P501S or HLA-B8 as a control antigen and either fixed and permeabilized as described

above or directly stained with 10E3-G4-D3 and analyzed as above. Specific recognition of P501S by 10E3-G4-D3 was found to require permeabilization, suggesting that the epitope recognized by this antibody is intracellular.

The reactivity of 10E3-G4-D3 with the three prostate tumor cell lines Lncap, PC-3 and DU-145, which are known to express high, medium and very low levels of P501S, respectively, was examined by permeabilizing the cells and treating them as described above. Higher reactivity of 10E3-G4-D3 was seen with Lncap than with PC-3, which in turn showed higher reactivity that DU-145. These results are in agreement with the real time PCR and demonstrate that the antibody specifically recognizes P501S in these tumor cell lines and that the epitope recognized in prostate tumor cell lines is also intracellular.

Specificity of 10E3-G4-D3 for P501S was also demonstrated by Western blot analysis. Lysates from the prostate tumor cell lines Lncap, DU-145 and PC-3, from P501S-transiently transfected HEK293 cells, and from non-transfected HEK293 cells were generated. Western blot analysis of these lysates with 10E3-G4-D3 revealed a 46 kDa immunoreactive band in Lncap, PC-3 and P501S-transfected HEK cells, but not in DU-145 cells or non-transfected HEK293 cells. P501S mRNA expression is consistent with these results since semi-quantitative PCR analysis revealed that P501S mRNA is expressed in Lncap, to a lesser but detectable level in PC-3 and not at all in DU-145 cells. Bacterially expressed and purified recombinant P501S (referred to as P501SStr2) was recognized by 10E3-G4-D3 (24 kDa), as was full-length P501S that was transiently expressed in HEK293 cells using either the expression vector VR1012 or pCEP4. Although the predicted molecular weight of P501S is 60.5 kDa, both transfected and "native" P501S run at a slightly lower mobility due to its hydrophobic nature.

Immunohistochemical analysis was performed on prostate tumor and a panel of normal tissue sections (prostate, adrenal, breast, cervix, colon, duodenum, gall bladder, ileum, kidney, ovary, pancreas, parotid gland, skeletal muscle, spleen and testis). Tissue samples were fixed in formalin solution for 24 hours and embedded in paraffin before being sliced into 10 micron sections. Tissue sections were permeabilized and incubated with 10E3-G4-D3 antibody for 1 hr. HRP-labeled anti-

mouse followed by incubation with DAB chromogen was used to visualize P501S immunoreactivity. P501S was found to be highly expressed in both normal prostate and prostate tumor tissue but was not detected in any of the other tissues tested.

To identify the epitope recognized by 10E3-G4-D3, an epitope mapping approach was pursued. A series of 13 overlapping 20-21 mers (5 amino acid overlap; SEQ ID NO: 489-501) was synthesized that spanned the fragment of P501S used to generate 10E3-G4-D3. Flat bottom 96 well microtiter plates were coated with either the peptides or the P501S fragment used to immunize mice, at 1 microgram/ml for 2 hours at 37 °C. Wells were then aspirated and blocked with phosphate buffered saline containing 1% (w/v) BSA for 2 hours at room temperature, and subsequently washed in PBS containing 0.1% Tween 20 (PBST). Purified antibody 10E3-G4-D3 was added at 2 fold dilutions (1000 ng – 16 ng) in PBST and incubated for 30 minutes at room temperature. This was followed by washing 6 times with PBST and subsequently incubating with HRP-conjugated donkey anti-mouse IgG (H+L)Affinipure F(ab') fragment (Jackson Immunoresearch, West Grove, PA) at 1:20000 for 30 minutes. Plates were then washed and incubated for 15 minutes in tetramethyl benzidine. Reactions were stopped by the addition of 1N sulfuric acid and plates were read at 450 nm using an ELISA plate reader. As shown in Fig. 8, reactivity was seen with the peptide of SEQ ID NO: 496 (corresponding to amino acids 439-459 of P501S) and with the P501S fragment but not with the remaining peptides, demonstrating that the epitope recognized by 10E3-G4-D3 is localized to amino acids 439-459 of SEQ ID NO: 113.

In order to further evaluate the tissue specificity of P501S, multi-array immunohistochemical analysis was performed on approximately 4700 different human tissues encompassing all the major normal organs as well as neoplasias derived from these tissues. Sixty-five of these human tissue samples were of prostate origin. Tissue sections 0.6 mm in diameter were formalin-fixed and paraffin embedded. Samples were pretreated with HIER using 10 mM citrate buffer pH 6.0 and boiling for 10 min. Sections were stained with 10E3-G4-D3 and P501S immunoreactivity was visualized with HRP. All the 65 prostate tissues samples (5 normal, 55 untreated prostate tumors,

5 hormone refractory prostate tumors) were positive, showing distinct perinuclear staining. All other tissues examined were negative for P501S expression.

c) Preparation and Characterization of Antibodies against P503S

A fragment of P503S (amino acids 113-241 of SEQ ID NO: 114) was expressed and purified from bacteria essentially as described above for P501S and used to immunize both rabbits and mice. Mouse monoclonal antibodies were isolated using standard hybridoma technology as described above. Rabbit monoclonal antibodies were isolated using Selected Lymphocyte Antibody Method (SLAM) technology at Immgenics Pharmaceuticals (Vancouver, BC, Canada). Table VI, below, lists the monoclonal antibodies that were developed against P503S.

Table VI

Antibody	Species
20D4	Rabbit
JA1	Rabbit
1A4	Mouse
1C3	Mouse
1C9	Mouse
1D12	Mouse
2A11	Mouse
2H9	Mouse
4H7	Mouse
8A8	Mouse
8D10	Mouse
9C12	Mouse
6D12	Mouse

The DNA sequences encoding the complementarity determining regions (CDRs) for the rabbit monoclonal antibodies 20D4 and JA1 were determined and are provided in SEQ ID NO: 502 and 503, respectively.

In order to better define the epitope binding region of each of the antibodies, a series of overlapping peptides were generated that span amino acids 109-213 of SEQ ID NO: 114. These peptides were used to epitope map the anti-P503S monoclonal antibodies by ELISA as follows. The recombinant fragment of P503S that was employed as the immunogen was used as a positive control. Ninety-six well microtiter plates were coated with either peptide or recombinant antigen at 20 ng/well overnight at 4 °C. Plates were aspirated and blocked with phosphate buffered saline containing 1% (w/v) BSA for 2 hours at room temperature then washed in PBS containing 0.1% Tween 20 (PBST). Purified rabbit monoclonal antibodies diluted in PBST were added to the wells and incubated for 30 min at room temperature. This was followed by washing 6 times with PBST and incubation with Protein-A HRP conjugate at a 1:2000 dilution for a further 30 min. Plates were washed six times in PBST and incubated with tetramethylbenzidine (TMB) substrate for a further 15 min. The reaction was stopped by the addition of 1N sulfuric acid and plates were read at 450 nm using at ELISA plate reader. ELISA with the mouse monoclonal antibodies was performed with supernatants from tissue culture run neat in the assay.

All of the antibodies bound to the recombinant P503S fragment, with the exception of the negative control SP2 supernatant. 20D4, JA1 and 1D12 bound strictly to peptide #2101 (SEQ ID NO: 504), which corresponds to amino acids 151-169 of SEQ ID NO: 114. 1C3 bound to peptide #2102 (SEQ ID NO: 505), which corresponds to amino acids 165-184 of SEQ ID NO: 114. 9C12 bound to peptide #2099 (SEQ ID NO: 522), which corresponds to amino acids 120-139 of SEQ ID NO: 114. The other antibodies bind to regions that were not examined in these studies.

Subsequent to epitope mapping, the antibodies were tested by FACS analysis on a cell line that stably expressed P503S to confirm that the antibodies bind to cell surface epitopes. Cells stably transfected with a control plasmid were employed as a negative control. Cells were stained live with no fixative. 0.5 ug of anti-P503S monoclonal antibody was added and cells were incubated on ice for 30 min before being washed twice and incubated with a FITC-labelled goat anti-rabbit or mouse secondary antibody for 20 min. After being washed twice, cells were analyzed with an Excalibur

fluorescent activated cell sorter. The monoclonal antibodies 1C3, 1D12, 9C12, 20D4 and JA1, but not 8D3, were found to bind to a cell surface epitope of P503S.

In order to determine which tissues express P503S, immunohistochemical analysis was performed, essentially as described above, on a panel of normal tissues (prostate, adrenal, breast, cervix, colon, duodenum, gall bladder, ileum, kidney, ovary, pancreas, parotid gland, skeletal muscle, spleen and testis). HRP-labeled anti-mouse or anti-rabbit antibody followed by incubation with TMB was used to visualize P503S immunoreactivity. P503S was found to be highly expressed in prostate tissue, with lower levels of expression being observed in cervix, colon, ileum and kidney, and no expression being observed in adrenal, breast, duodenum, gall bladder, ovary, pancreas, parotid gland, skeletal muscle, spleen and testis.

Western blot analysis was used to characterize anti-P503S monoclonal antibody specificity. SDS-PAGE was performed on recombinant (rec) P503S expressed in and purified from bacteria and on lysates from HEK293 cells transfected with full length P503S. Protein was transferred to nitrocellulose and then Western blotted with each of the anti-P503S monoclonal antibodies (20D4, JA1, 1D12, 6D12 and 9C12) at an antibody concentration of 1 ug/ml. Protein was detected using horse radish peroxidase (HRP) conjugated to either a goat anti-mouse monoclonal antibody or to protein A-sepharose. The monoclonal antibody 20D4 detected the appropriate molecular weight 14 kDa recombinant P503S (amino acids 113-241) and the 23.5 kDa species in the HEK293 cell lysates transfected with full length P503S. Other anti-P503S monoclonal antibodies displayed similar specificity by Western blot.

d) Preparation and Characterization of Antibodies against P703P

Rabbits were immunized with either a truncated (P703Ptr1; SEQ ID NO: 172) or full-length mature form (P703Pfl; SEQ ID NO: 523) of recombinant P703P protein was expressed in and purified from bacteria as described above. Affinity purified polyclonal antibody was generated using immunogen P703Pfl or P703Ptr1 attached to a solid support. Rabbit monoclonal antibodies were isolated using SLAM

technology at Immgenics Pharmaceuticals. Table VII below lists both the polyclonal and monoclonal antibodies that were generated against P703P.

Table VII

Antibody	Immunogen	Species/type
Aff. Purif. P703P (truncated); #2594	P703Ptrl	Rabbit polyclonal
Aff. Purif. P703P (full length); #9245	P703Pfl	Rabbit polyclonal
2D4	P703Ptrl	Rabbit monoclonal
8H2	P703Ptrl	Rabbit monoclonal
7H8	P703Ptrl	Rabbit monoclonal

The DNA sequences encoding the complementarity determining regions (CDRs) for the rabbit monoclonal antibodies 8H2, 7H8 and 2D4 were determined and are provided in SEQ ID NO: 506-508, respectively.

Epitope mapping studies were performed as described above. Monoclonal antibodies 2D4 and 7H8 were found to specifically bind to the peptides of SEQ ID NO: 509 (corresponding to amino acids 145-159 of SEQ ID NO: 172) and SEQ ID NO: 510 (corresponding to amino acids 11-25 of SEQ ID NO: 172), respectively. The polyclonal antibody 2594 was found to bind to the peptides of SEQ ID NO: 511-514, with the polyclonal antibody 9427 binding to the peptides of SEQ ID NO: 515-517.

The specificity of the anti-P703P antibodies was determined by Western blot analysis as follows. SDS-PAGE was performed on (1) bacterially expressed recombinant antigen; (2) lysates of HEK293 cells and Ltk-/- cells either untransfected or transfected with a plasmid expressing full length P703P; and (3) supernatant isolated from these cell cultures. Protein was transferred to nitrocellulose and then Western blotted using the anti-P703P polyclonal antibody #2594 at an antibody concentration of 1 ug/ml. Protein was detected using horse radish peroxidase (HRP) conjugated to an anti-rabbit antibody. A 35 kDa immunoreactive band could be observed with recombinant P703P. Recombinant P703P runs at a slightly higher molecular weight since it is epitope tagged. In lysates and supernatants from cells transfected with full length P703P, a 30 kDa band corresponding to P703P was observed. To assure

specificity, lysates from HEK293 cells stably transfected with a control plasmid were also tested and were negative for P703P expression. Other anti-P703P antibodies showed similar results.

Immunohistochemical studies were performed as described above, using anti-P703P monoclonal antibody. P703P was found to be expressed at high levels in normal prostate and prostate tumor tissue but was not detectable in all other tissues tested (breast tumor, lung tumor and normal kidney).

e) Preparation and Characterization of Antibodies against P504S

Full-length P504S (SEQ ID NO: 108) was expressed and purified from bacteria essentially as described above for P501S and employed to raise rabbit monoclonal antibodies using Selected Lymphocyte Antibody Method (SLAM) technology at Immgenics Pharmaceuticals (Vancouver, BC, Canada). The anti-P504S monoclonal antibody 13H4 was shown by Western blot to bind to both expressed recombinant P504S and to native P504S in tumor cells.

Immunohistochemical studies using 13H4 to assess P504S expression in various prostate tissues were performed as described above. A total of 104 cases, including 65 cases of radical prostatectomies with prostate cancer (PC), 26 cases of prostate biopsies and 13 cases of benign prostate hyperplasia (BPH), were stained with the anti-P504S monoclonal antibody 13H4. P504S showed strongly cytoplasmic granular staining in 64/65 (98.5%) of PCs in prostatectomies and 26/26 (100%) of PCs in prostatic biopsies. P504S was stained strongly and diffusely in carcinomas (4+ in 91.2% of cases of PC; 3+ in 5.5%; 2+ in 2.2% and 1+ in 1.1%) and high grade prostatic intraepithelial neoplasia (4+ in all cases). The expression of P504S did not vary with Gleason score. Only 17/91 (18.7%) of cases of NP/BPH around PC and 2/13 (15.4%) of BPH cases were focally (1+, no 2+ to 4+ in all cases) and weakly positive for P504S in large glands. Expression of P504S was not found in small atrophic glands, postatrophic hyperplasia, basal cell hyperplasia and transitional cell metaplasia in either biopsies or prostatectomies. P504S was thus found to be over-expressed in all Gleason scores of prostate cancer (98.5 to 100% of sensitivity) and exhibited only focal positivities in

large normal glands in 19/104 of cases (82.3% of specificity). These findings indicate that P504S may be usefully employed for the diagnosis of prostate cancer.

EXAMPLE 19

CHARACTERIZATION OF CELL SURFACE EXPRESSION AND CHROMOSOME LOCALIZATION OF THE PROSTATE-SPECIFIC ANTIGEN P501S

This example describes studies demonstrating that the prostate-specific antigen P501S is expressed on the surface of cells, together with studies to determine the probable chromosomal location of P501S.

The protein P501S (SEQ ID NO: 113) is predicted to have 11 transmembrane domains. Based on the discovery that the epitope recognized by the anti-P501S monoclonal antibody 10E3-G4-D3 (described above in Example 17) is intracellular, it was predicted that following transmembrane determinants would allow the prediction of extracellular domains of P501S. Fig. 9 is a schematic representation of the P501S protein showing the predicted location of the transmembrane domains and the intracellular epitope described in Example 17. Underlined sequence represents the predicted transmembrane domains, bold sequence represents the predicted extracellular domains, and italicized sequence represents the predicted intracellular domains. Sequence that is both bold and underlined represents sequence employed to generate polyclonal rabbit serum. The location of the transmembrane domains was predicted using HHMTOP as described by Tusnady and Simon (Principles Governing Amino Acid Composition of Integral Membrane Proteins: Applications to Topology Prediction, *J. Mol. Biol. 283*:489-506, 1998).

Based on Fig. 9, the P501S domain flanked by the transmembrane domains corresponding to amino acids 274-295 and 323-342 is predicted to be extracellular. The peptide of SEQ ID NO: 518 corresponds to amino acids 306-320 of P501S and lies in the predicted extracellular domain. The peptide of SEQ ID NO: 519, which is identical to the peptide of SEQ ID NO: 518 with the exception of the substitution of the histidine with an asparginine, was synthesized as described above. A

Cys-Gly was added to the C-terminus of the peptide to facilitate conjugation to the carrier protein. Cleavage of the peptide from the solid support was carried out using the following cleavage mixture: trifluoroacetic acid:ethanediol:thioanisol:water:phenol (40:1:2:2:3). After cleaving for two hours, the peptide was precipitated in cold ether. The peptide pellet was then dissolved in 10% v/v acetic acid and lyophilized prior to purification by C18 reverse phase hplc. A gradient of 5-60% acetonitrile (containing 0.05% TFA) in water (containing 0.05% TFA) was used to elute the peptide. The purity of the peptide was verified by hplc and mass spectrometry, and was determined to be >95%. The purified peptide was used to generate rabbit polyclonal antisera as described above.

Surface expression of P501S was examined by FACS analysis. Cells were stained with the polyclonal anti-P501S peptide serum at 10 μg/ml, washed, incubated with a secondary FITC-conjugated goat anti-rabbit Ig antibody (ICN), washed and analyzed for FITC fluorescence using an Excalibur fluorescence activated cell sorter. For FACS analysis of transduced cells, B-LCL were retrovirally transduced with P501S. To demonstrate specificity in these assays, B-LCL transduced with an irrelevant antigen (P703P) or nontransduced were stained in parallel. For FACS analysis of prostate tumor cell lines, Lncap, PC-3 and DU-145 were utilized. Prostate tumor cell lines were dissociated from tissue culture plates using cell dissociation medium and stained as above. All samples were treated with propidium iodide (PI) prior to FACS analysis, and data was obtained from PI-excluding (*i.e.,* intact and non-permeabilized) cells. The rabbit polyclonal serum generated against the peptide of SEQ ID NO: 519 was shown to specifically recognize the surface of cells transduced to express P501S, demonstrating that the epitope recognized by the polyclonal serum is extracellular.

To determine biochemically if P501S is expressed on the cell surface, peripheral membranes from Lncap cells were isolated and subjected to Western blot analysis. Specifically, Lncap cells were lysed using a dounce homogenizer in 5 ml of homogenization buffer (250 mM sucrose, 10 mM HEPES, 1mM EDTA, pH 8.0, 1 complete protease inhibitor tablet (Boehringer Mannheim)). Lysate samples were spun at 1000 g for 5 min at 4 °C. The supernatant was then spun at 8000g for 10 min at 4 °C.

Supernatant from the 8000g spin was recovered and subjected to a 100,000g spin for 30 min at 4 °C to recover peripheral membrane. Samples were then separated by SDS-PAGE and Western blotted with the mouse monoclonal antibody 10E3-G4-D3 (described above in Example 17) using conditions described above. Recombinant purified P501S, as well as HEK293 cells transfected with and over-expressing P501S were included as positive controls for P501S detection. LCL cell lysate was included as a negative control. P501S could be detected in Lncap total cell lysate, the 8000g (internal membrane) fraction and also in the 100,000g (plasma membrane) fraction. These results indicate that P501S is expressed at, and localizes to, the peripheral membrane.

To demonstrate that the rabbit polyclonal antiserum generated to the peptide of SEQ ID NO: 519 specifically recognizes this peptide as well as the corresponding native peptide of SEQ ID NO: 518, ELISA analyses were performed. For these analyses, flat-bottomed 96 well microtiter plates were coated with either the peptide of SEQ ID NO: 519, the longer peptide of SEQ ID NO: 520 that spans the entire predicted extracellular domain, the peptide of SEQ ID NO: 521 which represents the epitope recognized by the P501S-specific antibody 10E3-G4-D3, or a P501S fragment (corresponding to amino acids 355-526 of SEQ ID NO: 113) that does not include the immunizing peptide sequence, at 1 μg/ml for 2 hours at 37 °C. Wells were aspirated, blocked with phosphate buffered saline containing 1% (w/v) BSA for 2 hours at room temperature and subsequently washed in PBS containing 0.1% Tween 20 (PBST). Purified anti-P501S polyclonal rabbit serum was added at 2 fold dilutions (1000 ng - 125 ng) in PBST and incubated for 30 min at room temperature. This was followed by washing 6 times with PBST and incubating with HRP-conjugated goat anti-rabbit IgG (H+L) Affinipure F(ab') fragment at 1:20000 for 30 min. Plates were then washed and incubated for 15 min in tetramethyl benzidine. Reactions were stopped by the addition of 1N sulfuric acid and plates were read at 450 nm using an ELISA plate reader. As shown in Fig. 11, the anti-P501S polyclonal rabbit serum specifically recognized the peptide of SEQ ID NO: 519 used in the immunization as well as the longer peptide of

SEQ ID NO: 520, but did not recognize the irrelevant P501S-derived peptides and fragments.

In further studies, rabbits were immunized with peptides derived from the P501S sequence and predicted to be either extracellular or intracellular, as shown in Fig. 9. Polyclonal rabbit sera were isolated and polyclonal antibodies in the serum were purified, as described above. To determine specific reactivity with P501S, FACS analysis was employed, utilizing either B-LCL transduced with P501S or the irrelevant antigen P703P, of B-LCL infected with vaccinia virus-expressing P501S. For surface expression, dead and non-intact cells were excluded from the analysis as described above. For intracellular staining, cells were fixed and permeabilized as described above. Rabbit polyclonal serum generated against the peptide of SEQ ID NO: 548, which corresponds to amino acids 181-198 of P501S, was found to recognize a surface epitope of P501S. Rabbit polyclonal serum generated against the peptide SEQ ID NO: 551, which corresponds to amino acids 543-553 of P501S, was found to recognize an epitope that was either potentially extracellular or intracellular since in different experiments intact or permeabilized cells were recognized by the polyclonal sera. Based on similar deductive reasoning, the sequences of SEQ ID NO: 541-547, 549 and 550, which correspond to amino acids 109-122, 539-553, 509-520, 37-54, 342-359, 295-323, 217-274, 143-160 and 75-88, respectively, of P501S, can be considered to be potential surface epitopes of P501S recognized by antibodies.

In further studies, mouse monoclonal antibodies were raised against amino acids 296 to 322 to P501S, which are predicted to be in an extracellular domain. A/J mice were immunized with P501S/adenovirus, followed by subsequent boosts with an *E. coli* recombinant protein, referred to as P501N, that contains amino acids 296 to 322 of P501S, and with peptide 296-322 (SEQ ID NO: 898) coupled with KLH. The mice were subsequently used for splenic B cell fusions to generate anti-peptide hybridomas. The resulting 3 clones, referred to as 4F4 (IgG1,kappa), 4G5 (IgG2a,kappa) and 9B9 (IgG1,kappa), were grown for antibody production. The 4G5 mAb was purified by passing the supernatant over a Protein A-sepharose column,

followed by antibody elution using 0.2M glycine, pH 2.3. Purified antibody was neutralized by the addition of 1M Tris, pH 8, and buffer exchanged into PBS.

For ELISA analysis, 96 well plates were coated with P501S peptide 296-322 (referred to as P501-long), an irrelevant P775 peptide, P501S-N, P501TR2, P501S-long-KLH, P501S peptide 306-319 (referred to as P501-short)-KLH, or the irrelevant peptide 2073-KLH, all at a concentration of 2 ug/ml and allowed to incubate for 60 minutes at 37 °C. After coating, plates were washed 5X with PBS + 0.1% Tween and then blocked with PBS, 0.5% BSA, 0.4% Tween20 for 2 hours at room temperature. Following the addition of supernatants or purified mAb, the plates were incubated for 60 minutes at room temperature. Plates were washed as above and donkey anti-mouse IgHRP-linked secondary antibody was added and incubated for 30 minutes at room temperature, followed by a final washing as above. TMB peroxidase substrate was added and incubated 15 minutes at room temperature in the dark. The reaction was stopped by the addition of 1N H_2SO_4 and the OD was read at 450 nM. All three hybrid clones secreted mAb that recognized peptide 296-322 and the recombinant protein P501N.

For FACS analysis, HEK293 cells were transiently transfected with a P501S/VR1012 expression constructs using Fugene 6 reagent. After 2 days of culture, cells were harvested and washed, then incubated with purified 4G5 mAb for 30 minutes on ice. After several washes in PBS, 0.5% BSA, 0.01% azide, goat anti-mouse Ig-FITC was added to the cells and incubated for 30 minutes on ice. Cells were washed and resuspended in wash buffer including 1% propidium iodide and subjected to FACS analysis. The FACS analysis confirmed that amino acids 296-322 of P501S are in an extracellular domain and are cell surface expressed.

The chromosomal location of P501S was determined using the GeneBridge 4 Radiation Hybrid panel (Research Genetics). The PCR primers of SEQ ID NO: 528 and 529 were employed in PCR with DNA pools from the hybrid panel according to the manufacturer's directions. After 38 cycles of amplification, the reaction products were separated on a 1.2% agarose gel, and the results were analyzed through the Whitehead Institute/MIT Center for Genome Research web server

(http://www-genome.wi.mit.edu/cgi-bin/contig/rhmapper.pl) to determine the probable chromosomal location. Using this approach, P501S was mapped to the long arm of chromosome 1 at WI-9641 between q32 and q42. This region of chromosome 1 has been linked to prostate cancer susceptibility in hereditary prostate cancer (Smith *et al. Science 274*:1371-1374, 1996 and Berthon *et al. Am. J. Hum. Genet. 62*:1416-1424, 1998). These results suggest that P501S may play a role in prostate cancer malignancy.

EXAMPLE 20

REGULATION OF EXPRESSION OF THE PROSTATE-SPECIFIC ANTIGEN P501S

Steroid (androgen) hormone modulation is a common treatment modality in prostate cancer. The expression of a number of prostate tissue-specific antigens have previously been demonstrated to respond to androgen. The responsiveness of the prostate-specific antigen P501S to androgen treatment was examined in a tissue culture system as follows.

Cells from the prostate tumor cell line LNCaP were plated at 1.5 x 10^6 cells/T75 flask (for RNA isolation) or 3 x 10^5 cells/well of a 6-well plate (for FACS analysis) and grown overnight in RPMI 1640 media containing 10% charcoal-stripped fetal calf serum (BRL Life Technologies, Gaithersburg, MD). Cell culture was continued for an additional 72 hours in RPMI 1640 media containing 10% charcoal-stripped fetal calf serum, with 1 nM of the synthetic androgen Methyltrienolone (R1881; New England Nuclear) added at various time points. Cells were then harvested for RNA isolation and FACS analysis at 0, 1, 2, 4, 8, 16, 24, 28 and 72-hours post androgen addition. FACS analysis was performed using the anti-P501S antibody 10E3-G4-D3 and permeabilized cells.

For Northern analysis, 5-10 micrograms of total RNA was run on a formaldehyde denaturing gel, transferred to Hybond-N nylon membrane (Amersham Pharmacia Biotech, Piscataway, NJ), cross-linked and stained with methylene blue. The filter was then prehybridized with Church's Buffer (250 mM Na_2HPO_4, 70 mM H_3PO_4, 1 mM EDTA, 1% SDS, 1% BSA in pH 7.2) at 65 °C for 1 hour. P501S DNA was

labeled with 32P using High Prime random-primed DNA labeling kit (Boehringer Mannheim). Unincorporated label was removed using MicroSpin S300-HR columns (Amersham Pharmacia Biotech). The RNA filter was then hybridized with fresh Church's Buffer containing labeled cDNA overnight, washed with 1X SCP (0.1 M NaCl, 0.03 M $Na_2HPO_4.7H_2O$, 0.001 M Na_2EDTA), 1% sarkosyl (n-lauroylsarcosine) and exposed to X-ray film.

Using both FACS and Northern analysis, P501S message and protein levels were found in increase in response to androgen treatment.

EXAMPLE 21

PREPARATION OF FUSION PROTEINS OF PROSTATE-SPECIFIC ANTIGENS

The example describes the preparation of a fusion protein of the prostate-specific antigen P703P and a truncated form of the known prostate antigen PSA. The truncated form of PSA has a 21 amino acid deletion around the active serine site. The expression construct for the fusion protein also has a restriction site at 3' end, immediately prior to the termination codon, to aid in adding cDNA for additional antigens.

The full-length cDNA for PSA was obtained by RT-PCR from a pool of RNA from human prostate tumor tissues using the primers of SEQ ID NO: 607 and 608, and cloned in the vector pCR-Blunt II-TOPO. The resulting cDNA was employed as a template to make two different fragments of PSA by PCR with two sets of primers (SEQ ID NO: 609 and 610; and SEQ ID NO: 611 and 612). The PCR products having the expected size were used as templates to make truncated forms of PSA by PCR with the primers of SEQ ID NO: 611 and 613, which generated PSA (delta 208-218 in amino acids). The cDNA for the mature form of P703P with a 6X histidine tag at the 5' end, was prepared by PCR with P703P and the primers of SEQ ID NO: 614 and 615. The cDNA for the fusion of P703P with the truncated form of PSA (referred to as FOPP) was then obtained by PCR using the modified P703P cDNA and the truncated form of PSA cDNA as templates and the primers of SEQ ID NO: 614 and 615. The FOPP

cDNA was cloned into the NdeI site and XhoI site of the expression vector pCRX1, and confirmed by DNA sequencing. The determined cDNA sequence for the fusion construct FOPP is provided in SEQ ID NO: 616, with the amino acid sequence being provided in SEQ ID NO: 617.

The fusion FOPP was expressed as a single recombinant protein in *E. coli* as follows. The expression plasmid pCRX1FOPP was transformed into the *E. coli* strain BL21-CodonPlus RIL. The transformant was shown to express FOPP protein upon induction with 1 mM IPTG. The culture of the corresponding expression clone was inoculated into 25 ml LB broth containing 50 ug/ml kanamycin and 34 ug/ml chloramphenicol, grown at 37 °C to OD600 of about 1, and stored at 4 °C overnight. The culture was diluted into 1 liter of TB LB containing 50 ug/ml kanamycin and 34 ug/ml chloramphenicol, and grown at 37 °C to OD600 of 0.4. IPTG was added to a final concentration of 1 mM, and the culture was incubated at 30 °C for 3 hours. The cells were pelleted by centrifugation at 5,000 RPM for 8 min. To purify the protein, the cell pellet was suspended in 25 ml of 10 mM Tris-Cl pH 8.0, 2mM PMSF, complete protease inhibitor and 15 ug lysozyme. The cells were lysed at 4 °C for 30 minutes, sonicated several times and the lysate centrifuged for 30 minutes at 10,000 x g. The precipitate, which contained the inclusion body, was washed twice with 10 mM Tris-Cl pH 8.0 and 1% CHAPS. The inclusion body was dissolved in 40 ml of 10 mM Tris-Cl pH 8.0, 100 mM sodium phosphate and 8 M urea. The solution was bound to 8 ml Ni-NTA (Qiagen) for one hour at room temperature. The mixture was poured into a 25 ml column and washed with 50 ml of 10 mM Tris-Cl pH 6.3, 100 mM sodium phosphate, 0.5% DOC and 8M urea. The bound protein was eluted with 350 mM imidazole, 10 mM Tris-Cl pH 8.0, 100 mM sodium phosphate and 8 M urea. The fractions containing FOPP proteins were combined and dialyzed extensively against 10 mM Tris-Cl pH 4.6, aliquoted and stored at - 70 °C.

EXAMPLE 22

REAL-TIME PCR CHARACTERIZATION OF THE PROSTATE-SPECIFIC ANTIGEN P501S IN PERIPHERAL BLOOD OF PROSTATE CANCER PATIENTS

Circulating epithelial cells were isolated from fresh blood of normal individuals and metastatic prostate cancer patients, mRNA isolated and cDNA prepared using real-time PCR procedures. Real-time PCR was performed with the Taqman™ procedure using both gene specific primers and probes to determine the levels of gene expression.

Epithelial cells were enriched from blood samples using an immunomagnetic bead separation method (Dynal A.S., Oslo, Norway). Isolated cells were lysed and the magnetic beads removed. The lysate was then processed for poly A+ mRNA isolation using magnetic beads coated with Oligo(dT)25. After washing the beads in buffer, bead/poly A+ RNA samples were suspended in 10 mM Tris HCl pH 8.0 and subjected to reversed transcription. The resulting cDNA was subjected to real-time PCR using gene specific primers. Beta-actin content was also determined and used for normalization. Samples with P501S copies greater than the mean of the normal samples + 3 standard deviations were considered positive. Real time PCR on blood samples was performed using the Taqman™ procedure but extending to 50 cycles using forward and reverse primers and probes specific for P501S. Of the eight samples tested, 6 were positive for P501S and β-actin signal. The remaining 2 samples had no detectable β-actin or P501S. No P501S signal was observed in the four normal blood samples tested.

EXAMPLE 23

EXPRESSION OF THE PROSTATE-SPECIFIC ANTIGENS P703P AND P501S IN SCID MOUSE-PASSAGED PROSTATE TUMORS

When considering the effectiveness of antigens in the treatment of prostate cancer, the continued presence of the antigens in tumors during androgen

ablation therapy is important. The presence of the prostate-specific antigens P703P and P501S in prostate tumor samples grown in SCID mice in the presence of testosterone was evaluated as follows.

Two prostate tumors that had metastasized to the bone were removed from patients, implanted into SCID mice and grown in the presence of testosterone. Tumors were evaluated for mRNA expression of P703P, P501S and PSA using quantitative real time PCR with the SYBR green assay method. Expression of P703P and P501S in a prostate tumor was used as a positive control and the absence in normal intestine and normal heart as negative controls. In both cases, the specific mRNA was present in late passage tumors. Since the bone metastases were grown in the presence of testosterone, this implies that the presence of these genes would not be lost during androgen ablation therapy.

EXAMPLE 24

ANTI-P503S MONOCLONAL ANTIBODY INHIBITS TUMOR GROWTH *IN VIVO*

The ability of the anti-P503S monoclonal antibody 20D4 to suppress tumor formation in mice was examined as follows.

Ten SCID mice were injected subcutaneously with HEK293 cells that expressed P503S. Five mice received 150 micrograms of 20D4 intravenously at day 0 (time of tumor cell injection), day 5 and day 9. Tumor size was measured for 50 days. Of the five animals that received no 20D4, three formed detectable tumors after about 2 weeks which continued to enlarge throughout the study. In contrast, none of the five mice that received 20D4 formed tumors. These results demonstrate that the anti-P503S Mab 20D4 displays potent anti-tumor activity *in vivo*.

EXAMPLE 25

CHARACTERIZATION OF A T CELL RECEPTOR CLONE FROM A P501S-SPECIFIC T CELL CLONE

T cells have a limited lifespan. However, cloning of T cell receptor (TCR) chains and subsequent transfer essentially enables infinite propagation of the T

cell specificity. Cloning of tumor-antigen TCR chains allows the transfer of the specificity into T cells isolated from patients that share the TCR MHC-restricting allele. Such T cells could then be expanded and used in adoptive transfer settings to introduce the tumor antigen specificity into patients carrying tumors that express the antigen. T cell receptor alpha and beta chains from a CD8 T cell clone specific for the prostate-specific antigen P501S were isolated and sequenced as follows.

Total mRNA from 2 x 10^6 cells from CTL clone 4E5 (described above in Example 12) was isolated using Trizol reagent and cDNA was synthesized. To determine Va and Vb sequences in this clone, a panel of Va and Vb subtype-specific primers was synthesized and used in RT-PCR reactions with cDNA generated from each of the clones. The RT-PCR reactions demonstrated that each of the clones expressed a common Vb sequence that corresponded to the Vb7 subfamily. Futhermore, using cDNA generated from the clone, the Va sequence expressed was determined to be Va6. To clone the full TCR alpha and beta chains from clone 4E5, primers were designed that spanned the initiator and terminator-coding TCR nucleotides. The primers were as follows: TCR Valpha-6 5'(sense): GGATCC---GCCGCCACC—ATGTCACTTTCTAGCCTGCT (SEQ ID NO: 899) BamHI site Kozak TCR alpha sequence TCR alpha 3' (antisense): GTCGAC---TCAGCTGGACCACAGCCGCAG (SEQ ID NO: 900) SalI site TCR alpha constant sequence TCR Vbeta-7. 5'(sense): GGATCC---GCCGCCACC--ATGGGCTGCAGGCTGCTCT (SEQ ID NO: 901) BamHI site Kozak TCR alpha sequence TCR beta 3' (antisense): GTCGAC---TCAGAAATCCTTTCTCTTGAC (SEQ ID NO: 902) SalI site TCR beta constant sequence. Standard 35 cycle RT-PCR reactions were established using cDNA synthesized from the CTL clone and the above primers, employing the proofreading thermostable polymerase PWO (Roche, Nutley, NJ).

The resultant specific bands (approx. 850 bp for alpha and approx. 950 for beta) were ligated into the PCR blunt vector (Invitrogen) and transformed into *E. coli*. *E .coli* transformed with plasmids containing full-length alpha and beta chains were identified, and large scale preparations of the corresponding plasmids were generated. Plasmids containing full-length TCR alpha and beta chains were submitted

for sequencing. The sequencing reactions demonstrated the cloning of full-length TCR alpha and beta chains with the determined cDNA sequences for the Vb and Va chains being shown in SEQ ID NO: 903 and 904, respectively. The corresponding amino acid sequences are shown in SEQ ID NO: 905 and 906, respectively. The Va sequence was shown by nucleotide sequence alignment to be 99% identical (347/348) to Va6.2, and the Vb to be 99% identical to Vb7 (336/338).

EXAMPLE 26

CAPTURE OF PROSTATE SPECIFIC CELLS USING THE PROSTATE ANTIGEN P503S

As described above, P503S is found on the surface of prostate cells. Secondary coated microsphere beads specific for mouse IgG were coupled with the purified P503S-specific monoclonal antibody 1D12. The bound P503S antibody was then used to capture HEK cells expressing recombinant P503S. This provides a model system for prostate-specific cell capture which may be usefully employed in the detection of prostate cells in blood, and therefore in the detection of prostate cancer.

P503S-transfected HEK cells were harvested and redissolved in wash buffer (PBS, 0.1% BSA, 0.6% sodium citrate) at an appropriate volume to give at least 5^4 cells per sample. Round bottom Eppendorf tubes were used for all procedures involving beads. The stock concentrations were as shown below in Table VIII.

Table VIII

Stock concentrations	Sample concentration	Amount needed
Epithelial enrich beads 4^8 beads/ml (Dynal Biotech Inc. Lake Success, NY)	1^7 beads/ml	125 ul stock per 5 ml volume
1D12 ascites antibody 2 mg/ml	0.1 ug/ml (0.1X) to 5 ug/ml (5X) titrations	0.05 ul to 2.5 ul stock per sample
α- Mamma Mu 0.9 mg/ml	1 ug/ml (1X)	1.1 ul stock per sample
Pan-mouse IgG beads 4^8 beads/ml (Dynal Biotech)	1^7 beads/ml	125 ul stock per 5 ml volume

Blocked immunomagnetic beads were pre-washed as follows: all beads needed were pooled and washed once with 1 ml wash buffer. The beads were resuspended din a 3X volume of 1% BSA (v/v) in wash buffer and incubated for 15 min rotating at 4 °C. The beads were then washed three times with 2X volume of wash buffer and resuspended to original volume. Non-blocked beads were pooled, washed three times with 2X volume of wash buffer and resuspended to original volume.

Primary antibody was incubated with secondary beads in a fresh Eppendorf for 30 minutes, rotating at 4 °C. Approximately 200 ul wash buffer was added to increase the total volume for even mixing of the sample. The antibody-bead solution was transferred to a fresh Eppendorf, washed twice with an equal volume of wash buffer and resuspended to original volume. Target cells were added to each sample and incubated for 45 minutes, rotating at 4 °C. The tubes were transferred to a magnet, the supernatant removed, taking care not the agitate the beads, and the samples were washed twice with 1 ml wash buffer. The samples were then ready for RT-PCR using a Dynabeads mRNA direct microkit (Dynal Biotech).

Epithelial cell enrichment was placed in a magnet and supernant was removed. The epithelial enrichment beads were then resuspendedin 100 ul lysis/binding buffer fortified with Rnasin (2 U/ul per sample), and sotred at –70 °C until use. Oligo (dT_{25}) Dynabeads were pre-washed as follows: all beads needed were pooled (23 ul/sample), washed three times with an excess volume of lysis/binding buffer, and resuspsended ot original volume. The lysis supernant was separated with a magnet and transferred to a fresh Eppendorf. 20 ul oligo(dT25) Dynabeads were added per samplem ad rolled for 5 min at room temperature. Supernant was separated using a magnet and discarded, leaving the mRNA annealed ot the beads. The bead/mRNA complex was washed with buffer and resuspended in cold Tris-HCl.

For RT-PCR, the Tris-HCl supernatant was separated and discarded using MPS. For each sample containing 1^5 cells or less, the following was added to give a total volume of 30 ul: 14.25 ul H_2O; 1.5 ul BSA; 6 ul first strand buffer; 0.75 mL 10 mM dNTP mix; 3 ul Rnasin; 3 ul 0.1M dTT; and 1.5 ul Superscript II. The resulting solution was incubated for 1 hour at 42 °C, diluted 1:5 in H2O, heated at 80°C for 2 min

to detach cDNA from the beads, and immediately placed on MPS. The supernatant containing cDNA was transferred to a new tube and stored at –20 °C.

Table IX shows the percentage of capture of P503S-transfected HEK cells as determined by RT-PCR.

Table IX

	% capture P503S-transfected HEK cells	% capture LnCAP cells
0.1 ug/ml P503S Mab	36.90	0.00
0.5 ug/ml P503S Mab	67.40	2.93
1 ug/ml P503S Mab	40.22	0.00
5 ug/ml P503S Mab	13.11	0.00
Anti-Mu beads only, non-blocked	1.42	0.00
Anti-Mu beads only, blocked	15.65	20.21
Absolute control, non-capture cells	100.00	100.00

From the foregoing it will be appreciated that, although specific embodiments of the invention have been described herein for purposes of illustration, various modifications may be made without deviating from the spirit and scope of the invention. Accordingly, the invention is not limited except as by the appended claims.

CLAIMS

What is Claimed:

1. An isolated polynucleotide comprising a sequence selected from the group consisting of:

(a) sequences provided in SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-705, 709-774, 777, 789, 817, 823, 824, 878, 880-882, 894, 896, 907, 908, 916-919, 929-931, 938, 939 and 942;

(b) complements of the sequences provided in SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-705, 709-774, 777, 789, 817, 823, 824, 878, 880-882, 894, 896, 907, 908, 916-919, 929-931, 938, 939 and 942;

(c) sequences consisting of at least 20 contiguous residues of a sequence provided in SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-705, 709-774, 777, 789, 817, 823, 824, 878, 880-882, 894, 896, 907, 908, 916-919, 929-931, 938, 939 and 942;

(d) sequences that hybridize to a sequence provided in SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-705, 709-774, 777, 789, 817, 823, 824, 878, 880-882, 894, 896, 907, 908, 916-919, 929-931, 938, 939 and 942 under moderately stringent conditions;

(e) sequences having at least 75% identity to a sequence of SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-705, 709-774, 777, 789, 817, 823, 824, 878, 880-882, 894, 896, 907, 908, 916-919, 929-931, 938, 939 and 942;

(f) sequences having at least 90% identity to a sequence of SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-705, 709-774, 777, 789, 817, 823, 824, 878, 880-882, 894, 896, 907, 908, 916-919, 929-931, 938, 939 and 942; and

(g) degenerate variants of a sequence provided in SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-705, 709-774, 777, 789, 817, 823, 824, 878, 880-882, 894, 896, 907, 908, 916-919, 929-931, 938, 939 and 942.

2. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of:

(a) sequences recited in SEQ ID NO: 112-114, 172, 176, 178, 327, 329, 331, 336, 339, 376-380, 383, 477-483, 496, 504, 505, 519, 520, 522, 525, 527, 532, 534, 537-551, 553-568, 573-586, 588-590, 592, 706-708, 775, 776, 778, 780, 781, 811, 814, 818, 826, 827, 853, 855, 858, 860-862, 866-877, 879, 883-893, 895, 897, 898, 909-915, 920-928, 932-934, 940, 941 and 943;

(b) sequences having at least 70% identity to a sequence of SEQ ID NO: 112-114, 172, 176, 178, 327, 329, 331, 336, 339, 376-380, 383, 477-483, 496, 504, 505, 519, 520, 522, 525, 527, 532, 534, 537-551, 553-568, 573-586, 588-590, 592, 706-708, 775, 776, 778, 780, 781, 811, 814, 818, 826, 827, 853, 855, 858, 860-862, 866-877, 879, 883-893, 895, 897, 898, 909-915, 920-928, 932-934, 940, 941 and 943;

(c) sequences having at least 90% identity to a sequence of SEQ ID NO: 112-114, 172, 176, 178, 327, 329, 331, 336, 339, 376-380, 383, 477-483, 496, 504, 505, 519, 520, 522, 525, 527, 532, 534, 537-551, 553-568, 573-586, 588-590, 592, 706-708, 775, 776, 778, 780, 781, 811, 814, 818, 826, 827, 853, 855, 858, 860-862, 866-877, 879, 883-893, 895, 897, 898, 909-915, 920-928, 932-934, 940, 941 and 943;

(d) sequences encoded by a polynucleotide of claim 1;

(e) sequences having at least 70% identity to a sequence encoded by a polynucleotide of claim 1; and

(f) sequences having at least 90% identity to a sequence encoded by a polynucleotide of claim 1.

3. An expression vector comprising a polynucleotide of claim 1 operably linked to an expression control sequence.

4. A host cell transformed or transfected with an expression vector according to claim 3.

5. An isolated antibody, or antigen-binding fragment thereof, that specifically binds to a polypeptide of claim 2.

6. A method for detecting the presence of a cancer in a patient, comprising the steps of:

(a) obtaining a biological sample from the patient;

(b) contacting the biological sample with a binding agent that binds to a polypeptide of claim 2;

(c) detecting in the sample an amount of polypeptide that binds to the binding agent; and

(d) comparing the amount of polypeptide to a predetermined cut-off value and therefrom determining the presence of a cancer in the patient.

7. A fusion protein comprising at least one polypeptide according to claim 2.

8. An oligonucleotide that hybridizes to a sequence recited in SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591,

593-606, 618-705, 709-774, 777, 789, 817, 823, 824, 878, 880-882, 894, 896, 907, 908, 916-919, 929-931, 938, 939 and 942 under moderately stringent conditions.

9. A method for stimulating and/or expanding T cells specific for a tumor protein, comprising contacting T cells with at least one component selected from the group consisting of:

(a) polypeptides according to claim 2;

(b) polynucleotides according to claim 1; and

(c) antigen-presenting cells that express a polypeptide according to claim 2,

under conditions and for a time sufficient to permit the stimulation and/or expansion of T cells.

10. An isolated T cell population, comprising T cells prepared according to the method of claim 9.

11. A composition comprising a first component selected from the group consisting of physiologically acceptable carriers and immunostimulants, and a second component selected from the group consisting of:

(a) polypeptides according to claim 2;

(b) polynucleotides according to claim 1;

(c) antibodies according to claim 5;

(d) fusion proteins according to claim 7;

(e) T cell populations according to claim 10; and

(f) antigen presenting cells that express a polypeptide according to claim 2.

12. A method for stimulating an immune response in a patient, comprising administering to the patient a composition of claim 11.

13. A method for the treatment of a cancer in a patient, comprising administering to the patient a composition of claim 11.

14. A method for determining the presence of a cancer in a patient, comprising the steps of:

(a) obtaining a biological sample from the patient;

(b) contacting the biological sample with an oligonucleotide according to claim 8;

(c) detecting in the sample an amount of a polynucleotide that hybridizes to the oligonucleotide; and

(d) compare the amount of polynucleotide that hybridizes to the oligonucleotide to a predetermined cut-off value, and therefrom determining the presence of the cancer in the patient.

15. A diagnostic kit comprising at least one oligonucleotide according to claim 8.

16. A diagnostic kit comprising at least one antibody according to claim 5 and a detection reagent, wherein the detection reagent comprises a reporter group.

17. A method for inhibiting the development of a cancer in a patient, comprising the steps of:

(a) incubating CD4+ and/or CD8+ T cells isolated from a patient with at least one component selected from the group consisting of: (i) polypeptides according to claim 2; (ii) polynucleotides according to claim 1; and (iii) antigen presenting cells that express a polypeptide of claim 2, such that T cell proliferate;

(b) administering to the patient an effective amount of the proliferated T cells,

and thereby inhibiting the development of a cancer in the patient.

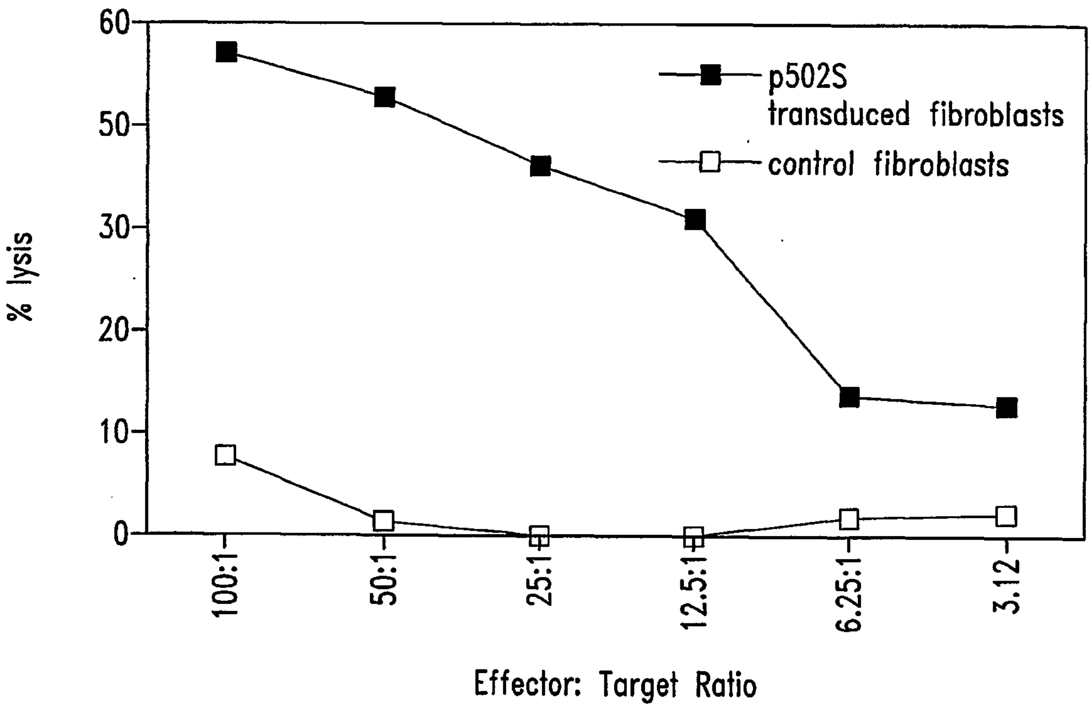

60
50
30
20
10
0
% lysis
p502S transduced fibroblasts
control fibroblasts
100:1
50:1
25:1
12.5:1
6.25:1
3.12
Effector: Target Ratio

Fig. 1

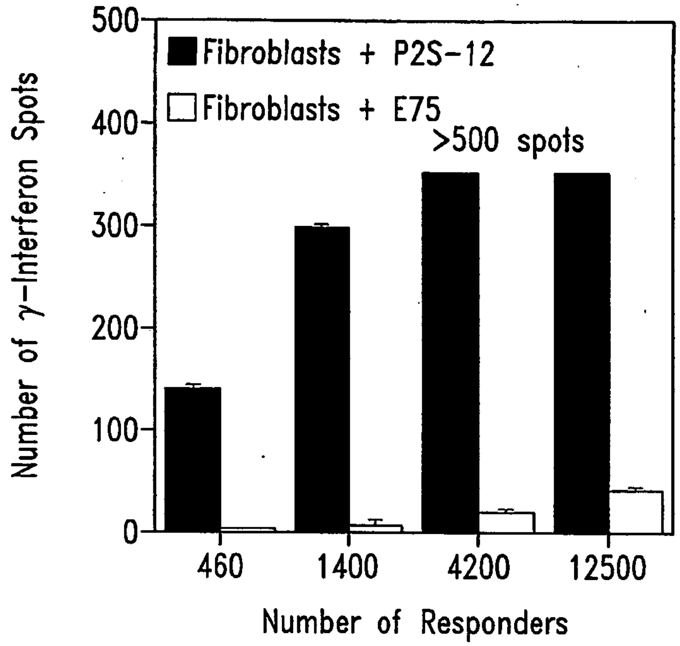

Fibroblasts + P2S-12
Fibroblasts + E75
>500 spots
Number of γ-Interferon Spots
500
400
300
200
100
0
460
1400
4200
12500
Number of Responders

Fig. 2A

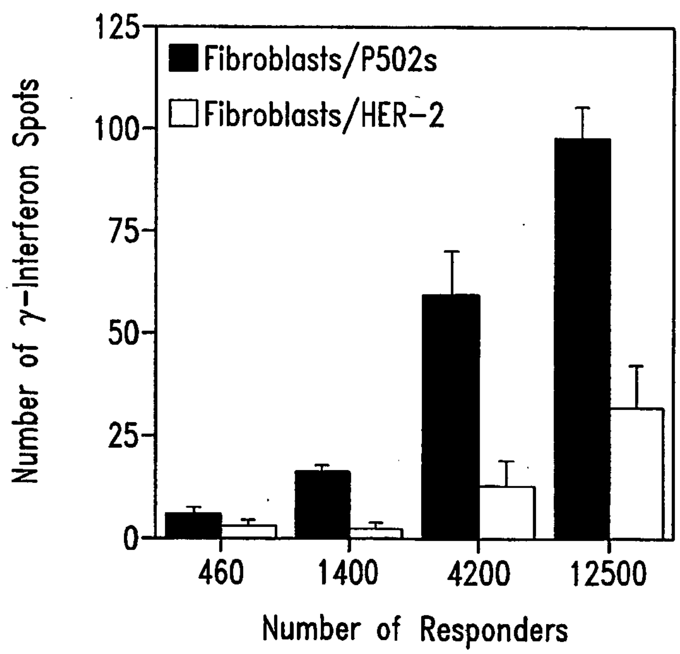
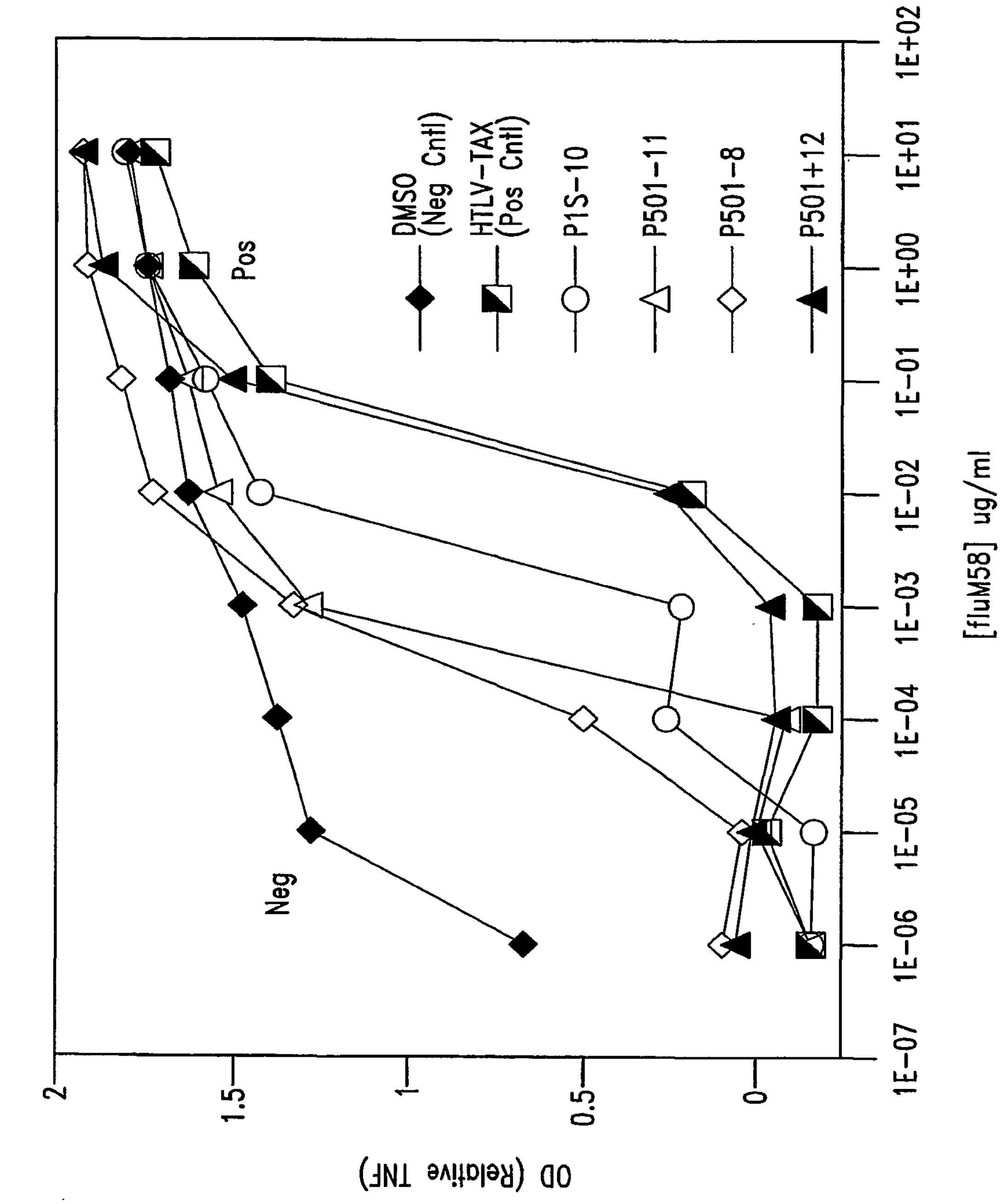

Fibroblasts/P502s
Fibroblasts/HER-2
Number of γ-Interferon Spots
125
100
75
50
25
0
460
1400
4200
12500
Number of Responders

Fig. 2B



OD (Relative TNF)
2
1.5
1
0.5
0
[fluM58] ug/ml
1E-07
1E-06
1E-05
1E-04
1E-03
1E-02
1E-01
1E+00
1E+01
1E+02
Neg
Pos
DMSO (Neg Cntl)
HTLV-TAX (Pos Cntl)
P1S-10
P501-11
P501-8
P501+12

Fig. 3

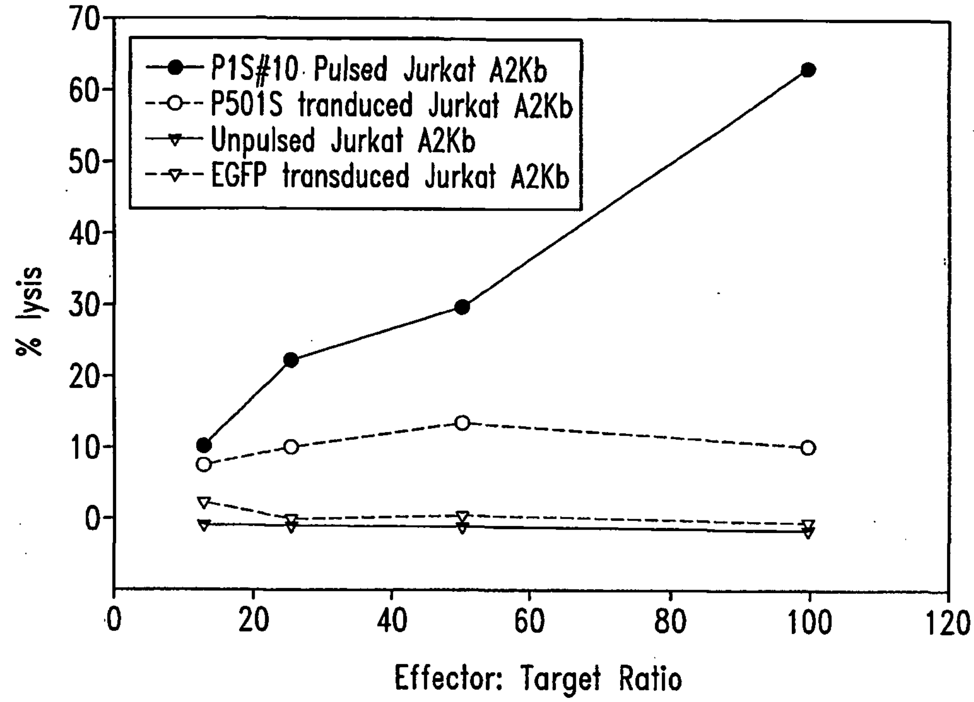

P1S#10 Pulsed Jurkat A2Kb
P501S tranduced Jurkat A2Kb
Unpulsed Jurkat A2Kb
EGFP transduced Jurkat A2Kb
% lysis
70
60
50
40
30
20
10
0
0
20
40
60
80
100
120
Effector: Target Ratio

Fig. 4

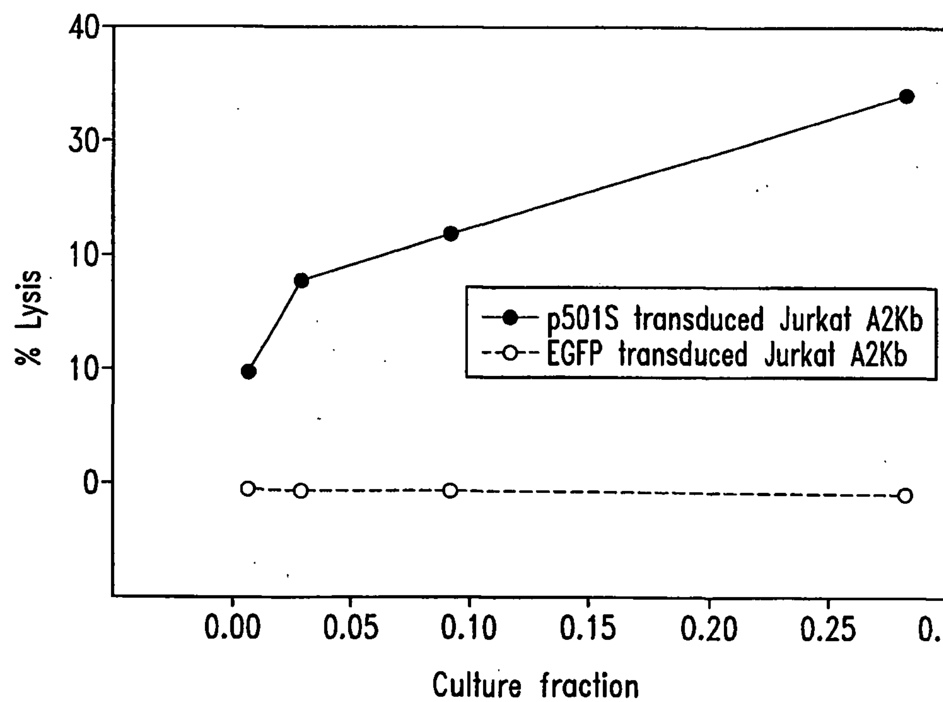

p501S transduced Jurkat A2Kb
EGFP transduced Jurkat A2Kb
% Lysis
40
30
10
10
0
0.00
0.05
0.10
0.15
0.20
0.25
0.30
Culture fraction

Fig. 5

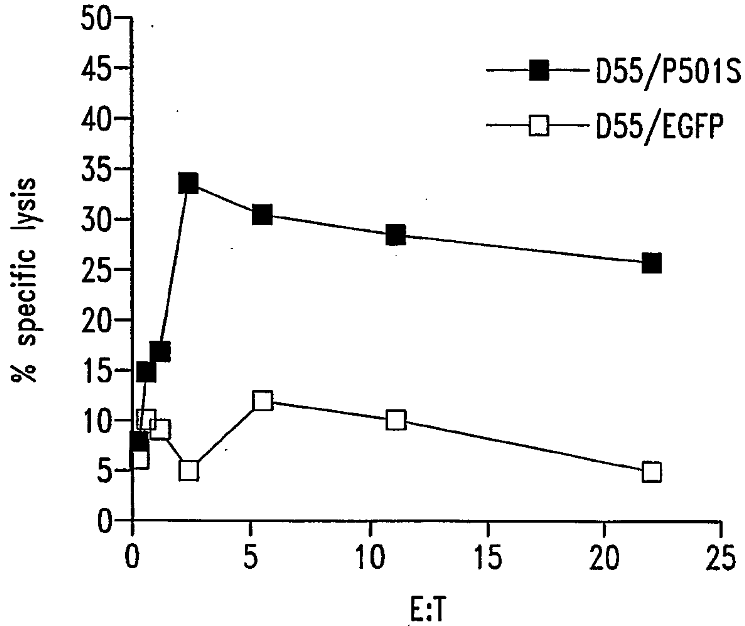

D55/P501S
D55/EGFP
% specific lysis
E:T
0
5
10
15
20
25
30
35
40
45
50

Fig. 6A

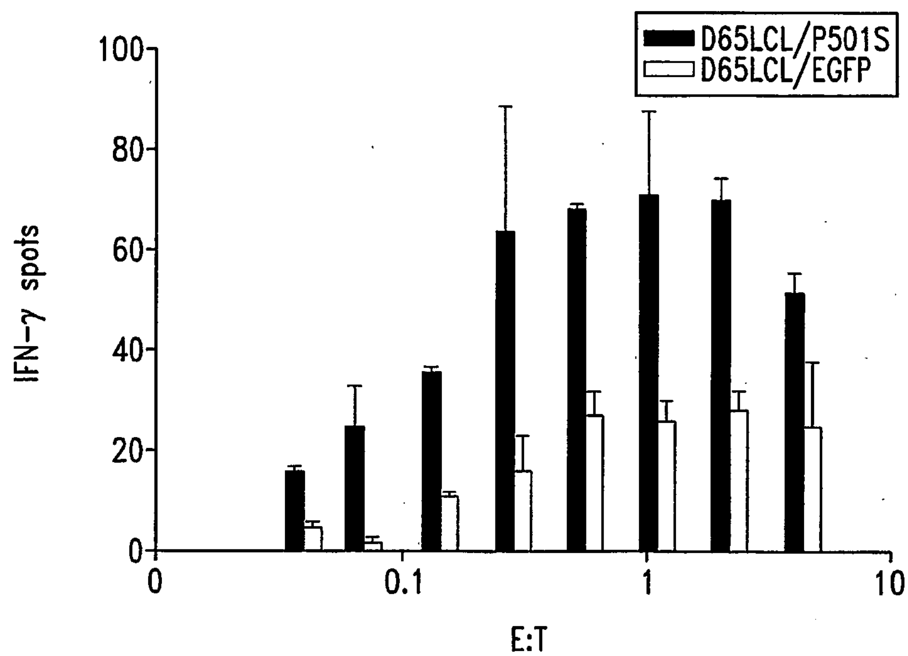
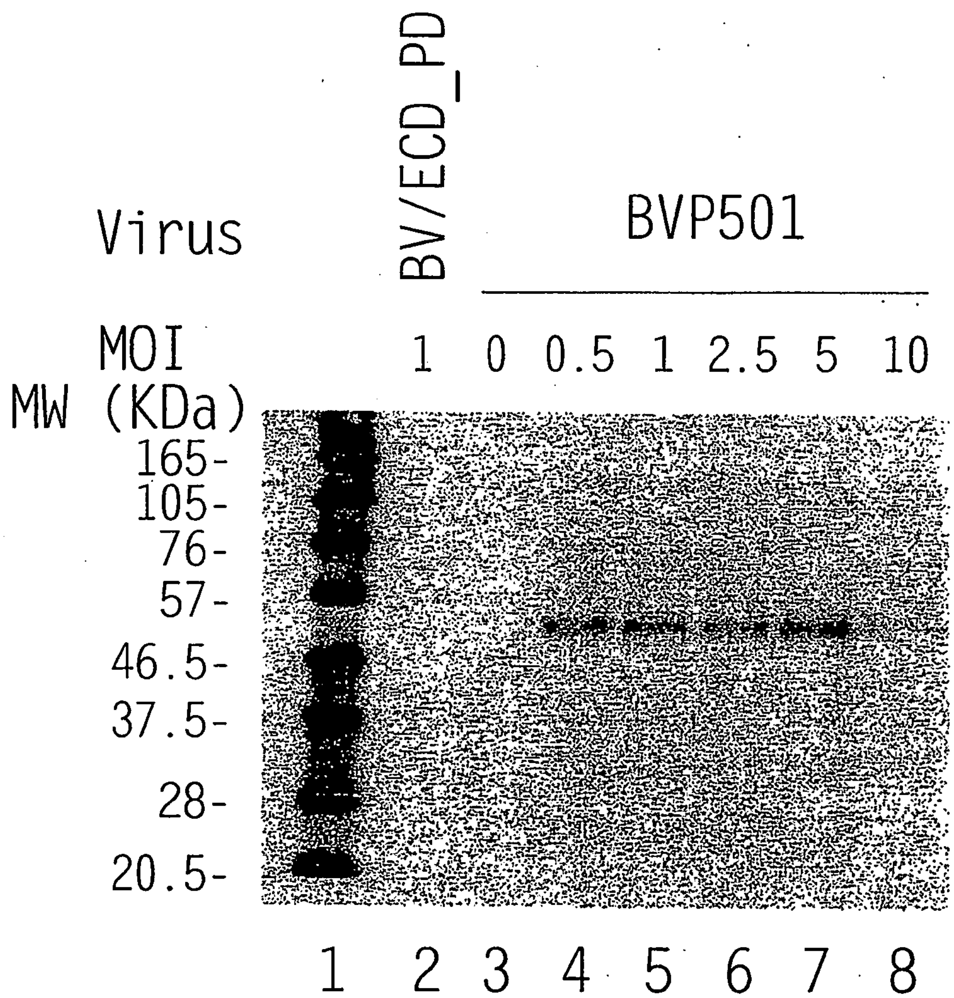

D65LCL/P501S
D65LCL/EGFP
IFN-γ spots
E:T
0
20
40
60
80
100
0.1
1
10

Fig. 6B

Expression of P501S
by the Baculovirus Expression System



0.6 million high 5 cells in 6-well plate were infected with an unrelated control virus BV/ECD_PD (lane2), without virus (lane3), or with recombinant baculovirus for P501 at different MOIs (lane 4-8). Cell lysates were run on SDS-PAGE under the reducing conditions and analyzed by Western blot with a monoclonal antibody against P501S (P501S-10E3-G4D3). Lane 1 is the biotinylated protein molecular weight marker (BioLabs).

Fig. 7

FIGURE 8. Mapping of the epitope recognized by 10E3-G4-D3

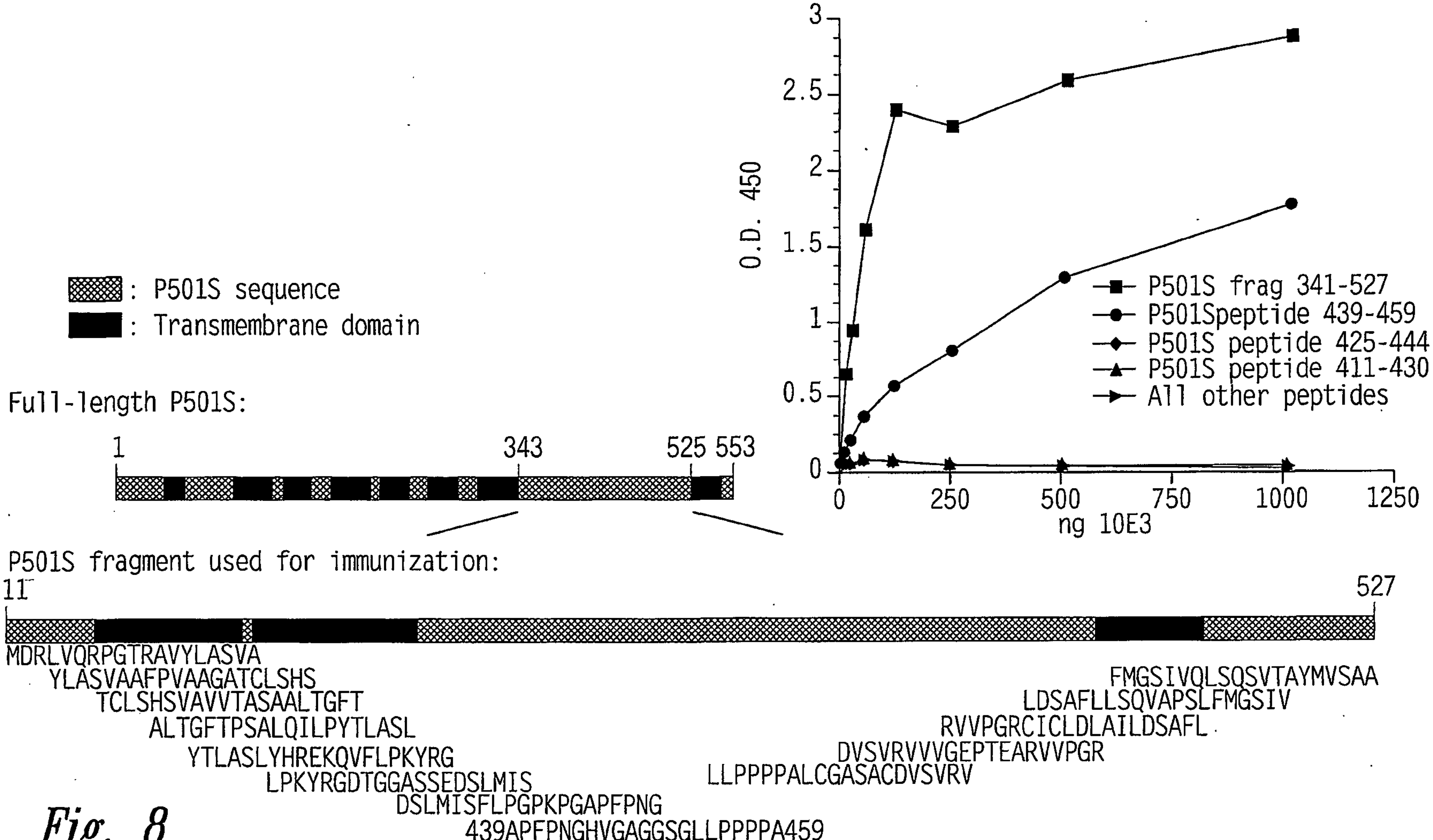


Fig. 8

Schematic of P501S with predicted
transmembrane, cytoplasmic, and extracellular regions

MVQRLWVSRLLRHRK AQLLLVNLLTFGLEVCLAAGIT **YVPPLLLEVGVEEKFM** TMVLGIGPVLGLVCYPLLGSAS

DHWRGRYGRRRP FIWALSLGILLSLFLIPRAGWL **AGLLCPDPRPLE** LALLILGVGLLDFCGQVCFTPL

EALLSDLFRDPDHCRQ AYSVYAFMISLGGCLGYLLPAI **DWDTSALAPYLGTQEE**

CLFGLLTLIFLTCVAATLLV *AEEAALGPTEPAEGLSAPSLSPHCCPCRARLAFRNLGALLPRL*

HQLCCRMPRTLRR LFVAELCSWMALMTFTLFYTDF **VGEGLYQGVPRAEPGTEARRHYDEGVR**

MGSLGLFLQCAISLVFSLVM *DRLVQRFGTRAVYLAS* VAAFPVAAGATCLSHSVAVVTA **SAA**

LTGFTFSALQILPYTLASLY *HREKQVFLPKYRGDTGGASSEDSLMTSFLPGPKPGAPFPNGHVGAGGSGL*

LPPPPALCGASACDVSVRVVVGEPTEARVVPGRG ICLDLAILDSAFLLSQVAPSLF **MGSIVQLSQS**

VTAYMVSAAGLGLVAIYFAT *QVVFDKSDLAKYSA*

Underlined sequence: Predicted transmembrane domain; **Bold sequence**: Predicted extracellular domain; *Italic sequence*: Predicted intracellular domain. Sequence in bold/underlined: used generate polyclonal rabbit serum

Localization of domains predicted using HMMTOP (G.E. Tusnady an I. Simon (1998) Principles Governing Amino Acid Composition of Integral Membrane Proteins: Applications to topology Prediction.J.Mol Biol. 283, 489-506.

Fig. 9

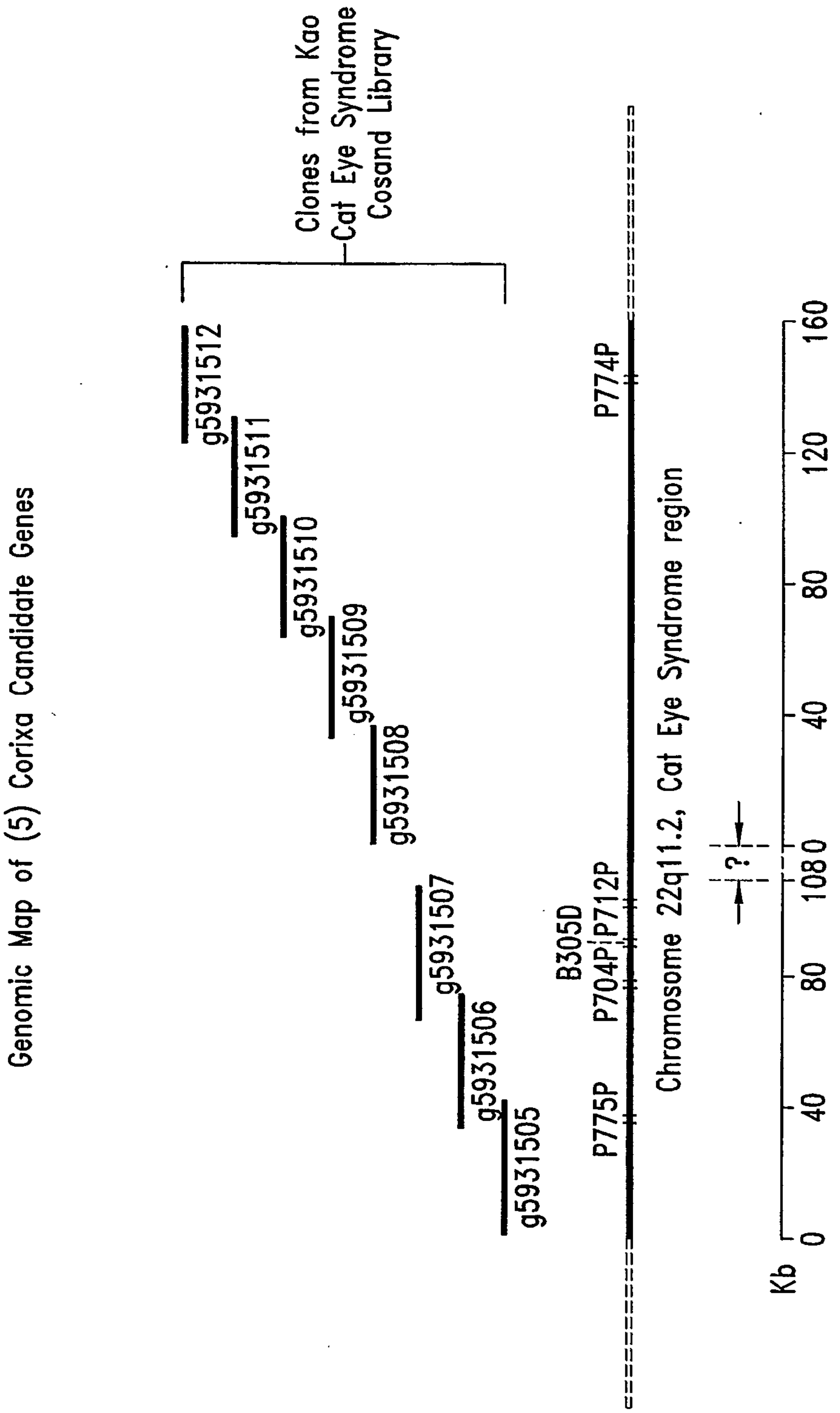

Genomic Map of (5) Corixa Candidate Genes
Clones from Kao
Cat Eye Syndrome
Cosand Library
g5931512
g5931511
g5931510
g5931509
g5931508
g5931507
g5931506
g5931505
P775P
B305D
P704P
P712P
P774P
Chromosome 22q11.2, Cat Eye Syndrome region
?
Kb
0
40
80
1080
40
80
120
160

Fig. 10

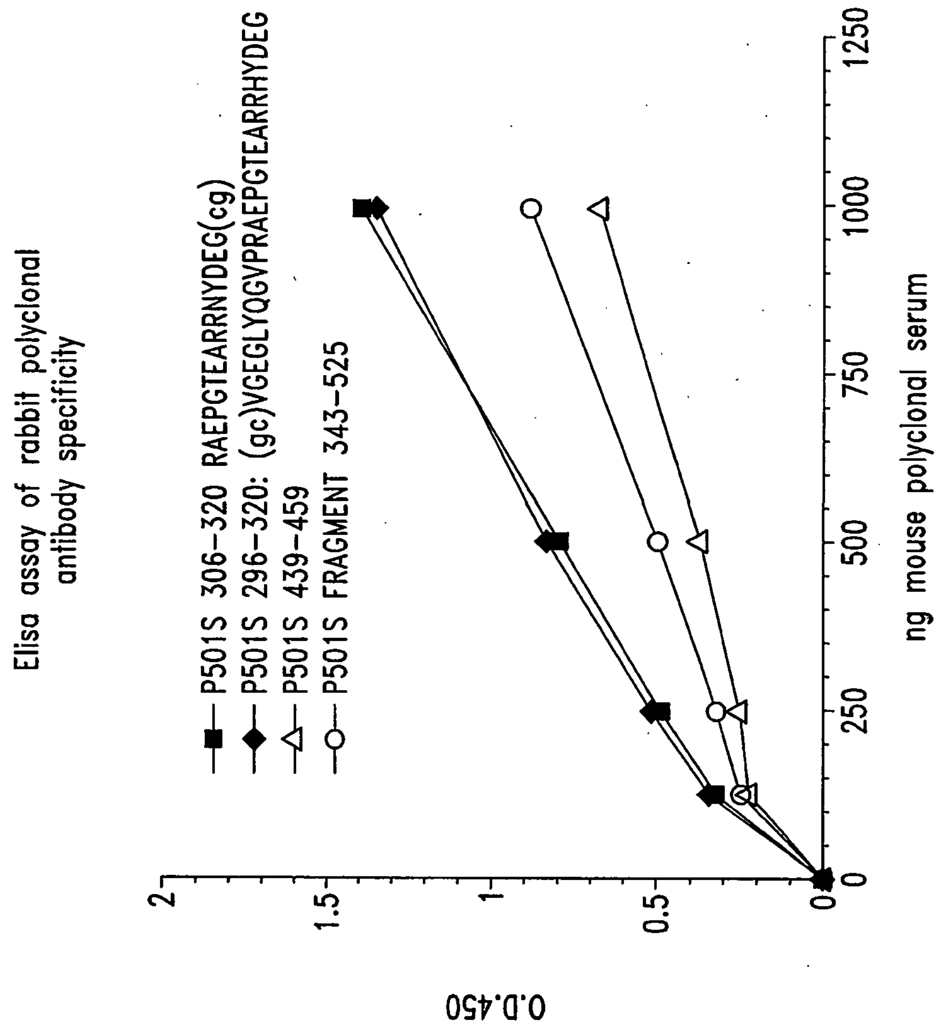

Elisa assay of rabbit polyclonal antibody specificity
P501S 306-320 RAEPGTEARRNYDEG(cg)
P501S 296-320: (gc)VGEGLYQGVPRAEPGTEARRHYDEG
P501S 439-459
P501S FRAGMENT 343-525
O.D.450
0
0.5
1
1.5
2
0
250
500
750
1000
1250
ng mouse polyclonal serum

Fig. 11

GTCACTTAGG AAAAGGTGTC CTTTCGGGCA GCCGGGCTCA GCATGAGGAA CAGAAGGAAT 60
GACACTCTGG ACAGCACCCG GACCCTGTAC TCCAGCGCGT CTCGGAGCAC AGACTTGTCT 120
TACAGTGAAA GCGACTTGGT GAATTTTATT CAAGCAAATT TTAAGAAACG AGAATGTGTC 180
TTCTTTACCA AAGATTCCAA GGCCACGGAG AATGTGTGCA AGTGTGGCTA TGCCCAGAGC 240
CAGCACATGG AAGGCACCCA GATCAACCAA AGTGAGAAAT GGAACTACAA GAAACACACC 300
AAGGAATTTC CTACCGACGC CTTTGGGGAT ATTCAGTTTG AGACACTGGG GAAGAAAGGG 360
AAGTATATAC GTCTGTCCTG CGACACGGAC GCGGAAATCC TTTACGAGCT GCTGACCCAG 420
CACTGGCACC TGAAAACACC CAACCTGGTC ATTTCTGTGA CCGGGGGCGC CAAGAACTTC 480
GCCCTGAAGC CGCGCATGCG CAAGATCTTC AGCCGGCTCA TCTACATCGC GCAGTCCAAA 540
GGTGCTTGGA TTCTCACGGG AGGCACCCAT TATGGCCTGA CGAAGTACAT CGGGGAGGTG 600
GTGAGAGATA ACACCATCAG CAGGAGTTCA GAGGAGAATA TTGTGGCCAT TGGCATAGCA 660
GCTTGGGGCA TGGTCTCCAA CCGGGACACC CTCATCAGGA ATTGCGATGC TGAGGGCTAT 720
TTTTTAGCCC AGTACCTTAT GGATGACTTC ACAAGGGATC CACTGTATAT CCTGGACAAC 780
AACCACACAC ATTTGCTGCT CGTGGACAAT GGCTGTCATG GACATCCCAC TGTCGAAGCA 840
AAGCTCCGGA ATCAGCTAGA GAAGCATATC TCTGAGCGCA CTATTCAAGA TTCCAACTAT 900
GGTGGCAAGA TCCCCATTGT GTGTTTTGCC CAAGGAGGTG GAAAAGAGAC TTTGAAAGCC 960
ATCAATACCT CCATCAAAAA TAAAATTCCT TGTGTGGTGG TGGAAGGCTC GGGCCGGATC 1020
GCTGATGTGA TCGCTAGCCT GGTGGAGGTG GAGGATGCCC CGACATCTTC TGCCGTCAAG 1080
GAGAAGCTGG TGCGCTTTTT ACCCCGCACG GTGTCCCGGC TGTCTGAGGA GGAGACTGAG 1140
AGTTGGATCA AATGGCTCAA AGAAATTCTC GAATGTTCTC ACCTATTAAC AGTTATTAAA 1200
ATGGAAGAAG CTGGGGATGA AATTGTGAGC AATGCCATCT CCTACGCTCT ATACAAAGCC 1260
TTCAGCACCA GTGAGCAAGA CAAGGATAAC TGGAATGGGC AGCTGAAGCT TCTGCTGGAG 1320
TGGAACCAGC TGGACTTAGC CAATGATGAG ATTTTCACCA ATGACCGCCG ATGGGAGTCT 1380
GCTGACCTTC AAGAAGTCAT GTTTACGGCT CTCATAAAGG ACAGACCCAA GTTTGTCCGC 1440
CTCTTTCTGG AGAATGGCTT GAACCTACGG AAGTTTCTCA CCCATGATGT CCTCACTGAA 1500
CTCTTCTCCA ACCACTTCAG CACGCTTGTG TACCGGAATC TGCAGATCGC CAAGAATTCC 1560
TATAATGATG CCCTCCTCAC GTTTGTCTGG AAACTGGTTG CGAACTTCCG AAGAGGCTTC 1620
CGGAAGGAAG ACAGAAATGG CCGGGACGAG ATGGACATAG AACTCCACGA CGTGTCTCCT 1680
ATTACTCGGC ACCCCCTGCA AGCTCTCTTC ATCTGGGCCA TTCTTCAGAA TAAGAAGGAA 1740
CTCTCCAAAG TCATTTGGGA GCAGACCAGG GGCTGCACTC TGGCAGCCCT GGGAGCCAGC 1800
AAGCTTCTGA AGACTCTGGC CAAAGTGAAG AACGACATCA ATGCTGCTGG GGAGTCCGAG 1860
GAGCTGGCTA ATGAGTACGA GACCCGGGCT GTTGAGCTGT TCACTGAGTG TTACAGCAGC 1920
GATGAAGACT TGGCAGAACA GCTGCTGGTC TATTCCTGTG AAGCTTGGGG TGGAAGCAAC 1980
TGTCTGGAGC TGGCGGTGGA GGCCACAGAC CAGCATTTCA CCGCCCAGCC TGGGGTCCAG 2040
AATTTTCTTT CTAAGCAATG GTATGGAGAG ATTTCCCGAG ACACCAAGAA CTGGAAGATT 2100

Fig. 12A (1)

ATCCTGTGTC TGTTTATTAT ACCCTTGGTG GGCTGTGGCT TTGTATCATT TAGGAAGAAA 2160
CCTGTCGACA AGCACAAGAA GCTGCTTTGG TACTATGTGG CGTTCTTCAC CTCCCCCTTC 2220
GTGGTCTTCT CCTGGAATGT GGTCTTCTAC ATCGCCTTCC TCCTGCTGTT TGCCTACGTG 2280
CTGCTCATGG ATTTCCATTC GGTGCCACAC CCCCCCGAGC TGGTCCTGTA CTCGCTGGTC 2340
TTTGTCCTCT TCTGTGATGA AGTGAGACAG TGGTACGTAA ATGGGGTGAA TTATTTTACT 2400
GACCTGTGGA ATGTGATGGA CACGCTGGGG CTTTTTTACT TCATAGCAGG AATTGTATTT 2460
CGGCTCCACT CTTCTAATAA AAGCTCTTTG TATTCTGGAC GAGTCATTTT CTGTCTGGAC 2520
TACATTATTT TCACTCTAAG ATTGATCCAC ATTTTTACTG TAAGCAGAAA CTTAGGACCC 2580
AAGATTATAA TGCTGCAGAG GATGCTGATC GATGTGTTCT TCTTCCTGTT CCTCTTTGCG 2640
GTGTGGATGG TGGCCTTTGG CGTGGCCAGG CAAGGGATCC TTAGGCAGAA TGAGCAGCGC 2700
TGGAGGTGGA TATTCCGTTC GGTCATCTAC GAGCCCTACC TGGCCATGTT CGGCCAGGTG 2760
CCCAGTGACG TGGATGGTAC CACGTATGAC TTTGCCCACT GCACCTTCAC TGGGAATGAG 2820
TCCAAGCCAC TGTGTGTGGA GCTGGATGAG CACAACCTGC CCCGGTTCCC CGAGTGGATC 2880
ACCATCCCCC TGGTGTGCAT CTACATGTTA TCCACCAACA TCCTGCTGGT CAACCTGCTG 2940
GTCGCCATGT TTGGCTACAC GGTGGGCACC GTCCAGGAGA ACAATGACCA GGTCTGGAAG 3000
TTCCAGAGGT ACTTCCTGGT GCAGGAGTAC TGCAGCCGCC TCAATATCCC CTTCCCCTTC 3060
ATCGTCTTCG CTTACTTCTA CATGGTGGTG AAGAAGTGCT TCAAGTGTTG CTGCAAGGAG 3120
AAAAACATGG AGTCTTCTGT CTGCTGTTTC AAAAATGAAG ACAATGAGAC TCTGGCATGG 3180
GAGGGTGTCA TGAAGGAAAA CTACCTTGTC AAGATCAACA CAAAAGCCAA CGACACCTCA 3240
GAGGAAATGA GGCATCGATT TAGACAACTG GATACAAAGC TTAATGATCT CAAGGGTCTT 3300
CTGAAAGAGA TTGCTAATAA AATCAAATAA AACTGTATGA AACTCTAATG GAGAAAAATC 3360
TAATTATAGC AAGATCATAT TAAGGAATGC TGATGAACAA TTTTGCTATC GACTACTAAA 3420
TGAGAGATTT TCAGACCCCT GGGTACATGG TGGATGATTT TAAATCACCC TAGTGTGCTG 3480
AGACCTTGAG AATAAAGTGT GTGATTGGTT TCATACTTGA AGACGGATAT AAAGGAAGAA 3540
TATTTCCTTT ATGTGTTTCT CCAGAATGGT GCCTGTTTCT CTCTGTGTCT CAATGCCTGG 3600
GACTGGAGGT TGATAGTTTA AGTGTGTTCT TACCGCCTCC TTTTTCCTTT AATCTTATTT 3660
TTGATGAACA CATATATAGG AGAACATCTA TCCTATGAAT AAGAACCTGG TCATGCTTTA 3720
CTCCTGTATT GTTATTTTGT TCATTTCCAA TTGATTCTCT ACTTTTCCCT TTTTTGTATT 3780
ATGTGACTAA TTAGTTGGCA TATTGTTAAA AGTCTCTCAA ATTAGGCCAG ATTCTAAAAC 3840
ATGCTGCAGC AAGAGGACCC CGCTCTCTTC AGGAAAAGTG TTTTCATTTC TCAGGATGCT 3900
TCTTACCTGT CAGAGGAGGT GACAAGGCAG TCTCTTGCTC TCTTGGACTC ACCAGGCTCC 3960
TATTGAAGGA ACCACCCCCA TTCCTAAATA TGTGAAAAGT CGCCCAAAAT GCAACCTTGA 4020
AAGGCACTAC TGACTTTGTT CTTATTGGAT ACTCCTCTTA TTTATTATTT TTCCATTAAA 4080
AATAATAGCT GGCTATTATA GAAAATTTAG ACCATACAGA GATGTAGAAA GAACATAAAT 4140
TGTCCCCATT ACCTTAAGGT AATCACTGCT AACAATTTCT GGATGGTTTT TCAAGTCTAT 4200
TTTTTTTCTA TGTATGTCTC AATTCTCTTT CAAAATTTTA CAGAATGTTA TCATACTACA 4260
TATATACTTT TTATGTAAGC TTTTTCACTT AGTATTTTAT CAAATATGTT TTTATTATAT 4320
TCATAGCCTT CTTAAACATT ATATCAATAA TTGCATAATA GGCAACCTCT AGCGATTACC 4380
ATAATTTTGC TCATTGAAGG CTATCTCCAG TTGATCATTG GGATGAGCAT CTTTGTGCAT 4440
GAATCCTATT GCTGTATTTG GGAAAATTTT CCAAGGTTAG ATTCCAATAA ATATCTATTT 4500
ATTATTAAAT ATTAAAATAT CGATTTATTA TTAAAACCAT TTATAAGGCT

Fig. 12A (2)

```
                                                          TTTTCATAAA 4560
TGTATAGCAA ATAGGAATTA TTAACTTGAG CATAAGATAT GAGATACATG AACCTGAACT 4620
ATTAAAATAA AATATTATAT TTAACCCTAG TTTAAGAAGA AGTCAATATG CTTATTTAAA 4680
TATTATGGAT GGTGGGCAGA TCACTTGAGG TCAGGAGTTC GAGACCAGCC TGGCCAACAT 4740
GGCAAAACCA CATCTCTACT AAAAATAAAA AAATTAGCTG GGTGTGGTGG TGCACTCCTG 4800
TAATCCCAGC TACTCAGAAG GCTGAGGTAC AAGAATTGCT GGAACCTGGG AGGCGGAGGT 4860
TGCAGTGAAC CAAGATTGCA CCACTGCACT CCAGCCGGGG TGACAGAGTG AGACTCCGAC 4920
TGAAAATAAA TAAATAAATA AATAAATAAA TAAATAAATA AATATTATGG ATGGTGAAGG 4980
GAATGGTATA GAATTGGAGA GATTATCTTA CTGAACACCT GTAGTCCCAG CTTTCTCTGG 5040
AAGTGGTGGT ATTTGAGCAG GATGTGCACA AGGCAATTGA AATGCCCATA ATTAGTTTCT 5100
CAGCTTTGAA TACACTATAA ACTCAGTGGC TGAAGGAGGA AATTTTAGAA GGAAGCTACT 5160
AAAAGATCTA ATTTGAAAAA CTACAAAAGC ATTAACTAAA AAAGTTTATT TTCCTTTTGT 5220
CTGGGCAGTA GTGAAAATAA CTACTCACAA CATTCACTAT GTTTGCAAGG AATTAACACA 5280
AATAAAAGAT GCCTTTTTAC TTAAACGCCA AGACAGAAAA CTTGCCCAAT ACTGAGAAGC 5340
AACTTGCATT AGAGAGGGAA CTGTTAAATG TTTTCAACCC AGTTCATCTG GTGGATGTTT 5400
TTGCAGGTTA CTCTGAGAAT TTTGCTTATG AAAAATCATT ATTTTTAGTG TAGTTCACAA 5460
TAATGTATTG AACATACTTC TAATCAAAGG TGCTATGTCC TTGTGTATGG TACTAAATGT 5520
GTCCTGTGTA CTTTTGCACA ACTGAGAATC CTGCGGCTTG GTTTAATGAG TGTGTTCATG 5580
AAATAAATAA TGGAGGAATT GTCAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 5640
AAAAAAAAAA AAAAAAAAAA AAAAAAAA                                   5668
```

Fig. 12A (3)

MRNRRNDTLDSTRTLYSSASRSTDLSYSESDLVNFIQANFKKRECVFFTKDSKATENVCKCGYAQSQHME
GTQINQSEKWNYKKHTKEFPTDAFGDIQFETLGKKGKYIRLSCDTDAEILYELLTQHWHLKTPNLVISVT
GGAKNFALKPRMRKIFSRLIYIAQSKGAWILTGGTHYGLTKYIGEVVRDNTISRSSEENIVAIGIAAWGM
VSNRDTLIRNCDAEGYFLAQYLMDDFTRDPLYILDNNHTHLLLVDNGCHGHPTVEAKLRNQLEKHISERT
IQDSNYGGKIPIVCFAQGGGKETLKAINTSIKNKIPCVVVEGSGRIADVIASLVEVEDAPTSSAVKEKLV
RFLPRTVSRLSEEETESWIKWLKEILECSHLLTVIKMEEAGDEIVSNAISYALYKAFSTSEQDKDNWNGQ
LKLLLEWNQLDLANDEIFTNDRRWESADLQEVMFTALIKDRPKFVRLFLENGLNLRKFLTHDVLTELFSN
HFSTLVYRNLQIAKNSYNDALLTFVWKLVANFRRGFRKEDRNGRDEMDIELHDVSPITRHPLQALFIWAI
LQNKKELSKVIWEQTRGCTLAALGASKLLKTLAKVKNDINAAGESEELANEYETRAVELFTECYSSDEDL
AEQLLVYSCEAWGGSNCLELAVEATDQHFTAQPGVQNFLSKQWYGEISRDTKNWKIILCLFIIPLVGCGF
VSFRKKPVDKHKKLLWYYVAFFTSPFVVFSWNVVFYIAFLLLFAYVLLMDFHSVPHPPELVLYSLVFVLF
CDEVRQWYVNGVNYFTDLWNVMDTLGLFYFIAGIVFRLHSSNKSSLYSGRVIFCLDYIIFTLRLIHIFTV
SRNLGPKIIMLQRMLIDVFFFLFLFAVWMVAFGVARQGILRQNEQRWRWIFRSVIYEPYLAMFGQVPSDV
DGTTYDFAHCTFTGNESKPLCVELDEHNLPRFPEWITIPLVCIYMLSTNILLVNLLVAMFGYTVGTVQEN
NDQVWKFQRYFLVQEYCSRLNIPFPFIVFAYFYMVVKKCFKCCCKEKNMESSVCCFKNEDNETLAWEGVM
KENYLVKINTKANDTSEEMRHRFRQLDTKLNDLKGLLKEIANKIK

Fig. 12B

SEQUENCE LISTING

<110> Corixa Corporation
Xu, Jiangchun
Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
Yuqui, Jiang
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
Li, Samuel
Wang, Aijun
Skeiky, Yasir A.W.
Hepler, William
Henderson, Robert A.

<120> COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF PROSTATE CANCER

<130> 210121.42723PC

<140> PCT
<141> 2001-03-27

<160> 943

<170> FastSEQ for Windows Version 3.0

<210> 1
<211> 814
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(814)
<223> n = A,T,C or G

<400> 1
tttttttttt tttttcacag tataacagct ctttatttct gtgagttcta ctaggaaatc 60
atcaaatctg agggttgtct ggaggacttc aatacacctc cccccatagt gaatcagctt 120
ccagggggtc cagtccctct ccttacttca tccccatccc atgccaaagg aagaccctcc 180
ctccttggct cacagccttc tctaggcttc ccagtgcctc caggacagag tgggttatgt 240
tttcagctcc atccttgctg tgagtgtctg gtgcgttgtg cctccagctt ctgctcagtg 300
cttcatggac agtgtccagc acatgtcact ctccactctc tcagtgtgga tccactagtt 360
ctagagcggc cgccaccgcg gtggagctcc agcttttgtt ccctttagtg agggttaatt 420
gcgcgcttgg cgtaatcatg gtcataactg tttcctgtgt gaaattgtta tccgctcaca 480
attccacaca acatacgagc cggaagcata aagtgtaaag cctggggtgc ctaatgagtg 540
anctaactca cattaattgc gttgcgctca ctgnccgctt tccagtcngg aaaactgtcg 600
tgccagctgc attaatgaat cggccaacgc ncggggaaaa gcggtttgcg ttttgggggc 660
tcttccgctt ctcgctcact nantcctgcg ctcggtcntt cggctgcggg gaacggtatc 720
actcctcaaa ggnggtatta cggttatccn naaatcnggg gatacccngg aaaaanttt 780

aacaaaaggg cancaaaggg cngaaacgta aaaa 814

<210> 2
<211> 816
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(816)
<223> n = A,T,C or G

<400> 2
acagaaatgt tggatggtgg agcacctttc tatacgactt acaggacagc agatggggaa 60
ttcatggctg ttggagcaat agaaccccag ttctacgagc tgctgatcaa aggacttgga 120
ctaaagtctg atgaacttcc caatcagatg agcatggatg attggccaga aatgaagaag 180
aagtttgcag atgtatttgc aaagaagacg aaggcagagt ggtgtcaaat ctttgacggc 240
acagatgcct gtgtgactcc ggttctgact tttgaggagg ttgttcatca tgatcacaac 300
aaggaacggg gctcgtttat caccagtgag gagcaggacg tgagcccccg ccctgcacct 360
ctgctgttaa acaccccagc catcccttct ttcaaaaggg atccactagt tctagaagcg 420
gccgccaccg cggtggagct ccagcttttg ttccctttag tgagggttaa ttgcgcgctt 480
ggcgtaatca tggtcatagc tgtttcctgt gtgaaattgt tatccgctca caattccccc 540
aacatacgag ccggaacata aagtgttaag cctggggtgc ctaatgantg agctaactcn 600
cattaattgc gttgcgctca ctgcccgctt tccagtcggg aaaactgtcg tgccactgcn 660
ttantgaatc ngccaccccc cgggaaaagg cggttgcntt ttgggcctct tccgctttcc 720
tcgctcattg atcctngcnc ccggtcttcg gctgcggnga acggttcact cctcaaaggc 780
ggtntnccgg ttatccccaa acnggggata cccnga 816

<210> 3
<211> 773
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(773)
<223> n = A,T,C or G

<400> 3
cttttgaaag aagggatggc tggggtgttt aacagcagag gtgcagggcg ggggctcacg 60
tcctgctcct cactggtgat aaacgagccc cgttccttgt tgtgatcatg atgaacaacc 120
tcctcaaaag tcagaaccgg agtcacacag gcatctgtgc cgtcaaagat ttgacaccac 180
tctgccttcg tcttctttgc aaatacatct gcaaacttct tcttcatttc tggccaatca 240
tccatgctca tctgattggg aagttcatca gactttagtc canntccttt gatcagcagc 300
tcgtagaact ggggttctat tgctccaaca gccatgaatt ccccatctgc tgtcctgtaa 360
gtcgtataga aaggtgctcc accatccaac atgttctgtc ctcgaggggg ggcccggtac 420
ccaattcgcc ctatantgag tcgtattacg cgcgctcact ggccgtcgtt ttacaacgtc 480
gtgactggga aaaccctggg cgttacccaac ttaatcgcct tgcagcacat ccccctttcg 540
ccagctggcg gtaatancga aaaggcccgc accgatcgcc cttccaacag ttgcgcacct 600
gaatgggnaa atgggacccc cctgttaccg cgcattnaac ccccgcnggg tttngttgtt 660
acccccacnt nnaccgctta cactttgcca gcgccttanc gcccgctccc tttcnccttt 720
cttcccttcc tttcncnccn ctttcccccg gggtttcccc cntcaaaccc cna 773

<210> 4
<211> 828
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(828)
<223> n = A,T,C or G

<400> 4
```
cctcctgagt cctactgacc tgtgctttct ggtgtggagt ccagggctgc taggaaaagg      60
aatgggcaga cacaggtgta tgccaatgtt tctgaaatgg gtataatttc gtcctctcct     120
tcggaacact ggctgtctct gaagacttct cgctcagttt cagtgaggac acacacaaag     180
acgtgggtga ccatgttgtt tgtggggtgc agagatggga ggggtggggc ccaccctgga     240
agagtggaca gtgacacaag gtggacactc tctacagatc actgaggata agctggagcc     300
acaatgcatg aggcacacac acagcaagga tgacnctgta aacatagccc acgctgtcct     360
gngggcactg ggaagcctan atnaggccgt gagcanaaag aaggggagga tccactagtt     420
ctanagcggc cgccaccgcg gtgganctcc ancttttgtt ccctttagtg agggttaatt     480
gcgcgcttgg cntaatcatg gtcatanctn tttcctgtgt gaaattgtta tccgctcaca     540
attccacaca acatacganc cggaaacata aantgtaaac ctggggtgcc taatgantga     600
ctaactcaca ttaattgcgt tgcgctcact gcccgctttc caatcnggaa acctgtcttg     660
ccncttgcat tnatgaatcn gccaaccccc ggggaaaagc gtttgcgttt tgggcgctct     720
tccgcttcct cnctcantta ntccctncnc tcggtcattc cggctgcngc aaaccggttc     780
accncctcca aaggggtat tccggtttcc ccnaatccgg gganancc                   828
```

<210> 5
<211> 834
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(834)
<223> n = A,T,C or G

<400> 5
```
tttttttttt tttttactga tagatggaat ttattaagct tttcacatgt gatagcacat      60
agttttaatt gcatccaaag tactaacaaa aactctagca atcaagaatg gcagcatgtt     120
attttataac aatcaacacc tgtggctttt aaaatttggt tttcataaga taatttatac     180
tgaagtaaat ctagccatgc ttttaaaaaa tgctttaggt cactccaagc ttggcagtta     240
acatttggca taaacaataa taaaacaatc acaatttaat aaataacaaa tacaacattg     300
taggccataa tcatatacag tataaggaaa aggtggtagt gttgagtaag cagttattag     360
aatagaatac cttggcctct atgcaaatat gtctagacac tttgattcac tcagccctga     420
cattcagttt tcaaagtagg agacaggttc tacagtatca ttttacagtt tccaacacat     480
tgaaaacaag tagaaaatga tgagttgatt tttattaatg cattacatcc tcaagagtta     540
tcaccaaccc ctcagttata aaaaatttc aagttatatt agtcatataa cttggtgtgc      600
ttattttaaa ttagtgctaa atggattaag tgaagacaac aatggtcccc taatgtgatt     660
gatattggtc atttttacca gcttctaaat ctnaactttc aggcttttga actggaacat     720
tgnatnacag tgttccanag ttncaaccta ctggaacatt acagtgtgct tgattcaaaa     780
tgttattttg ttaaaaatta aattttaacc tggtggaaaa ataatttgaa atna           834
```

<210> 6
<211> 818
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(818)
<223> n = A,T,C or G

<400> 6

```
tttttttttt tttttttttt aagaccctca tcaatagatg gagacataca gaaatagtca      60
aaccacatct acaaaatgcc agtatcaggc ggcggcttcg aagccaaagt gatgtttgga     120
tgtaaagtga aatattagtt ggcggatgaa gcagatagtg aggaaagttg agccaataat     180
gacgtgaagt ccgtggaagc ctgtggctac aaaaaatgtt gagccgtaga tgccgtcgga     240
aatggtgaag ggagactcga agtactctga ggcttgtagg agggtaaaat agagacccag     300
taaaattgta ataagcagtg cttgaattat ttggtttcgg ttgttttcta ttagactatg     360
gtgagctcag gtgattgata ctcctgatgc gagtaatacg gatgtgttta ggagtgggac     420
ttctaggggа tttagcgggg tgatgcctgt tgggggccag tgccctccta gttggggggt     480
aggggctagg ctggagtggt aaaaggctca gaaaaatcct gcgaagaaaa aaacttctga     540
ggtaataaat aggattatcc cgtatcgaag gccttttttgg acaggtggtg tgtggtggcc    600
ttggtatgtg ctttctcgtg ttacatcgcg ccatcattgg tatatggtta gtgtgttggg     660
ttantanggc ctantatgaa gaacttttgg antggaatta aatcaatngc ttggccggaa     720
gtcattanga nggctnaaaa ggccctgtta ngggtctggg ctnggtttta cccnacccat     780
ggaatncncc ccccggacna ntgnatccct attcttaa                             818
```

<210> 7
<211> 817
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(817)
<223> n = A,T,C or G

<400> 7

```
tttttttttt tttttttttt tggctctaga gggggtagag ggggtgctat agggtaaata      60
cgggccctat ttcaaagatt tttaggggaa ttaattctag gacgatgggt atgaaactgt     120
ggtttgctcc acagatttca gagcattgac cgtagtatac ccccggtcgt gtagcggtga     180
aagtggtttg gtttagacgt ccgggaattg catctgtttt taagcctaat gtggggacag     240
ctcatgagtg caagacgtct tgtgatgtaa ttattatacn aatgggggct tcaatcggga     300
gtactactcg attgtcaacg tcaaggagtc gcaggtcgcc tggttctagg aataatgggg     360
gaagtatgta ggaattgaag attaatccgc cgtagtcggt gttctcctag gttcaatacc     420
attggtggcc aattgatttg atggtaaggg gagggatcgt tgaactcgtc tgttatgtaa     480
aggatncctt ngggatggga aggcnatnaa ggactangga tnaatggcgg gcangatatt     540
tcaaacngtc tctanttcct gaaacgtctg aaatgttaat aanaattaan tttngttatt     600
gaatnttnng gaaaaggget tacaggacta gaaaccaaat angaaaanta atnntaangg     660
cnttatcntn aaaggtnata accnctccta tnatcccacc caatngnatt ccccacncnn     720
acnattggat nccccanttc canaaanggc cnccccccgg tgnanncenc cttttgttcc     780
cttnantgan ggttattcnc ccctngcntt atcancc                              817
```

<210> 8
<211> 799
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(799)
<223> n = A,T,C or G

<400> 8

```
catttccggg tttactttct aaggaaagcc gagcggaagc tgctaacgtg ggaatcggtg      60
cataaggaga actttctgct ggcacgcgct agggacaagc gggagagcga ctccgagcgt     120
ctgaagcgca cgtcccagaa ggtggacttg gcactgaaac agctgggaca catccgcgag     180
tacgaacagc gcctgaaagt gctggagcgg gaggtccagc agtgtagccg cgtcctgggg     240
tgggtggccg angcctganc cgctctgcct tgctgccccc angtgggccg ccaccccctg     300
acctgcctgg gtccaaacac tgagccctgc tggcggactt caagganaac ccccacangg     360
```

```
ggattttgct cctanantaa ggctcatctg ggcctcggcc cccccacctg gttggccttg     420
tctttgangt gagccccatg tccatctggg ccactgtcng gaccaccttt ngggagtgtt     480
ctccttacaa ccacannatg cccggctcct cccggaaacc antcccancc tgngaaggat     540
caagncctgn atccactnnt nctanaaccg gccnccnccg cngtggaacc cnccttntgt     600
tccttttcnt tnagggttaa tnncgccttg gccttnccan ngtcctncnc nttttccnnt     660
gttnaaattg ttangcnccc nccnntcccn cnncnncnan cccgacccnn annttnnann     720
ncctgggggt nccnncngat tgacccnncc nccctntant tgcnttnggg nncnntgccc     780
ctttccctct ngggannccg                                                 799
```

<210> 9
<211> 801
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(801)
<223> n = A,T,C or G

<400> 9

```
acgccttgat cctcccaggc tgggactggt tctgggagga gccgggcatg ctgtggtttg      60
taangatgac actcccaaag gtggtcctga cagtggccca gatggacatg gggctcacct     120
caaggacaag gccaccaggt gcgggggccg aagcccacat gatccttact ctatgagcaa     180
aatcccctgt gggggcttct ccttgaagtc cgccancagg gctcagtctt tggacccang     240
caggtcatgg ggttgtngnc caactggggg ccncaacgca aaanggcnca gggcctcngn     300
cacccatccc angacgcggc tacactnctg gacctcccnc tccaccactt tcatgcgctg     360
ttcntacccg cgnatntgtc ccanctgttt cngtgccnac tccancttct nggacgtgcg     420
ctacatacgc ccggantcnc nctcccgctt tgtccctatc cacgtnccan caacaaattt     480
cnccntantg caccnattcc cacntttnnc agntttccnc nncgngcttc cttntaaaag     540
ggttganccc cggaaaatnc cccaaagggg gggggccngg tacccaactn cccccctnata     600
gctgaantcc ccatnaccnn gnctcnatgg ancentccnt tttaannacn ttctnaactt     660
gggaanancc ctcgnccntn ccccccnttaa tcccnccttg cnangnncnt cccccnntcc     720
ncccnnntng gcntntnann cnaaaaaggc ccnnnancaa tctcctnncn cctcanttcg     780
ccanccctcg aaatcggccn c                                               801
```

<210> 10
<211> 789
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(789)
<223> n = A,T,C or G

<400> 10

```
cagtctatnt ggccagtgtg gcagctttcc ctgtggctgc cggtgccaca tgcctgtccc      60
acagtgtggc cgtggtgaca gcttcagccg ccctcaccgg gttcaccttc tcagccctgc     120
agatcctgcc ctacacactg gcctccctct accaccggga gaagcaggtg ttcctgccca     180
aataccgagg ggacactgga ggtgctagca gtgaggacag cctgatgacc agcttcctgc     240
caggccctaa gcctggagct cccttcccta atggacacgt gggtgctgga ggcagtggcc     300
tgctcccacc tccacccgcg ctctgcgggg cctctgcctg tgatgtctcc gtacgtgtgg     360
tggtgggtga gcccaccgan gccagggtgg ttccgggccg gggcatctgc ctggacctcg     420
ccatcctgga tagtgcttcc tgctgtccca ngtggcccca tccctgttta tgggctccat     480
tgtccagctc agccagtctg tcactgccta tatggtgtct gccgcaggcc tgggtctggt     540
cccatttact ttgctacaca ggtantattt gacaagaacg anttggccaa atactcagcg     600
ttaaaaaatt ccagcaacat tgggggtgga aggcctgcct cactgggtcc aactccccgc     660
tcctgttaac cccatggggc tgccggcttg gccgccaatt tctgttgctg ccaaantnat     720
```

```
gtggctctct gctgccacct gttgctggct gaagtgcnta cngcncanct ngggggg tng      780
ggngttccc                                                               789

      &lt;210&gt; 11
      &lt;211&gt; 772
      &lt;212&gt; DNA
      &lt;213&gt; Homo sapien

      &lt;220&gt;
      &lt;221&gt; misc_feature
      &lt;222&gt; (1)...(772)
      &lt;223&gt; n = A,T,C or G

      &lt;400&gt; 11
cccaccctac ccaaatatta gacaccaaca cagaaaagct agcaatggat tcccttctac        60
tttgttaaat aaataagtta aatatttaaa tgcctgtgtc tctgtgatgg caacagaagg       120
accaacaggc cacatcctga taaaaggtaa gagggggg tg gatcagcaaa aagacagtgc      180
tgtgggctga ggggacctgg ttcttgtgtg ttgcccctca ggactcttcc cctacaaata       240
actttcatat gttcaaatcc catggaggag tgtttcatcc tagaaactcc catgcaagag       300
ctacattaaa cgaagctgca ggttaagggg cttanagatg ggaaaccagg tgactgagtt       360
tattcagctc ccaaaaaccc ttctctaggt gtgtctcaac taggaggcta gctgttaacc       420
ctgagcctgg gtaatccacc tgcagagtcc ccgcattcca gtgcatggaa cccttctggc       480
ctccctgtat aagtccagac tgaaaccccc ttggaaggnc tccagtcagg cagccctana       540
aactggggaa aaaagaaaag gacgccccan cccccagctg tgcanctacg cacctcaaca       600
gcacagggtg gcagcaaaaa aaccacttta ctttggcaca aacaaaaact nggggggca       660
accccggcac cccnangggg gttaacagga ancngggnaa cntggaaccc aattnaggca       720
ggcccnccac cccnaatntt gctgggaaat ttttcctccc ctaaattntt tc               772

      &lt;210&gt; 12
      &lt;211&gt; 751
      &lt;212&gt; DNA
      &lt;213&gt; Homo sapien

      &lt;220&gt;
      &lt;221&gt; misc_feature
      &lt;222&gt; (1)...(751)
      &lt;223&gt; n = A,T,C or G

      &lt;400&gt; 12
gccccaattc cagctgccac accacccacg gtgactgcat tagttcggat gtcatacaaa        60
agctgattga agcaaccctc tactttttgg tcgtgagcct tttgcttggt gcaggtttca       120
ttggctgtgt tggtgacgtt gtcattgcaa cagaatgggg gaaaggcact gttctctttg       180
aagtanggtg agtcctcaaa atccgtatag ttggtgaagc cacagcactt gagccctttc       240
atggtggtgt tccacacttg agtgaagtct tcctgggaac cataatcttt cttgatggca       300
ggcactacca gcaacgtcag ggaagtgctc agccattgtg gtgtacacca aggcgaccac       360
agcagctgcn acctcagcaa tgaagatgan gaggangatg aagaagaacg tcncgagggc       420
acacttgctc tcagtcttan caccatanca gcccntgaaa accaananca aagaccacna       480
cnccggctgc gatgaagaaa tnaccccncg ttgacaaact tgcatggcac tggganccac       540
agtggcccna aaaatcttca aaaaggatgc cccatcnatt gaccccccaa atgcccactg       600
ccaacagggg ctgccccacn cncnnaacga tganccnatt gnacaagatc tncntggtct       660
tnatnaacnt gaaccctgcn tngtggctcc tgttcaggnc cnnggcctga cttctnaann       720
aangaactcn gaagncccca cnggananne g                                      751

      &lt;210&gt; 13
      &lt;211&gt; 729
      &lt;212&gt; DNA
      &lt;213&gt; Homo sapien
```

<220>
<221> misc_feature
<222> (1)...(729)
<223> n = A,T,C or G

<400> 13
gagccaggcg tccctctgcc tgcccactca gtggcaacac ccgggagctg ttttgtcctt 60
tgtggancct cagcagtncc ctctttcaga actcantgcc aaganccctg aacaggagcc 120
accatgcagt gcttcagctt cattaagacc atgatgatcc tcttcaattt gctcatcttt 180
ctgtgtggtg cagccctgtt ggcagtgggc atctgggtgt caatcgatgg ggcatccttt 240
ctgaagatct tcgggccact gtcgtccagt gccatgcagt ttgtcaacgt gggctacttc 300
ctcatcgcag ccggcgttgt ggtcttagct ctaggtttcc tgggctgcta tggtgctaag 360
actgagagca agtgtgccct cgtgacgttc ttcttcatcc tcctcctcat cttcattgct 420
gaggttgcaa tgctgtggtc gccttggtgt acaccacaat ggctgagcac ttcctgacgt 480
tgctggtaat gcctgccatc aanaaaagat tatgggttcc caggaaactt tcactcaagt 540
gttggaacac caccatgaaa gggctcaagt gctgtggctt cnnccaacta tacggatttt 600
gaagantcac ctacttcaaa gaaaanagtg cctttccccc atttctgttg caattgacaa 660
acgtccccaa cacagccaat tgaaaacctg cacccaaccc aaangggtcc ccaaccanaa 720
attnaaggg 729

<210> 14
<211> 816
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(816)
<223> n = A,T,C or G

<400> 14
tgctcttcct caaagttgtt cttgttgcca taacaaccac cataggtaaa gcgggcgcag 60
tgttcgctga aggggttgta gtaccagcgc gggatgctct ccttgcagag tcctgtgtct 120
ggcaggtcca cgcagtgccc tttgtcactg gggaaatgga tgcgctggag ctcgtcaaag 180
ccactcgtgt atttttcaca ggcagcctcg tccgacgcgt cggggcagtt gggggtgtct 240
tcacactcca ggaaactgtc natgcagcag ccattgctgc agcggaactg ggtgggctga 300
cangtgccag agcacactgg atggcgcctt tccatgnnan gggccctgng ggaaagtccc 360
tganccccan anctgcctct caaangcccc accttgcaca ccccgacagg ctagaatgga 420
atcttcttcc cgaaaggtag ttnttcttgt tgcccaancc anccccntaa acaaactctt 480
gcanatctgc tccgnggggg tcntantacc ancgtgggaa aagaacccca ggcngcgaac 540
caancttgtt tggatncgaa gcnataatct nctnttctgc ttggtggaca gcaccantna 600
ctgtnnanct ttagnccntg gtcctcntgg gttgnncttg aacctaatcn ccnntcaact 660
gggacaaggt aantngccnt cctttnaatt cccnancntn cccccctggtt tggggttttn 720
cncnctccta ccccagaaan nccgtgttcc cccccaacta ggggccnaaa ccnnttnttc 780
cacaaccctn ccccacccac gggttcngnt ggttng 816

<210> 15
<211> 783
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(783)
<223> n = A,T,C or G

<400> 15
ccaaggcctg ggcaggcata nacttgaagg tacaacccca ggaacccctg gtgctgaagg 60

```
atgtggaaaa cacagattgg cgcctactgc ggggtgacac ggatgtcagg gtagagagga     120
aagacccaaa ccaggtggaa ctgtggggac tcaaggaang cacctacctg ttccagctga     180
cagtgactag ctcagaccac ccagaggaca cggccaacgt cacagtcact gtgctgtcca     240
ccaagcagac agaagactac tgcctcgcat ccaacaangt gggtcgctgc cggggctctt     300
tcccacgctg gtactatgac ccccacggagc agatctgcaa gagtttcgtt tatggaggct    360
gcttgggcaa caagaacaac taccttcggg aagaagagtg cattctancc tgtcngggtg     420
tgcaaggtgg gcctttgana ngcanctctg gggctcangc gactttcccc cagggcccct     480
ccatggaaag gcgccatcca ntgttctctg gcacctgtca gcccacccag ttccgctgca     540
ncaatggctg ctgcatcnac antttcctng aattgtgaca acaccccccca ntgcccccaa    600
ccctcccaac aaagcttccc tgttnaaaaa tacnccantt ggcttttnac aaacnccccgg    660
cncctccntt ttccccnntn aacaaagggc nctngcnttt gaactgcccn aacccnggaa     720
tctnccnngg aaaaantncc cccccctggtt cctnnaancc cctccncnaa anctnccccc    780
ccc                                                                   783
```

<210> 16
<211> 801
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(801)
<223> n = A,T,C or G

<400> 16
```
gccccaattc cagctgccac accacccacg gtgactgcat tagttcggat gtcatacaaa      60
agctgattga agcaaccctc tactttttgg tcgtgagcct tttgcttggt gcaggtttca     120
ttggctgtgt tggtgacgtt gtcattgcaa cagaatgggg gaaaggcact gttctctttg     180
aagtagggtg agtcctcaaa atccgtatag ttggtgaagc cacagcactt gagccctttc     240
atggtggtgt tccacacttg agtgaagtct tcctgggaac cataatcttt cttgatggca     300
ggcactacca gcaacgtcag gaagtgctca gccattgtgg tgtacaccaa ggcgaccaca     360
gcagctgcaa cctcagcaat gaagatgagg aggaggatga agaagaacgt cncgagggca     420
cacttgctct ccgtcttagc accatagcag cccangaaac caagagcaaa gaccacaacg     480
ccngctgcga atgaaagaaa ntacccacgt tgacaaactg catggccact ggacgacagt     540
tggcccgaan atcttcagaa aagggatgcc ccatcgattg aacacccana tgcccactgc     600
cnacagggct gcnccncncn gaaagaatga gccattgaag aaggatcntc ntggtcttaa     660
tgaactgaaa ccntgcatgg tggcccctgt tcagggctct tggcagtgaa ttctganaaa     720
aaggaacngc ntnagccccc ccaaangana aaacaccccc gggtgttgcc ctgaattggc     780
ggccaaggan ccctgccccn g                                               801
```

<210> 17
<211> 740
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(740)
<223> n = A,T,C or G

<400> 17
```
gtgagagcca ggcgtccctc tgcctgccca ctcagtggca acacccggga gctgttttgt      60
cctttgtgga gcctcagcag ttccctcttt cagaactcac tgccaagagc cctgaacagg     120
agccaccatg cagtgcttca gcttcattaa gaccatgatg atcctcttca atttgctcat     180
ctttctgtgt ggtgcagccc tgttggcagt gggcatctgg gtgtcaatcg atggggcatc     240
ctttctgaag atcttcgggc cactgtcgtc cagtgccatg cagtttgtca acgtgggcta     300
cttcctcatc gcagccggcg ttgtggtctt tgctcttggt ttcctgggct gctatggtgc     360
taagacggag agcaagtgtg ccctcgtgac gttcttcttc atcctcctcc tcatcttcat     420
```

```
tgctgaagtt gcagctgctg tggtcgcctt ggtgtacacc acaatggctg aaccattcct     480
gacgttgctg gtantgcctg ccatcaanaa agattatggg ttcccaggaa aaattcactc     540
aantntggaa caccnccatg aaaagggctc caatttctgn tggcttcccc aactataccg     600
gaattttgaa agantcnccc tacttccaaa aaaaaanant tgcctttncc cccnttctgt     660
tgcaatgaaa acntcccaan acngccaatn aaaacctgcc cnnncaaaaa ggntcncaaa     720
caaaaaaant nnaagggttn                                                 740
```

<210> 18
<211> 802
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(802)
<223> n = A,T,C or G

<400> 18

```
ccgctggttg cgctggtcca gngnagccac gaagcacgtc agcatacaca gcctcaatca      60
caaggtcttc cagctgccgc acattacgca gggcaagagc ctccagcaac actgcatatg     120
ggatacactt tactttagca gccagggtga caactgagag gtgtcgaagc ttattcttct     180
gagcctctgt tagtggagga agattccggg cttcagctaa gtagtcagcg tatgtcccat     240
aagcaaacac tgtgagcagc cggaaggtag aggcaaagtc actctcagcc agctctctaa     300
cattgggcat gtccagcagt tctccaaaca cgtagacacc agnggcctcc agcacctgat     360
ggatgagtgt ggccagcgct gccccttgg ccgacttggc taggagcaga aattgctcct      420
ggttctgccc tgtcaccttc acttccgcac tcatcactgc actgagtgtg gggacttgg      480
gctcaggatg tccagagacg tggttccgcc ccctcnctta atgacaccgn ccanncaacc     540
gtcggctccc gccgantgng ttcgtcgtnc ctgggtcagg gtctgctggc cnctacttgc     600
aancttcgtc nggcccatgg aattcaccnc accggaactn gtangatcca ctnnttctat     660
aaccggncgc caccgcnnnt ggaactccac tcttnttncc tttacttgag ggttaaggtc     720
acccttnncg ttaccttggt ccaaaccntn ccntgtgtcg anatngtnaa tcnggnccna     780
tnccanccnc atangaagcc ng                                              802
```

<210> 19
<211> 731
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(731)
<223> n = A,T,C or G

<400> 19

```
cnaagcttcc aggtnacggg ccgcnaancc tgacccnagg tancanaang cagncngcgg      60
gagcccaccg tcacgnggng gngtctttat nggagggggc ggagccacat cnctggacnt     120
cntgacccca actccccncc ncncantgca gtgatgagtg cagaactgaa ggtnacgtgg     180
caggaaccaa gancaaannc tgctccnntc caagtcggcn nagggggcgg ggctggccac     240
gcncatccnt cnagtgctgn aaagccccnn cctgtctact tgtttggaga acngcnnnga     300
catgcccagn gttanataac nggcngagag tnantttgcc tctcccttcc ggctgcgcan     360
cgngtntgct tagnggacat aacctgacta cttaactgaa cccnngaatc tnccnccccct    420
ccactaagct cagaacaaaa aacttcgaca ccactcantt gtcacctgnc tgctcaagta     480
aagtgtaccc catncccaat gtntgctnga ngctctgncc tgcnttangt tcggtcctgg     540
gaagacctat caattnaagc tatgtttctg actgcctctt gctccctgna acaancnacc     600
cnncnntcca aggggggggnc ggcccccaat ccccccaacc ntnaattnan tttanccccn    660
cccccnggcc cggcctttta cnancntcnn nnacngggna aaaccnnngc tttncccaac     720
nnaatccncc t                                                          731
```

<210> 20
<211> 754
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(754)
<223> n = A,T,C or G

<400> 20
```
tttttttttt tttttttttt taaaaacccc ctccattnaa tgnaaacttc cgaaattgtc      60
caaccccctc ntccaaatnn ccntttccgg gngggggttc caaacccaan ttannttttgg    120
annttaaatt aaatnttnnt tggnggnnna anccnaatgt nangaaagtt naacccanta     180
tnancttnaa tncctggaaa ccngtngntt ccaaaaatnt ttaaccctta antccctccg     240
aaatngttna nggaaaaccc aanttctcnt aaggttgttt gaaggntnaa tnaaaanccc     300
nnccaattgt ttttngccac gcctgaatta attggnttcc gntgttttcc nttaaaanaa     360
ggnnancccc ggttantnaa tccccccnnc cccaattata ccganttttt ttngaattgg     420
gancccncgg gaattaacgg ggnnnntccc tnttgggggg cnggnncccc ccccntcggg     480
ggttngggnc aggncnnaat tgtttaaggg tccgaaaaat ccctccnaga aaaaaanctc     540
ccaggntgag nntngggttt nccccccccc canggcccct ctcgnanagt tggggtttgg     600
ggggcctggg attttntttc ccctnttncc tccccccccc ccngggganag aggttngngt    660
tttgntcnnc ggccccnccn aagancttttn ccganttnan ttaaatccnt gcctnggcga    720
agtccnttgn agggntaaan ggcccccctnn cggg                                754
```

<210> 21
<211> 755
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(755)
<223> n = A,T,C or G

<400> 21
```
atcancccat gaccccnaac nngggaccnc tcanccggnc nnncnaccnc cggccnatca      60
nngtnagnnc actncnnttn natcacnccc cnccnactac gcccncnanc cnacgcncta     120
nncanatncc actganngcg cgangtngan ngagaaanct nataccanag ncaccanacn     180
ccagctgtcc nanaangcct nnnatacngg nnnatccaat ntgnancctc cnaagtattn     240
nncnncanat gattttcctn anccgattac ccntnccccc tancccctcc cccccaacna     300
cgaaggcnct ggnccnaagg nngcgncncc ccgctagntc cccnncaagt cncncnccta     360
aactcanccn nattacncgc ttcntgagta tcactccccg aatctcaccc tactcaactc     420
aaaaanatcn gatacaaaat aatncaagcc tgnttatnac actntgactg ggtctctatt     480
ttagnggtcc ntnaancntc ctaatacttc cagtctncct tcnccaattt ccnaanggct     540
ctttcngaca gcatnttttg gttcccnntt gggttcttan ngaattgccc ttcntngaac     600
gggctcntct tttccttcgg ttancctggn ttcnnccggc cagttattat ttcccntttt     660
aaattcntnc cntttanttt tggcnttcna aacccccggc cttgaaaacg gccccctggt     720
aaaaggttgt tttganaaaa tttttgtttt gttcc                                755
```

<210> 22
<211> 849
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(849)

<223> n = A,T,C or G

<400> 22
```
tttttttttt tttttangtg tngtcgtgca ggtagaggct tactacaant gtgaanacgt    60
acgctnggan taangcgacc cganttctag gannencccct aaaatcanac tgtgaagatn   120
atcctgnnna cggaanggtc accggnngat nntgctaggg tgnccnctcc cannncnttn   180
cataactcng nggccctgcc caccaccttc ggcggcccng ngnccgggcc cgggtcattn    240
gnnttaaccn cactnngcna ncggtttccn nccccnncng acccnggcga tccggggtnc    300
tctgtcttcc cctgnagncn anaaantggg ccncggnccc ctttacccct nnacaagcca   360
cngccntcta nccncngccc cccctccant nnggggggact gccnanngct ccgttnctng   420
nnaccccnnn gggtncctcg gttgtcgant cnaccgnang ccanggattc cnaaggaagg   480
tgcgttnttg gcccctaccc ttcgctncgg nncacccttc ccgacnanga nccgctcccg   540
cncnncgnng cctcncctcg caacacccgc nctcntcngt ncggnnnccc ccccacccgc   600
nccctcncnc ngncgnancn ctccnccncc gtctcannca ccaccccgcc ccgccaggcc   660
ntcanccacn ggnngacnng nagcncnntc gcnccgcgcn gcgncnccct cgccncngaa   720
ctncntcngg ccantnncgc tcaanccnna cnaaacgccg ctgcgcggcc cgnagcgncc   780
ncctccncga gtcctcccgn cttccnaccc angnnttccn cgaggacacn nnaccccgcc   840
nncangcgg                                                           849
```

<210> 23
<211> 872
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(872)
<223> n = A,T,C or G

<400> 23
```
gcgcaaacta tacttcgctc gnactcgtgc gcctcgctnc tcttttcctc cgcaaccatg    60
tctgacnanc ccgattnggc ngatatcnan aagntcganc agtccaaact gantaacaca   120
cacacncnan aganaaatcc nctgccttcc anagtanacn attgaacnng agaaccangc   180
nggcgaatcg taatnaggcg tgcgccgcca atntgtcncc gtttattntn ccagcntcnc   240
ctnccnaccc tacntcttcn nagctgtcnn acccctngtn cgnacccccc naggtcggga   300
tcgggtttnn nntgaccgng cnnccccctcc ccccntccat nacganccnc ccgcaccacc   360
nanngcncgc nccccgnnct cttcgccncc ctgtcctntn cccctgtngc ctggcncngn   420
accgcattga ccctcgccnn ctncnngaaa ncgnanacgt ccgggttgnn annancgctg   480
tgggnnngcg tctgcncccgc gttccttccn ncnncttcca ccatcttcnt tacngggtct  540
ccncgccntc tcnnncacnc cctgggacgc tntcctntgc ccccсttnac tcccccccctt  600
cgncgtgncc cgncccccacc ntcatttnca nacgntcttc acaannncct ggntnnctcc  660
cnancngncn gtcanccnag ggaagggngg ggnnccnntg nttgacgttg nggngangtc   720
cgaanantcc tcnccntcan cnctacccct cgggcgnnct ctcngttncc aacttancaa   780
ntctcccccg ngngcncntc tcagcctcnc ccnccccnct ctctgcantg tnctctgctc   840
tnaccnntac gantnttcgn cnccctcttt cc                                 872
```

<210> 24
<211> 815
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(815)
<223> n = A,T,C or G

<400> 24
```
gcatgcaagc ttgagtattc tatagngtca cctaaatanc ttggcntaat catggtcnta    60
```

```
nctgncttcc tgtgtcaaat gtatacnaan tanatatgaa tctnatntga caaganngta     120
tcntncatta gtaacaantg tnntgtccat cctgtcngan canattccca tnnattncgn     180
cgcattcncn gcncantatn taatngggaa ntcnnntnnn ncaccnncat ctatcntncc     240
gcnccctgac tggnagagat ggatnanttc tnntntgacc nacatgttca tcttggattn     300
aananccccc cgcngnccac cggttngnng cnagccnntc ccaagacctc ctgtggaggt     360
aacctgcgtc aganncatca aacntgggaa acccgcnncc angtnnaagt ngnnncanan     420
gatcccgtcc aggnttnacc atcccttcnc agcgcccccct ttngtgcctt anagngnagc    480
gtgtccnanc cnctcaacat ganacgcgcc agnccanccg caattnggca caatgtcgnc     540
gaaccccccta gggggantna tncaaanccc caggattgtc cncncangaa atcccncanc    600
cccnccctac ccnnctttgg gacngtgacc aantcccgga gtnccagtcc ggccngnctc     660
ccccaccggt nnccntgggg gggtgaanct cngnntcanc cngncgaggn ntcgnaagga     720
accggncctn ggncgaanng ancnntcnga agngccncnt cgtataaccc cccctcncca     780
nccnacngnt agntcccccc cngggtncgg aangg                                815
```

<210> 25
<211> 775
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(775)
<223> n = A,T,C or G

<400> 25

```
ccgagatgtc tcgctccgtg gccttagctg tgctcgcgct actctctctt tctggcctgg      60
aggctatcca gcgtactcca aagattcagg tttactcacg tcatccagca gagaatggaa     120
agtcaaattt cctgaattgc tatgtgtctg ggtttcatcc atccgacatt gaanttgact     180
tactgaagaa tgganagaga attgaaaaag tggagcattc agacttgtct ttcagcaagg     240
actggtcttt ctatctcntg tactacactg aattcacccc cactgaaaaa gatgagtatg     300
cctgccgtgt gaaccatgtg actttgtcac agcccaagat agttaagtgg gatcgagaca     360
tgtaagcagn cnncatggaa gtttgaagat gccgcatttg gattggatga attccaaatt     420
ctgcttgctt gcnttttaat antgatatgc ntatacaccc taccctttat gnccccaaat     480
tgtaggggtt acatnantgt tcncntngga catgatcttc ctttataant ccnccnttcg     540
aattgcccgt cncccngttn ngaatgtttc cnnaaccacg gttggctccc ccaggtcncc     600
tcttacggaa gggcctgggc cnctttncaa ggttggggga accnaaaatt tcncttntgc     660
ccnccccnca cnntcttgng nncncanttt ggaacccttc cnattcccct tggcctcnna     720
nccttnncta anaaaacttn aaancgtngc naaannttn acttcccccc ttacc          775
```

<210> 26
<211> 820
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(820)
<223> n = A,T,C or G

<400> 26

```
anattantac agtgtaatct tttcccagag gtgtgtanag ggaacggggc ctagaggcat      60
cccanagata ncttatanca acagtgcttt gaccaagagc tgctgggcac atttcctgca     120
gaaaaggtgg cggtccccat cactcctcct ctcccatagc catcccagag gggtgagtag     180
ccatcangcc ttcggtggga gggagtcang gaaacaacan accacagagc anacagacca     240
ntgatgacca tgggcgggag cgagcctctt ccctgnaccg gggtggcana nganagccta     300
nctgaggggt cacactataa acgttaacga ccnagatnan cacctgcttc aagtgcaccc     360
ttcctacctg acnaccagng accnnnaact gcngcctggg gacagcnctg ggancagcta     420
acnnagcact cacctgcccc cccatggccg tncgcntccc tggtcctgnc aagggaagct     480
```

```
cccctgttgga attncgggga naccaaggga ncccccctcct ccanctgtga aggaaaaann     540
gatggaattt tnccccttccg gccnntcccc tcttccttta cacgcccccct nntactcntc     600
tccctctntt ntcctgncnc acttttnacc ccnnnatttc ccttnattga tcggannctn     660
ganattccac tnncgcctnc cntcnatcng naanacnaaa nactntctna cccngggggat     720
gggnncctcg ntcatcctct ctttttcnct accnccnntt ctttgcctct ccttngatca     780
tccaaccntc gntggccntn cccccccnnn tcctttnccc                           820
```

<210> 27
<211> 818
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(818)
<223> n = A,T,C or G

<400> 27

```
tctgggtgat ggcctcttcc tcctcaggga cctctgactg ctctgggcca aagaatctct      60
tgtttcttct ccgagcccca ggcagcggtg attcagccct gcccaacctg attctgatga     120
ctgcggatgc tgtgacggac ccaaggggca aatagggtcc cagggtccag ggagggggcgc     180
ctgctgagca cttccgcccc tcaccctgcc cagcccctgc catgagctct gggctgggtc     240
tccgcctcca gggttctgct cttccangca ngccancaag tggcgctggg ccacactggc     300
ttcttcctgc cccntccctg gctctgantc tctgtcttcc tgtcctgtgc angcnccttg     360
gatctcagtt tccctcnctc anngaactct gtttctgann tcttcantta actntgantt     420
tatnaccnan tggnctgtnc tgtcnnactt taatgggccn gaccggctaa tccctccctc     480
nctcccttcc anttcnnnna accngcttnc cntcntctcc ccntanccccg ccngggaanc     540
ctcctttgcc ctnaccangg gccnnnaccg cccntnnctn ggggggcnng gtnnctncnc     600
ctgntnnccc cnctcncnnt tncctcgtcc cnncnncgcn nngcanntc ncngtcccnn     660
tnnctcttcn ngtntcgnaa ngntcncntn tnnnnngncn ngntnntncn tccctctcnc     720
cnnntgnang tnnttnnnnc ncngnncccc nnnncnnnnn nggnnntnnn tctncncngc     780
cccnnccccc ngnattaagg cctccnntct ccggccnc                             818
```

<210> 28
<211> 731
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(731)
<223> n = A,T,C or G

<400> 28

```
aggaagggcg gagggatatt gtangggatt gagggatagg agnataangg gggaggtgtg      60
tcccaacatg anggtgnngt tctcttttga angagggttg ngtttttann ccnggtgggt     120
gattnaaccc cattgtatgg agnnaaaggn tttnagggat ttttcggctc ttatcagtat     180
ntanattcct gtnaatcgga aaatnatntt tcnncnggaa aatnttgctc ccatccgnaa     240
attnctcccg ggtagtgcat nttngggggn cngccangtt tcccaggctg ctanaatcgt     300
actaaagntt naagtgggan tncaaatgaa aacctnncac agagnatccn tacccgactg     360
tnnnttncct tcgccctntg actctgcnng agcccaatac ccnngngnat gtcncccngn     420
nnngcgncnc tgaaannnnc tcgnggctnn gancatcang gggtttcgca tcaaaagcnn     480
cgtttcncat naaggcactt tngcctcatc caaccnctng ccctcnncca tttngccgtc     540
nggttcncct acgctnntng cncctnnntn ganattttnc ccgcctnggg naancctcct     600
gnaatgggta gggncttntc ttttnaccnn gnggtntact aatcnnctnc acgcntnctt     660
tctcnacccc cccccttttt caatcccanc ggcnaatggg gtctccccnn cganggggggg     720
nnncccannc c                                                           731
```

<210> 29
<211> 822
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(822)
<223> n = A,T,C or G

<400> 29
actagtccag tgtggtggaa ttccattgtg ttggggncnc ttctatgant antnttagat 60
cgctcanacc tcacanccte ccnacnangc ctataangaa nannaataga nctgtncnnt 120
atntntacnc tcatannect cnnnacccac tccctcttaa cccntactgt gcctatngcn 180
tnnctantct ntgccgcctn cnanccaccn gtgggccnac cncnngnatt ctcnatctcc 240
tcnccatntn gcctananta ngtncatacc ctatacctac nccaatgcta nnnctaancn 300
tccatnantt annntaacta ccactgacnt ngactttcnc atnanctcct aatttgaatc 360
tactctgact cccacngcct annnattagc ancntccccc nacnatntct caaccaaatc 420
ntcaacaacc tatctanctg ttcnccaacc nttncctccg atccccnnac aaccccccte 480
ccaaataccc nccacctgac ncctaacccn caccatcccg gcaagccnan ggncatttan 540
ccactggaat cacnatngga naaaaaaaac ccnaactctc tancncnnat ctccctaana 600
aatnctcctn naatttactn ncantnccat caancccacn tgaaacnnaa cccctgtttt 660
tanatccctt ctttcgaaaa ccnacccttt annncccaac ctttngggcc cccccnctnc 720
ccnaatgaag gncncccaat cnangaaacg nccntgaaaa ancnaggcna anannntccg 780
canatcctat cccttanttn ggggncccctt ncccngggcc cc 822

<210> 30
<211> 787
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(787)
<223> n = A,T,C or G

<400> 30
cggccgcctg ctctggcaca tgcctcctga atggcatcaa aagtgatgga ctgcccattg 60
ctagagaaga ccttctctcc tactgtcatt atggagccct gcagactgag ggctcccctt 120
gtctgcagga tttgatgtct gaagtcgtgg agtgtggctt ggagctcctc atctacatna 180
gctggaagcc ctggagggcc tctctcgcca gcctccccct tctctccacg ctctccangg 240
acaccagggg ctccaggcag cccattattc ccagnangac atggtgtttc tccacgcgga 300
cccatggggc ctgnaaggcc agggtctcct ttgacaccat ctctcccgtc ctgcctggca 360
ggccgtggga tccactantt ctanaacggn cgccaccncg gtgggagctc cagcttttgt 420
tcccnttaat gaaggttaat tgcncgcttg gcgtaatcat nggtcanaac tntttcctgt 480
gtgaaattgt ttntcccctc ncnattccnc ncnacatacn aacccggaan cataaagtgt 540
taaagcctgg gggtngcctn nngaatnaac tnaactcaat taattgcgtt ggctcatggc 600
ccgctttccn ttcnggaaaa ctgtcntccc ctgcnttnnt gaatcggcca ccccccnggg 660
aaaagcggtt tgcnttttng ggggntcctt ccncttcccc cctcnctaan ccctncgcct 720
cggtcgttnc nggtngcggg gaangggnat nnnctcccnc naagggggng agnnngntat 780
ccccaaa 787

<210> 31
<211> 799
<212> DNA
<213> Homo sapien

<220>

<221> misc_feature
<222> (1)...(799)
<223> n = A,T,C or G

<400> 31
tttttttttt tttttttggc gatgctactg tttaattgca ggaggtgggg gtgtgtgtac 60
catgtaccag ggctattaga agcaagaagg aaggagggag ggcagagcgc cctgctgagc 120
aacaaaggac tcctgcagcc ttctctgtct gtctcttggc gcaggcacat ggggaggcct 180
cccgcagggt gggggccacc agtccagggg tgggagcact acanggggtg ggagtgggtg 240
gtggctggtn cnaatggcct gncacanatc cctacgattc ttgacacctg gatttcacca 300
ggggaccttc tgttctccca nggnaacttc ntnnatctcn aaagaacaca actgtttctt 360
cngcanttct ggctgttcat ggaaagcaca ggtgtccnat ttnggctggg acttggtaca 420
tatggttccg gcccacctct cccntcnaan aagtaattca ccccccccn ccntctnttg 480
cctgggccct taantaccca caccggaact canttantta ttcatcttng gntgggcttg 540
ntnatcnccn cctgaangcg ccaagttgaa aggccacgcc gtncccnctc cccatagnan 600
nttttnncnt canctaatgc ccccccnggc aacnatccaa tcccccccn tggggggcccc 660
agcccanggc ccccgnctcg ggnnnccngn cncgnantcc ccaggntctc ccantcngnc 720
ccnnngcncc cccgcacgca gaacanaagg ntngagccnc cgcannnnnn nggtnncnac 780
ctcgcccccc ccnncgnng 799

<210> 32
<211> 789
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(789)
<223> n = A,T,C or G

<400> 32
tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 60
ttttnccnag ggcaggttta ttgacaacct cncgggacac aancaggctg gggacaggac 120
ggcaacaggc tccggcggcg gcggcggcgg ccctacctgc ggtaccaaat ntgcagcctc 180
cgctcccgct tgatnttcct ctgcagctgc aggatgccnt aaaacagggc ctcggccntn 240
ggtgggcacc ctgggatttn aatttccacg ggcacaatgc ggtcgcancc cctcaccacc 300
nattaggaat agtggtntta cccnccnccg ttggcncact ccccntggaa accacttntc 360
gcggctccgg catctggtct taaaccttgc aaacnctggg gccctctttt tggttantnt 420
nccngccaca atcatnactc agactggcnc gggctggccc caaaaaancn ccccaaaacc 480
ggnccatgtc ttnncggggt tgctgcnatn tncatcacct cccgggcnca ncaggncaac 540
ccaaaagttc ttgnggcccn caaaaaanct ccgggggggnc ccagtttcaa caaagtcatc 600
cccttggcc cccaaatcct cccccgntt nctgggtttg ggaacccacg cctctnnctt 660
tggnnggcaa gntggntccc ccttcgggcc cccggtgggc ccnnctctaa ngaaaacncc 720
ntcctnnnca ccatcccccc nngnnacgnc tancaangna tccctttttt tanaaacggg 780
cccccncg 789

<210> 33
<211> 793
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(793)
<223> n = A,T,C or G

<400> 33
gacagaacat gttggatggt ggagcacctt tctatacgac ttacaggaca gcagatgggg 60

aattcatggc tgttggagca atanaacccc agttctacga gctgctgatc aaaggacttg 120
gactaaagtc tgatgaactt cccaatcaga tgagcatgga tgattggcca gaaatgaana 180
agaagtttgc agatgtattt gcaaagaaga cgaaggcaga gtggtgtcaa atctttgacg 240
gcacagatgc ctgtgtgact ccggttctga cttttgagga ggttgttcat catgatcaca 300
acaangaacg gggctcgttt atcaccantg aggagcagga cgtgagcccc cgccctgcac 360
ctctgctgtt aaacacccca gccatccctt ctttcaaaag ggatccacta cttctagagc 420
ggncgccacc gcggtggagc tccagctttt gttcccttta gtgagggtta attgcgcgct 480
tggcgtaatc atggtcatan ctgtttcctg tgtgaaattg ttatccgctc acaattccac 540
acaacatacg anccggaagc atnaaatttt aaagcctggn ggtngcctaa tgantgaact 600
nactcacatt aattggcttt gcgctcactg cccgctttcc agtccggaaa acctgtcctt 660
gccagctgcc nttaatgaat cnggccaccc cccggggaaa aggcngtttg cttnttgggg 720
cgcncttccc gctttctcgc ttcctgaant ccttcccccc ggtctttcgg cttgcggcna 780
acggtatcna cct 793

<210> 34
<211> 756
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(756)
<223> n = A,T,C or G

<400> 34
gccgcgaccg gcatgtacga gcaactcaag ggcgagtgga accgtaaaag ccccaatctt 60
ancaagtgcg gggaanagct gggtcgactc aagctagttc ttctggagct caacttcttg 120
ccaaccacag ggaccaagct gaccaaacag cagctaattc tggcccgtga catactggag 180
atcggggccc aatggagcat cctacgcaan gacatcccct ccttcgagcg ctacatggcc 240
cagctcaaat gctactactt tgattacaan gagcagctcc ccgagtcagc ctatatgcac 300
cagctcttgg gcctcaacct cctcttcctg ctgtcccaga accgggtggc tgantnccac 360
acgganttgg ancggctgcc tgcccaanga catacanacc aatgtctaca tcnaccacca 420
gtgtcctgga gcaatactga tgganggcag ctaccncaaa gtnttcctgg ccnagggtaa 480
catccccgc cgagagctac accttcttca ttgacatcct gctcgacact atcagggatg 540
aaaatcgcng ggttgctcca gaaaggctnc aanaanatcc ttttcnctga aggcccccgg 600
atncnctagt nctagaatcg gcccgccatc gcggtgganc ctccaacctt tcgttnccct 660
ttactgaggg ttnattgccg cccttggcgt tatcatggtc acnccngttn cctgtgttga 720
aattnttaac cccccacaat tccacgccna cattng 756

<210> 35
<211> 834
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(834)
<223> n = A,T,C or G

<400> 35
ggggatctct anatcnacct gnatgcatgg ttgtcggtgt ggtcgctgtc gatgaanatg 60
aacaggatct tgcccttgaa gctctcggct gctgtntttta agttgctcag tctgccgtca 120
tagtcagaca cnctcttggg caaaaaacan caggatntga gtcttgattt cacctccaat 180
aatcttcngg gctgtctgct cggtgaactc gatgacnang ggcagctggt tgtgtntgat 240
aaantccanc angttctcct tggtgacctc cccttcaaag ttgttccggc cttcatcaaa 300
cttctnnaan angannancc canctttgtc gagctggnat ttgganaaca cgtcactgtt 360
ggaaactgat cccaaatggt atgtcatcca tcgcctctgc tgcctgcaaa aaacttgctt 420
ggcncaaatc cgactccccn tccttgaaag aagccnatca cacccccctc cctggactcc 480

```
nncaangact ctnccgctnc cccntccnng cagggttggt ggcannccgg gcccntgcgc     540
ttcttcagcc agttcacnat nttcatcagc ccctctgcca gctgttntat tccttggggg     600
ggaanccgtc tctcccttcc tgaannaact ttgaccgtng gaatagccgc gcntcnccnt     660
acntnctggg ccgggttcaa antccctccn ttgncnntcn cctcgggcca ttctggattt     720
nccnaacttt ttccttcccc cnccccncgg ngtttggntt tttcatnggg ccccaactct     780
gctnttggcc antcccctgg gggcntntan cnccccctnt ggtcccntng ggcc           834

      <210> 36
      <211> 814
      <212> DNA
      <213> Homo sapien

      <220>
      <221> misc_feature
      <222> (1)...(814)
      <223> n = A,T,C or G

      <400> 36
cggncgcttt ccngccgcgc cccgtttcca tgacnaaggc tcccttcang ttaaatacnn      60
cctagnaaac attaatgggt tgctctacta atacatcata cnaaccagta agcctgccca     120
naacgccaac tcaggccatt cctaccaaag gaagaaaggc tggtctctcc accccctgta     180
ggaaaggcct gccttgtaag acaccacaat ncggctgaat ctnaagtctt gtgttttact     240
aatggaaaaa aaaaataaac aanaggtttt gttctcatgg ctgcccaccg cagcctggca     300
ctaaaacanc ccagcgctca cttctgcttg ganaaatatt ctttgctctt ttggacatca     360
ggcttgatgg tatcactgcc acntttccac ccagctgggc nccccttcccc catntttgtc    420
antganctgg aaggcctgaa ncttagtctc caaaagtctc ngcccacaag accggccacc     480
aggggangtc ntttncagtg gatctgccaa anantacccn tatcatcnnt gaataaaaag     540
gcccctgaac ganatgcttc cancanccttt taagacccat aatcctngaa ccatggtgcc   600
cttccggtct gatccnaaag gaatgttcct gggtcccant ccctcctttg ttncttacgt     660
tgtnttggac ccntgctngn atnacccaan tganatcccc ngaagcaccc tnccccctggc    720
atttganttt cntaaattct ctgccctacn nctgaaagca cnattccctn ggcnccnaan     780
ggngaactca agaaggtctn ngaaaaacca cncn                                 814

      <210> 37
      <211> 760
      <212> DNA
      <213> Homo sapien

      <220>
      <221> misc_feature
      <222> (1)...(760)
      <223> n = A,T,C or G

      <400> 37
gcatgctgct cttcctcaaa gttgttcttg ttgccataac aaccaccata ggtaaagcgg      60
gcgcagtgtt cgctgaaggg gttgtagtac cagcgcggga tgctctcctt gcagagtcct     120
gtgtctggca ggtccacgca atgccctttg tcactgggga aatggatgcg ctggagctcg     180
tcnaanccac tcgtgtattt ttcacangca gcctcctccg aagcntccgg gcagttgggg     240
gtgtcgtcac actccactaa actgtcgatn cancagccca ttgctgcagc ggaactgggt     300
gggctgacag gtgccagaac acactggatn ggcctttcca tggaagggcc tgggggaaat     360
cncctnancc caaactgcct ctcaaaggcc accttgcaca ccccgacagg ctagaaatgc     420
actcttcttc ccaaaggtag ttgttcttgt tgcccaagca ncctccanca aaccaaaanc     480
ttgcaaaatc tgctccgtgg gggtcatnnn taccanggtt ggggaaanaa acccggcngn     540
gancencctt gtttgaatgc naaggnaata atcctcctgt cttgcttggg tggaanagca     600
caattgaact gttaacnttg ggccgngttc cnctngggtg gtctgaaact aatcaccgtc     660
actggaaaaa ggtangtgcc ttccttgaat tcccaaantt cccctngntt tgggtnnttt     720
ctcctctncc ctaaaaatcg tnttcccccc ccntanggcg                          760
```

<210> 38
<211> 724
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(724)
<223> n = A,T,C or G

<400> 38
```
tttttttttt tttttttttt tttttttttt tttttaaaaa ccccctccat tgaatgaaaa      60
cttccnaaat tgtccaaccc cctcnnccaa atnnccattt ccgggggggg gttccaaacc     120
caaattaatt ttggantttа aattaaatnt tnattngggg aanaanccaa atgtnaagaa     180
aatttaaccc attatnaact taaatncctn gaaacccntg gnttccaaaa atttttaacc     240
cttaaatccc tccgaaattg ntaanggaaa accaaattcn cctaaggctn tttgaaggtt     300
ngatttaaac cccсttnant tnttttnacc cnngnctnaa ntatttngnt tccggtgttt     360
tcctnttaan cntnggtaac tcccgntaat gaannnccct aanccaatta aaccgaattt     420
tttttgaatt ggaaattccn ngggaattna ccggggtttt tcccntttgg gggccatncc     480
cccnctttcg gggtttgggn ntaggttgaa tttttnnang ncccaaaaaa ncccccaana     540
aaaaaactcc caagnnttaa ttngaatntc cccсttccca ggcctttttgg gaaaggnggg     600
tttntggggg ccngggantt cnttccccсn ttnccncccc ccccccnggt aaanggttat     660
ngnntttggt ttttgggccc cttnanggac cttccggatn gaaattaaat ccccgggncg     720
gccg                                                                  724
```

<210> 39
<211> 751
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(751)
<223> n = A,T,C or G

<400> 39
```
tttttttttt tttttctttg ctcacattta atttttattt tgattttttt taatgctgca      60
caacacaata tttatttcat ttgtttcttt tatttcattt tatttgtttg ctgctgctgt     120
tttatttatt tttactgaaa gtgagaggga acttttgtgg ccttttttcc tttttctgta     180
ggccgcctta agctttctaa atttggaaca tctaagcaag ctgaanggaa aaggggggttt    240
cgcaaaatca ctcgggggaa nggaaaggtt gctttgttaa tcatgcccta tggtgggtga     300
ttaactgctt gtacaattac ntttcacttt taattaattg tgctnaangc tttaattana     360
cttgggggtt ccctccccan accaaccccn ctgacaaaaa gtgccngccc tcaaatnatg     420
tcccggcnnt cnttgaaaca cacngcngaa ngttctcatt ntccccncnc caggtnaaaa     480
tgaagggtta ccatntttaa cnccacctcc acntggcnnn gcctgaatcc tcnaaaancn     540
ccctcaancn aattnctnng ccccggtcnc gcntnngtcc cncccgggct ccgggaantn     600
caccccсnga anncnntnnc naacnaaatt ccgaaaatat tcccnntcnc tcaattcccc     660
cnnagactnt cctcnncnan cncaattttc ttttnntcac gaacncgnnc cnnaaaatgn     720
nnnncncctc cnctngtccn naatcnccan c                                    751
```

<210> 40
<211> 753
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(753)

<223> n = A,T,C or G

<400> 40
gtggtatttt ctgtaagatc aggtgttcct ccctcgtagg tttagaggaa acaccctcat 60
agatgaaaac ccccccgaga cagcagcact gcaactgcca agcagccggg gtaggagggg 120
cgccctatgc acagctgggc ccttgagaca gcagggcttc gatgtcaggc tcgatgtcaa 180
tggtctggaa gcggcggctg tacctgcgta ggggcacacc gtcagggccc accaggaact 240
tctcaaagtt ccaggcaacn tcgttgcgac acaccggaga ccaggtgatn agcttggggt 300
cggtcataan cgcggtggcg tcgtcgctgg gagctggcag ggcctcccgc aggaaggcna 360
ataaaaggtg cgccccgca ccgttcanct cgcacttctc naanaccatg angttgggct 420
cnaacccacc accannccgg acttccttga nggaattccc aaatctcttc gntcttgggc 480
ttctnctgat gccctanctg gttgcccngn atgccaanca nccccaancc ccggggtcct 540
aaancacccn cctcctcntt tcatctgggt tnttntcccc ggaccntggt tcctctcaag 600
gganccccata tctcnaccan tactcaccnt ncccccccnt gnnacccanc cttctanngn 660
ttcccncccg ncctctggcc cntcaaanan gcttncacna cctgggtctg ccttcccccc 720
tnccctatct gnaccccncn tttgtctcan tnt 753

<210> 41
<211> 341
<212> DNA
<213> Homo sapien

<400> 41
actatatcca tcacaacaga catgcttcat cccatagact tcttgacata gcttcaaatg 60
agtgaaccca tccttgattt atatacatat atgttctcag tattttggga gcctttccac 120
ttctttaaac cttgttcatt atgaacactg aaaataggaa tttgtgaaga gttaaaaagt 180
tatagcttgt ttacgtagta agtttttgaa gtctacattc aatccagaca cttagttgag 240
tgttaaactg tgatttttaa aaaatatcat ttgagaatat tctttcagag gtattttcat 300
ttttactttt tgattaattg tgttttatat attagggtag t 341

<210> 42
<211> 101
<212> DNA
<213> Homo sapien

<400> 42
acttactgaa tttagttctg tgctcttcct tatttagtgt tgtatcataa atactttgat 60
gtttcaaaca ttctaaataa ataattttca gtggcttcat a 101

<210> 43
<211> 305
<212> DNA
<213> Homo sapien

<400> 43
acatctttgt tacagtctaa gatgtgttct taaatcacca ttccttcctg gtcctcaccc 60
tccagggtgg tctcacactg taattagagc tattgaggag tctttacagc aaattaagat 120
tcagatgcct tgctaagtct agagttctag agttatgttt cagaaagtct aagaaaccca 180
cctcttgaga ggtcagtaaa gaggacttaa tatttcatat ctacaaaatg accacaggat 240
tggatacaga acgagagtta tcctggataa ctcagagctg agtacctgcc cgggggccgc 300
tcgaa 305

<210> 44
<211> 852
<212> DNA
<213> Homo sapien

<220>

<221> misc_feature
<222> (1)...(852)
<223> n = A,T,C or G

<400> 44
```
acataaatat cagagaaaag tagtctttga aatatttacg tccaggagtt ctttgtttct      60
gattatttgg tgtgtgtttt ggtttgtgtc caaagtattg gcagcttcag ttttcatttt     120
ctctccatcc tcgggcattc ttcccaaatt tatataccag tcttcgtcca tccacacgct     180
ccagaatttc tcttttgtag taatatctca tagctcggct gagcttttca taggtcatgc     240
tgctgttgtt cttcttttta ccccatagct gagccactgc ctctgatttc aagaacctga     300
agacgccctc agatcggtct tcccatttta ttaatcctgg gttcttgtct gggttcaaga     360
ggatgtcgcg gatgaattcc cataagtgag tccctctcgg gttgtgcttt ttggtgtggc     420
acttggcagg ggggtcttgc tcctttttca tatcaggtga ctctgcaaca ggaaggtgac     480
tggtggttgt catggagatc tgagcccggc agaaagtttt gctgtccaac aaatctactg     540
tgctaccata gttggtgtca tataaatagt tctngtcttt ccaggtgttc atgatggaag     600
gctcagtttg ttcagtcttg acaatgacat tgtgtgtgga ctggaacagg tcactactgc     660
actggccgtt ccacttcaga tgctgcaagt tgctgtagag gagntgcccc gccgtccctg     720
ccgcccgggt gaactcctgc aaactcatgc tgcaaaggtg ctcgccgttg atgtcgaact     780
cntggaaagg gatacaattg gcatccagct ggttggtgtc caggaggtga tggagccact     840
cccacacctg gt                                                         852
```

<210> 45
<211> 234
<212> DNA
<213> Homo sapien

<400> 45
```
acaacagacc cttgctcgct aacgacctca tgctcatcaa gttggacgaa tccgtgtccg      60
agtctgacac catccggagc atcagcattg cttcgcagtg ccctaccgcg gggaactctt     120
gcctcgtttc tggctggggt ctgctggcga acggcagaat gcctaccgtg ctgcagtgcg     180
tgaacgtgtc ggtggtgtct gaggaggtct gcagtaagct ctatgacccg ctgt           234
```

<210> 46
<211> 590
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(590)
<223> n = A,T,C or G

<400> 46
```
actttttatt taaatgttta taaggcagat ctatgagaat gatagaaaac atggtgtgta      60
atttgatagc aatattttgg agattacaga gttttagtaa ttaccaatta cacagttaaa     120
aagaagataa tatattccaa gcanatacaa aatatctaat gaaagatcaa ggcaggaaaa     180
tgantataac taattgacaa tggaaaatca atttaatgt gaattgcaca ttatccttta      240
aaagctttca aaanaaaanaa ttattgcagt ctanttaatt caaacagtgt taaatggtat   300
caggataaan aactgaaggg canaaagaat taattttcac ttcatgtaac ncacccanat     360
ttacaatggc ttaaatgcan ggaaaaagca gtggaagtag ggaagtantc aaggtctttc     420
tggtctctaa tctgccttac tctttgggtg tggctttgat cctctggaga cagctgccag     480
ggctcctgtt atatccacaa tcccagcagc aagatgaagg gatgaaaaag gacacatgct     540
gccttccttt gaggagactt catctcactg gccaacactc agtcacatgt                590
```

<210> 47
<211> 774
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(774)
<223> n = A,T,C or G

<400> 47
```
acaaggggc ataatgaagg agtggggana gattttaaag aaggaaaaaa aacgaggccc      60
tgaacagaat tttcctgnac aacggggctt caaaataatt ttcttgggga ggttcaagac     120
gcttcactgc ttgaaactta aatggatgtg ggacanaatt ttctgtaatg accctgaggg     180
cattacagac gggactctgg gaggaaggat aaacagaaag gggacaaagg ctaatcccaa     240
aacatcaaag aaaggaaggt ggcgtcatac ctcccagcct acacagttct ccagggctct     300
cctcatccct ggaggacgac agtggaggaa caactgacca tgtccccagg ctcctgtgtg     360
ctggctcctg gtcttcagcc cccagctctg gaagcccacc ctctgctgat cctgcgtggc     420
ccacactcct tgaacacaca tccccaggtt atattcctgg acatggctga acctcctatt     480
cctacttccg agatgccttg ctccctgcag cctgtcaaaa tcccactcac cctccaaacc     540
acggcatggg aagcctttct gacttgcctg attactccag catcttggaa caatccctga     600
ttccccactc cttagaggca agatagggtg gttaagagta gggctggacc acttggagcc     660
aggctgctgg cttcaaattn tggctcattt acgagctatg ggaccttggg caagtnatct     720
tcacttctat gggcntcatt ttgttctacc tgcaaaatgg gggataataa tagt           774
```

<210> 48
<211> 124
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(124)
<223> n = A,T,C or G

<400> 48
```
canaaattga aattttataa aaaggcattt ttctcttata tccataaaat gatataattt      60
ttgcaantat anaaatgtgt cataaattat aatgttcctt aattacagct caacgcaact     120
tggt                                                                  124
```

<210> 49
<211> 147
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(147)
<223> n = A,T,C or G

<400> 49
```
gccgatgcta ctattttatt gcaggaggtg gggtgtttt tattattctc tcaacagctt      60
tgtggctaca ggtggtgtct gactgcatna aaaanttttt tacgggtgat tgcaaaaatt     120
ttagggcacc catatcccaa gcantgt                                         147
```

<210> 50
<211> 107
<212> DNA
<213> Homo sapien

<400> 50
```
acattaaatt aataaaagga ctgttggggt tctgctaaaa cacatggctt gatatattgc      60
```

atggtttgag gttaggagga gttaggcata tgttttggga gaggggt 107

<210> 51
<211> 204
<212> DNA
<213> Homo sapien

<400> 51
gtcctaggaa gtctagggga cacacgactc tggggtcacg gggccgacac acttgcacgg 60
cgggaaggaa aggcagagaa gtgacaccgt caggggggaaa tgacagaaag gaaaatcaag 120
gccttgcaag gtcagaaagg ggactcaggg cttccaccac agccctgccc cacttggcca 180
cctccctttt gggaccagca atgt 204

<210> 52
<211> 491
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(491)
<223> n = A,T,C or G

<400> 52
acaaagataa catttatctt ataacaaaaa tttgatagtt ttaaaggtta gtattgtgta 60
gggtattttc caaaagacta aagagataac tcaggtaaaa agttagaaat gtataaaaca 120
ccatcagaca ggtttttaaa aaacaacata ttacaaaatt agacaatcat ccttaaaaaa 180
aaaacttctt gtatcaattt cttttgttca aaatgactga cttaantatt tttaaatatt 240
tcanaaacac ttcctcaaaa attttcaana tggtagcttt canatgtncc ctcagtccca 300
atgttgctca gataaataaa tctcgtgaga acttaccacc caccacaagc tttctggggc 360
atgcaacagt gtcttttctt tnctttttct tttttttttt ttacaggcac agaaactcat 420
caattttatt tggataacaa agggtctcca aattatattg aaaaataaat ccaagttaat 480
atcactcttg t 491

<210> 53
<211> 484
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(484)
<223> n = A,T,C or G

<400> 53
acataattta gcagggctaa ttaccataag atgctattta ttaanaggtn tatgatctga 60
gtattaacag ttgctgaagt ttggtatttt tatgcagcat tttctttttg ctttgataac 120
actacagaac ccttaaggac actgaaaatt agtaagtaaa gttcagaaac attagctgct 180
caatcaaatc tctacataac actatagtaa ttaaaacgtt aaaaaaaagt gttgaaatct 240
gcactagtat anaccgctcc tgtcaggata anactgcttt ggaacagaaa gggaaaaanc 300
agctttgant ttctttgtgc tgatangagg aaaggctgaa ttaccttgtt gcctctccct 360
aatgattggc aggtcnggta aatnccaaaa catattccaa ctcaacactt cttttccncg 420
tancttgant ctgtgtattc cagganacagg cggatggaat gggccagccc ncggatgttc 480
cant 484

<210> 54
<211> 151
<212> DNA

<213> Homo sapien

<400> 54
actaaacctc gtgcttgtga actccataca gaaaacggtg ccatccctga acacggctgg 60
ccactgggta tactgctgac aaccgcaaca acaaaaacac aaatccttgg cactggctag 120
tctatgtcct ctcaagtgcc tttttgtttg t 151

<210> 55
<211> 91
<212> DNA
<213> Homo sapien

<400> 55
acctggcttg tctccgggtg gttcccggcg ccccccacgg tccccagaac ggacactttc 60
gccctccagt ggatactcga gccaaagtgg t 91

<210> 56
<211> 133
<212> DNA
<213> Homo sapien

<400> 56
ggcggatgtg cgttggttat atacaaatat gtcattttat gtaagggact tgagtatact 60
tggattttg gtatctgtgg gttgggggga cggtccagga accaataccc catggatacc 120
aagggacaac tgt 133

<210> 57
<211> 147
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(147)
<223> n = A,T,C or G

<400> 57
actctggaga acctgagccg ctgctccgcc tctgggatga ggtgatgcan gcngtggcgc 60
gactgggagc tgagcccttc cctttgcgcc tgcctcagag gattgttgcc gacntgcana 120
tctcantggg ctggatncat gcagggt 147

<210> 58
<211> 198
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(198)
<223> n = A,T,C or G

<400> 58
acagggatat aggtttnaag ttattgtnat tgtaaaatac attgaatttt ctgtatactc 60
tgattacata catttatcct ttaaaaaaga tgtaaatctt aatttttatg ccatctatta 120
atttaccaat gagttacctt gtaaatgaga agtcatgata gcactgaatt ttaactagtt 180
ttgacttcta agtttggt 198

<210> 59

<211> 330
<212> DNA
<213> Homo sapien

<400> 59
acaacaaatg ggttgtgagg aagtcttatc agcaaaactg gtgatggcta ctgaaaagat 60
ccattgaaaa ttatcattaa tgattttaaa tgacaagtta tcaaaaactc actcaatttt 120
cacctgtgct agcttgctaa aatgggagtt aactctagag caaatatagt atcttctgaa 180
tacagtcaat aaatgacaaa gccagggcct acaggtggtt tccagacttt ccagacccag 240
cagaaggaat ctattttatc acatggatct ccgtctgtgc tcaaaatacc taatgatatt 300
tttcgtcttt attggacttc tttgaagagt 330

<210> 60
<211> 175
<212> DNA
<213> Homo sapien

<400> 60
accgtgggtg ccttctacat tcctgacggc tccttcacca acatctggtt ctacttcggc 60
gtcgtgggct ccttcctctt catcctcatc cagctggtgc tgctcatcga ctttgcgcac 120
tcctggaacc agcggtggct gggcaaggcc gaggagtgcg attcccgtgc ctggt 175

<210> 61
<211> 154
<212> DNA
<213> Homo sapien

<400> 61
accccacttt tcctcctgtg agcagtctgg acttctcact gctacatgat gagggtgagt 60
ggttgttgct cttcaacagt atcctcccct ttccggatct gctgagccgg acagcagtgc 120
tggactgcac agccccgggg ctccacattg ctgt 154

<210> 62
<211> 30
<212> DNA
<213> Homo sapien

<400> 62
cgctcgagcc ctatagtgag tcgtattaga 30

<210> 63
<211> 89
<212> DNA
<213> Homo sapien

<400> 63
acaagtcatt tcagcaccct ttgctcttca aaactgacca tcttttatat ttaatgcttc 60
ctgtatgaat aaaaatggtt atgtcaagt 89

<210> 64
<211> 97
<212> DNA
<213> Homo sapien

<400> 64
accggagtaa ctgagtcggg acgctgaatc tgaatccacc aataaataaa ggttctgcag 60
aatcagtgca tccaggattg gtccttggat ctggggt 97

<210> 65
<211> 377
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(377)
<223> n = A,T,C or G

<400> 65
acaacaanaa ntcccttctt taggccactg atggaaacct ggaaccccct tttgatggca 60
gcatggcgtc ctaggccttg acacagcggc tggggtttgg gctntcccaa accgcacacc 120
ccaaccctgg tctacccaca nttctggcta tgggctgtct ctgccactga acatcagggt 180
tcggtcataa natgaaatcc caangggac agaggtcagt agaggaagct caatgagaaa 240
ggtgctgttt gctcagccag aaaacagctg cctggcattc gccgctgaac tatgaacccg 300
tggggtgaa ctacccccan gaggaatcat gcctgggcga tgcaanggtg ccaacaggag 360
gggcgggagg agcatgt 377

<210> 66
<211> 305
<212> DNA
<213> Homo sapien

<400> 66
acgcctttcc ctcagaattc agggaagaga ctgtcgcctg ccttcctccg ttgttgcgtg 60
agaacccgtg tgccccttcc caccatatcc accctcgctc catctttgaa ctcaaacacg 120
aggaactaac tgcaccctgg tcctctcccc agtccccagt tcaccctcca tccctcacct 180
tcctccactc taaggatat caacactgcc cagcacaggg gccctgaatt tatgtggttt 240
ttatatattt tttaataaga tgcactttat gtcatttttt aataaagtct gaagaattac 300
tgttt 305

<210> 67
<211> 385
<212> DNA
<213> Homo sapien

<400> 67
actacacaca ctccacttgc ccttgtgaga cactttgtcc cagcacttta ggaatgctga 60
ggtcggacca gccacatctc atgtgcaaga ttgcccagca gacatcaggt ctgagagttc 120
cccttttaaa aaaggggact tgcttaaaaa agaagtctag ccacgattgt gtagagcagc 180
tgtgctgtgc tggagattca cttttgagag agttctcctc tgagacctga tctttagagg 240
ctgggcagtc ttgcacatga gatggggctg gtctgatctc agcactcctt agtctgcttg 300
cctctcccag ggccccagcc tggccacacc tgcttacagg gcactctcag atgcccatac 360
catagtttct gtgctagtgg accgt 385

<210> 68
<211> 73
<212> DNA
<213> Homo sapien

<400> 68
acttaaccag atatattttt accccagatg gggatattct ttgtaaaaaa tgaaaataaa 60
gttttttaa tgg 73

<210> 69
<211> 536
<212> DNA

<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(536)
<223> n = A,T,C or G

<400> 69
actagtccag tgtggtggaa ttccattgtg ttgggggctc tcaccctcct ctcctgcagc 60
tccagctttg tgctctgcct ctgaggagac catggcccag catctgagta ccctgctgct 120
cctgctggcc accctagctg tggccctggc ctggagcccc aaggaggagg ataggataat 180
cccgggtggc atctataacg cagacctcaa tgatgagtgg gtacagcgtg cccttcactt 240
cgccatcagc gagtataaca aggccaccaa agatgactac tacagacgtc cgctgcgggt 300
actaagagcc aggcaacaga ccgttggggg ggtgaattac ttcttcgacg tagaggtggg 360
ccgaaccata tgtaccaagt cccagcccaa cttggacacc tgtgccttcc atgaacagcc 420
agaactgcag aagaaacagt tgtgctcttt cgagatctac gaagttccct ggggagaaca 480
gaangtccct gggtgaaatc caggtgtcaa gaaatcctan ggatctgttg ccaggc 536

<210> 70
<211> 477
<212> DNA
<213> Homo sapien

<400> 70
atgaccccta acaggggccc tctcagccct cctaatgacc tccggcctag ccatgtgatt 60
tcacttccac tccataacgc tcctcatact aggcctacta accaacacac taaccatata 120
ccaatgatgg cgcgatgtaa cacgagaaag cacataccaa ggccaccaca caccacctgt 180
ccaaaaaggc cttcgatacg ggataatcct atttattacc tcagaagttt ttttcttcgc 240
agggattttt ctgagccttt taccactcca gcctagcccc taccccccaa ctaggagggc 300
actggccccc aacaggcatc accccgctaa atcccctaga agtcccactc ctaaacacat 360
ccgtattact cgcatcagga gtatcaatca cctgagctca ccatagtcta atagaaaaca 420
accgaaacca aattattcaa agcactgctt attacaattt tactgggtct ctattt 477

<210> 71
<211> 533
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(533)
<223> n = A,T,C or G

<400> 71
agagctatag gtacagtgtg atctcagctt tgcaaacaca ttttctacat agatagtact 60
aggtattaat agatatgtaa agaaagaaat cacaccatta ataatggtaa gattggttta 120
tgtgatttta gtggtatttt tggcaccctt atatatgttt tccaaacttt cagcagtgat 180
attatttcca taacttaaaa agtgagtttg aaaaagaaaa tctccagcaa gcatctcatt 240
taaataaagg tttgtcatct ttaaaaatac agcaatatgt gactttttaa aaaagctgtc 300
aaataggtgt gaccctacta ataattatta gaaatacatt taaaaacatc gagtacctca 360
agtcagtttg ccttgaaaaa tatcaaatat aactcttaga gaaatgtaca taaaagaatg 420
cttcgtaatt ttggagtang aggttccctc ctcaattttg tatttttaaa aagtacatgg 480
taaaaaaaaa aattcacaac agtatataag gctgtaaaat gaagaattct gcc 533

<210> 72
<211> 511
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(511)
<223> n = A,T,C or G

<400> 72
tattacggaa aaacacacca cataattcaa ctancaaaga anactgcttc agggcgtgta 60
aaatgaaagg cttccaggca gttatctgat taaagaacac taaaagaggg acaaggctaa 120
aagccgcagg atgtctacac tatancaggc gctatttggg ttggctggag gagctgtgga 180
aaacatggan agattggtgc tgganatcgc cgtggctatt cctcattgtt attacanagt 240
gaggttctct gtgtgcccac tggtttgaaa accgttctnc aataatgata gaatagtaca 300
cacatgagaa ctgaaatggc ccaaacccag aaagaaagcc caactagatc ctcagaanac 360
gcttctaggg acaataaccg atgaagaaaa gatggcctcc ttgtgccccc gtctgttatg 420
atttctctcc attgcagcna naaacccgtt cttctaagca aacncaggtg atgatggcna 480
aaatacaccc cctcttgaag naccnggagg a 511

<210> 73
<211> 499
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(499)
<223> n = A,T,C or G

<400> 73
cagtgccagc actggtgcca gtaccagtac caataacagt gccagtgcca gtgccagcac 60
cagtggtggc ttcagtgctg gtgccagcct gaccgccact ctcacatttg ggctcttcgc 120
tggccttggt ggagctggtg ccagcaccag tggcagctct ggtgcctgtg gtttctccta 180
caagtgagat tttagatatt gttaatcctg ccagtctttc tcttcaagcc agggtgcatc 240
ctcagaaacc tactcaacac agcactctag gcagccacta tcaatcaatt gaagttgaca 300
ctctgcatta aatctatttg ccatttctga aaaaaaaaaa aaaaaaaggg cggccgctcg 360
antctagagg gcccgtttaa acccgctgat cagcctcgac tgtgccttct anttgccagc 420
catctgttgt ttgcccctcc cccgntgcct tccttgaccc tggaaagtgc cactcccact 480
gtcctttcct aantaaaat 499

<210> 74
<211> 537
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(537)
<223> n = A,T,C or G

<400> 74
tttcatagga gaacacactg aggagatact tgaagaattt ggattcagcc gcgaagagat 60
ttatcagctt aactcagata aaatcattga aagtaataag gtaaaagcta gtctctaact 120
tccaggccca cggctcaagt gaatttgaat actgcattta cagtgtagag taacacataa 180
cattgtatgc atggaaacat ggaggaacag tattacagtg tcctaccact ctaatcaaga 240
aaagaattac agactctgat tctacagtga tgattgaatt ctaaaaatgg taatcattag 300
ggcttttgat ttataanact ttgggtactt atactaaatt atggtagtta tactgccttc 360
cagtttgctt gatatatttg ttgatattaa gattcttgac ttatattttg aatgggttct 420
actgaaaaan gaatgatata ttcttgaaga catcgatata catttattta cactcttgat 480
tctacaatgt agaaaatgaa ggaaatgccc caaattgtat ggtgataaaa gtcccgt 537

<210> 75
<211> 467
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(467)
<223> n = A,T,C or G

<400> 75
caaanacaat tgttcaaaag atgcaaatga tacactactg ctgcagctca caaacacctc 60
tgcatattac acgtacctcc tcctgctcct caagtagtgt ggtctatttt gccatcatca 120
cctgctgtct gcttagaaga acggctttct gctgcaangg agagaaatca taacagacgg 180
tggcacaagg aggccatctt ttcctcatcg gttattgtcc ctagaagcgt cttctgagga 240
tctagttggg ctttctttct gggtttgggc catttcantt ctcatgtgtg tactattcta 300
tcattattgt ataacggttt tcaaaccngt gggcacncag agaacctcac tctgtaataa 360
caatgaggaa tagccacggt gatctccagc accaaatctc tccatgttnt tccagagctc 420
ctccagccaa cccaaatagc cgctgctatn gtgtagaaca tccctgn 467

<210> 76
<211> 400
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(400)
<223> n = A,T,C or G

<400> 76
aagctgacag cattcgggcc gagatgtctc gctccgtggc cttagctgtg ctcgcgctac 60
tctctctttc tggcctggag gctatccagc gtactccaaa gattcaggtt tactcacgtc 120
atccagcaga gaatggaaag tcaaatttcc tgaattgcta tgtgtctggg tttcatccat 180
ccgacattga agttgactta ctgaagaatg gagagagaat tgaaaaagtg gagcattcag 240
acttgtcttt cagcaaggac tggtctttct atctcttgta ctacactgaa ttcacccccca 300
ctgaaaaaga tgagtatgcc tgccgtgtga accatgtgac tttgtcacag cccaagatng 360
ttnagtggga tcganacatg taagcagcan catgggaggt 400

<210> 77
<211> 248
<212> DNA
<213> Homo sapien

<400> 77
ctggagtgcc ttggtgtttc aagcccctgc aggaagcaga atgcaccttc tgaggcacct 60
ccagctgccc cggcggggga tgcgaggctc ggagcaccct tgcccggctg tgattgctgc 120
caggcactgt tcatctcagc ttttctgtcc ctttgctccc ggcaagcgct tctgctgaaa 180
gttcatatct ggagcctgat gtcttaacga ataaaggtcc catgctccac ccgaaaaaaa 240
aaaaaaa 248

<210> 78
<211> 201
<212> DNA
<213> Homo sapien

<400> 78

```
actagtccag tgtggtggaa ttccattgtg ttgggcccaa cacaatggct acctttaaca      60
tcacccagac cccgccctgc ccgtgcccca cgctgctgct aacgacagta tgatgcttac     120
tctgctactc ggaaactatt tttatgtaat taatgtatgc tttcttgttt ataaatgcct     180
gatttaaaaa aaaaaaaaaa a                                               201

      <210> 79
      <211> 552
      <212> DNA
      <213> Homo sapien

      <220>
      <221> misc_feature
      <222> (1)...(552)
      <223> n = A,T,C or G

      <400> 79
tccttttgtt aggtttttga gacaacccta gacctaaact gtgtcacaga cttctgaatg      60
tttaggcagt gctagtaatt tcctcgtaat gattctgtta ttactttcct attctttatt     120
cctctttctt ctgaagatta atgaagttga aaattgaggt ggataaatac aaaaaggtag     180
tgtgatagta taagtatcta agtgcagatg aaagtgtgtt atatatatcc attcaaaatt     240
atgcaagtta gtaattactc agggttaact aaattacttt aatatgctgt tgaacctact     300
ctgttccttg gctagaaaaa attataaaca ggactttgtt agtttgggaa gccaaattga     360
taatattcta tgttctaaaa gttgggctat acataaaanta tnaagaaata tggaatttta     420
ttcccaggaa tatggggttc atttatgaat antacccggg anagaagttt tgantnaaac     480
cngttttggt taatacgtta atatgtcctn aatnaacaag gcntgactta tttccaaaaa     540
aaaaaaaaaa aa                                                         552

      <210> 80
      <211> 476
      <212> DNA
      <213> Homo sapien

      <220>
      <221> misc_feature
      <222> (1)...(476)
      <223> n = A,T,C or G

      <400> 80
acagggattt gagatgctaa ggccccagag atcgtttgat ccaaccctct tattttcaga      60
ggggaaaatg gggcctagaa gttacagagc atctagctgg tgcgctggca cccctggcct     120
cacacagact cccgagtagc tgggactaca ggcacacagt cactgaagca ggccctgttt     180
gcaattcacg ttgccacctc caacttaaac attcttcata tgtgatgtcc ttagtcacta     240
aggttaaact ttcccaccca gaaaaggcaa cttagataaa atcttagagt actttcatac     300
tcttctaagt cctcttccag cctcactttg agtcctcctt gggggttgat aggaantntc     360
tcttggcttt ctcaataaaa tctctatcca tctcatgttt aatttggtac gcntaaaaat     420
gctgaaaaaa ttaaaatgtt ctggtttcnc tttaaaaaaa aaaaaaaaaa aaaaaa         476

      <210> 81
      <211> 232
      <212> DNA
      <213> Homo sapien

      <220>
      <221> misc_feature
      <222> (1)...(232)
      <223> n = A,T,C or G

      <400> 81
```

```
ttttttttg tatgccntcn ctgtggngtt attgttgctg ccaccctgga ggagcccagt      60
ttcttctgta tctttctttt ctgggggatc ttcctggctc tgcccctcca ttcccagcct    120
ctcatcccca tcttgcactt ttgctagggt tggaggcgct ttcctggtag cccctcagag    180
actcagtcag cgggaataag tcctaggggt gggggtgtg gcaagccggc ct             232

      <210> 82
      <211> 383
      <212> DNA
      <213> Homo sapien

      <220>
      <221> misc_feature
      <222> (1)...(383)
      <223> n = A,T,C or G

      <400> 82
aggcgggagc agaagctaaa gccaaagccc aagaagagtg gcagtgccag cactggtgcc     60
agtaccagta ccaataacat gccagtgcca gtgccagcac cagtggtggc ttcagtgctg    120
gtgccagcct gaccgccact ctcacatttg ggctcttcgc tggccttggt ggagctggtg    180
ccagcaccag tggcagctct ggtgcctgtg gtttctccta caagtgagat tttagatatt    240
gttaatcctg ccagtctttc tcttcaagcc agggtgcatc ctcagaaacc tactcaacac    300
agcactctng gcagccacta tcaatcaatt gaagttgaca ctctgcatta aatctatttg    360
ccatttcaaa aaaaaaaaaa aaa                                            383

      <210> 83
      <211> 494
      <212> DNA
      <213> Homo sapien

      <220>
      <221> misc_feature
      <222> (1)...(494)
      <223> n = A,T,C or G

      <400> 83
accgaattgg gaccgctggc ttataagcga tcatgtcctc cagtattacc tcaacgagca     60
gggagatcga gtctatacgc tgaagaaatt tgacccgatg ggacaacaga cctgctcagc    120
ccatcctgct cggttctccc cagatgacaa atactctcga caccgaatca ccatcaagaa    180
acgcttcaag gtgctcatga cccagcaacc gcgccctgtc ctctgagggt ccttaaactg    240
atgtcttttc tgccacctgt tacccctcgg agactccgta accaaactct tcggactgtg    300
agccctgatg cctttttgcc agccatactc tttggcntcc agtctctcgt ggcgattgat    360
tatgcttgtg tgaggcaatc atggtggcat cacccatnaa gggaacacat ttgantttt     420
tttcncatat tttaaattac naccagaata nttcagaata aatgaattga aaaactctta    480
aaaaaaaaaa aaaa                                                      494

      <210> 84
      <211> 380
      <212> DNA
      <213> Homo sapien

      <220>
      <221> misc_feature
      <222> (1)...(380)
      <223> n = A,T,C or G

      <400> 84
gctggtagcc tatggcgtgg ccacggangg gctcctgagg cacgggacag tgacttccca     60
agtatcctgc gccgcgtctt ctaccgtccc tacctgcaga tcttcgggca gattccccag    120
```

gaggacatgg acgtggccct catggagcac agcaactgct cgtcggagcc cggcttctgg 180
gcacaccctc ctggggccca ggcgggcacc tgcgtctccc agtatgccaa ctggctggtg 240
gtgctgctcc tcgtcatctt cctgctcgtg gccaacatcc tgctggtcac ttgctcattg 300
ccatgttcag ttacacattc ggcaaagtac agggcaacag cnatctctac tgggaaggcc 360
agcgttnccg cctcatccgg 380

<210> 85
<211> 481
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(481)
<223> n = A,T,C or G

<400> 85
gagttagctc ctccacaacc ttgatgaggt cgtctgcagt ggcctctcgc ttcataccgc 60
tnccatcgtc atactgtagg tttgccacca cctcctgcat cttggggcgg ctaatatcca 120
ggaaactctc aatcaagtca ccgtcnatna aacctgtggc tggttctgtc ttccgctcgg 180
tgtgaaagga tctccagaag gagtgctcga tcttccccac acttttgatg actttattga 240
gtcgattctg catgtccagc aggaggttgt accagctctc tgacagtgag gtcaccagcc 300
ctatcatgcc nttgaacgtg ccgaagaaca ccgagccttg tgtggggggt gnagtctcac 360
ccagattctg cattaccaga nagccgtggc aaaaganatt gacaactcgc ccaggnngaa 420
aaagaacacc tcctggaagt gctngccgct cctcgtccnt tggtggnngc gcntnccttt 480
t 481

<210> 86
<211> 472
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(472)
<223> n = A,T,C or G

<400> 86
aacatcttcc tgtataatgc tgtgtaatat cgatccgatn ttgtctgctg agaattcatt 60
acttggaaaa gcaacttnaa gcctggacac tggtattaaa attcacaata tgcaacactt 120
taaacagtgt gtcaatctgc tcccttactt tgtcatcacc agtctgggaa taagggtatg 180
ccctattcac acctgttaaa agggcgctaa gcatttttga ttcaacatct tttttttga 240
cacaagtccg aaaaaagcaa aagtaaacag ttnttaattt gttagccaat tcactttctt 300
catgggacag agccatttga tttaaaaagc aaattgcata atattgagct ttgggagctg 360
atatntgagc ggaagantag cctttctact tcaccagaca caactccttt catattggga 420
tgttnacnaa agttatgtct cttacagatg ggatgctttt gtggcaattc tg 472

<210> 87
<211> 413
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(413)
<223> n = A,T,C or G

<400> 87

```
agaaaccagt atctctnaaa acaacctctc ataccttgtg gacctaattt tgtgtgcgtg      60
tgtgtgtgcg cgcatattat atagacaggc acatcttttt tacttttgta aaagcttatg     120
cctctttggt atctatatct gtgaaagttt taatgatctg ccataatgtc ttggggacct     180
ttgtcttctg tgtaaatggt actagagaaa acacctatnt tatgagtcaa tctagttngt     240
tttattcgac atgaaggaaa tttccagatn acaacactna caaactctcc cttgactagg     300
ggggacaaag aaaagcanaa ctgaacatna gaaacaattn cctggtgaga aattncataa     360
acagaaattg ggtngtatat tgaaananng catcattnaa acgttttttt ttt            413
```

<210> 88
<211> 448
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(448)
<223> n = A,T,C or G

<400> 88

```
cgcagcgggt cctctctatc tagctccagc ctctcgcctg ccccactccc cgcgtcccgc      60
gtcctagccn accatggccg ggcccctgcg cgccccgctg ctcctgctgg ccatcctggc     120
cgtggccctg gccgtgagcc ccgcggccgg ctccagtccc ggcaagccgc cgcgcctggt     180
gggaggccca tggaccccgc gtggaagaag aaggtgtgcg gcgtgcactg gactttgccg     240
tcggcnanta caacaaaccc gcaacnactt ttaccnagcn cgcgctgcag gttgtgccgc     300
cccaancaaa ttgttactng gggtaantaa ttcttggaag ttgaacctgg gccaaacnng     360
tttaccagaa ccnagccaat tngaacaatt ncccctccat aacagcccct tttaaaaagg     420
gaancantcc tgntcttttc caaatttt                                        448
```

<210> 89
<211> 463
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(463)
<223> n = A,T,C or G

<400> 89

```
gaattttgtg cactggccac tgtgatggaa ccattgggcc aggatgcttt gagtttatca      60
gtagtgattc tgccaaagtt ggtgttgtaa catgagtatg taaaatgtca aaaaattagc     120
agaggtctag gtctgcatat cagcagacag tttgtccgtg tattttgtag ccttgaagtt     180
ctcagtgaca agttnnttct gatgcgaagt tctnattcca gtgttttagt cctttgcatc     240
tttnatgttn agacttgcct ctntnaaatt gcttttgtnt tctgcaggta ctatctgtgg     300
tttaacaaaa tagaannact tctctgcttn gaanatttga atatcttaca tctnaaaatn     360
aattctctcc ccatannaaa acccangccc ttggganaat ttgaaaaang gntccttcnn     420
aattcnnana anttcagntn tcatacaaca naacngganc ccc                       463
```

<210> 90
<211> 400
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(400)
<223> n = A,T,C or G

```
<400> 90
agggattgaa ggtctnttnt actgtcggac tgttcancca ccaactctac aagttgctgt     60
cttccactca ctgtctgtaa gcntnttaac ccagactgta tcttcataaa tagaacaaat    120
tcttcaccag tcacatcttc taggaccttt ttggattcag ttagtataag ctcttccact    180
tcctttgtta agacttcatc tggtaaagtc ttaagttttg tagaaaggaa tttaattgct    240
cgttctctaa caatgtcctc tccttgaagt atttggctga acaacccacc tnaagtccct    300
ttgtgcatcc attttaaata tacttaatag ggcattggtn cactaggtta aattctgcaa    360
gagtcatctg tctgcaaaag ttgcgttagt atatctgcca                          400

<210> 91
<211> 480
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(480)
<223> n = A,T,C or G

<400> 91
gagctcggat ccaataatct ttgtctgagg gcagcacaca tatncagtgc catggnaact     60
ggtctacccc acatgggagc agcatgccgt agntatataa ggtcattccc tgagtcagac    120
atgcctcttt gactaccgtg tgccagtgct ggtgattctc acacacctcc nnccgctctt    180
tgtggaaaaa ctggcacttg nctggaacta gcaagacatc acttacaaat tcacccacga    240
gacacttgaa aggtgtaaca aagcgactct tgcattgctt tttgtccctc cggcaccagt    300
tgtcaatact aaccccgctgg tttgcctcca tcacatttgt gatctgtagc tctggataca   360
tctcctgaca gtactgaaga acttcttctt ttgtttcaaa agcaactctt ggtgcctgtt    420
ngatcaggtt cccatttccc agtccgaatg ttcacatggc atatnttact tcccacaaaa    480

<210> 92
<211> 477
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(477)
<223> n = A,T,C or G

<400> 92
atacagccca natcccacca cgaagatgcg cttgttgact gagaacctga tgcggtcact     60
ggtcccgctg tagccccagc gactctccac ctgctggaag cggttgatgc tgcactcctt    120
cccacgcagg cagcagcggg gccggtcaat gaactccact cgtggcttgg ggttgacggt    180
taantgcagg aagaggctga ccacctcgcg gtccaccagg atgcccgact gtgcgggacc    240
tgcagcgaaa ctcctcgatg gtcatgagcg ggaagcgaat gangcccagg gccttgccca    300
gaaccttccg cctgttctct ggcgtcacct gcagctgctg ccgctnacac tcggcctcgg    360
accagcggac aaacggcgtt gaacagccgc acctcacgga tgcccantgt gtcgcgctcc    420
aggaacggcn ccagcgtgtc caggtcaatg tcggtgaanc ctccgcgggt aatggcg       477

<210> 93
<211> 377
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(377)
<223> n = A,T,C or G
```

<400> 93
gaacggctgg accttgcctc gcattgtgct gctggcagga ataccttggc aagcagctcc 60
agtccgagca gccccagacc gctgccgccc gaagctaagc ctgcctctgg ccttcccctc 120
cgcctcaatg cagaaccant agtgggagca ctgtgtttag agttaagagt gaacactgtn 180
tgattttact tgggaatttc ctctgttata tagcttttcc caatgctaat ttccaaacaa 240
caacaacaaa ataacatgtt tgcctgttna gttgtataaa agtangtgat tctgtatnta 300
aagaaaatat tactgttaca tatactgctt gcaanttctg tatttattgg tnctctggaa 360
ataaatatat tattaaa 377

<210> 94
<211> 495
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(495)
<223> n = A,T,C or G

<400> 94
ccctttgagg ggttagggtc cagttcccag tggaagaaac aggccaggag aantgcgtgc 60
cgagctgang cagatttccc acagtgaccc cagagccctg ggctatagtc tctgacccct 120
ccaaggaaag accaccttct ggggacatgg gctggagggc aggacctaga ggcaccaagg 180
gaaggcccca ttccggggct gttccccgag gaggaaggga aggggctctg tgtgcccccc 240
acgaggaana ggccctgant cctgggatca nacacccctt cacgtgtatc cccacacaaa 300
tgcaagctca ccaaggtccc ctctcagtcc cttccctaca ccctgaacgg ncactggccc 360
acacccaccc agancancca cccgccatgg ggaatgtnct caaggaatcg cngggcaacg 420
tggactctng tcccnnaagg gggcagaatc tccaatagan gganngaacc cttgctnana 480
aaaaaaaana aaaaa 495

<210> 95
<211> 472
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(472)
<223> n = A,T,C or G

<400> 95
ggttacttgg tttcattgcc accacttagt ggatgtcatt tagaaccatt ttgtctgctc 60
cctctggaag ccttgcgcag agcggacttt gtaattgttg gagaataact gctgaatttt 120
tagctgtttt gagttgattc gcaccactgc accacaactc aatatgaaaa ctatttnact 180
tatttattat cttgtgaaaa gtatacaatg aaaattttgt tcatactgta tttatcaagt 240
atgatgaaaa gcaatagata tatattcttt tattatgttn aattatgatt gccattatta 300
atcggcaaaa tgtggagtgt atgttctttt cacagtaata tatgcctttt gtaacttcac 360
ttggttattt tattgtaaat gaattacaaa attcttaatt taagaaaatg gtangttata 420
tttanttcan taatttcttt ccttgtttac gttaattttg aaaagaatgc at 472

<210> 96
<211> 476
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature

<222> (1)...(476)
<223> n = A,T,C or G

<400> 96
ctgaagcatt tcttcaaact tntctacttt tgtcattgat acctgtagta agttgacaat 60
gtggtgaaat ttcaaaatta tatgtaactt ctactagttt tactttctcc cccaagtctt 120
ttttaactca tgatttttac acacacaatc cagaacttat tatatagcct ctaagtcttt 180
attcttcaca gtagatgatg aaagagtcct ccagtgtctt gngcaaatg ttctagntat 240
agctggatac atacngtggg agttctataa actcatacct cagtgggact naaccaaaat 300
tgtgttagtc tcaattccta ccacactgag ggagcctccc aaatcactat attcttatct 360
gcaggtactc ctccagaaaa acngacaggg caggcttgca tgaaaaagtn acatctgcgt 420
tacaaagtct atcttcctca nangtctgtn aaggaacaat ttaatcttct agcttt 476

<210> 97
<211> 479
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(479)
<223> n = A,T,C or G

<400> 97
actctttcta atgctgatat gatcttgagt ataagaatgc atatgtcact agaatggata 60
aaataatgct gcaaacttaa tgttcttatg caaaatggaa cgctaatgaa acacagctta 120
caatcgcaaa tcaaaactca caagtgctca tctgttgtag atttagtgta ataagactta 180
gattgtgctc cttcggatat gattgtttct canatcttgg gcaatnttcc ttagtcaaat 240
caggctacta gaattctgtt attggatatn tgagagcatg aaatttttaa naatacactt 300
gtgattatna aattaatcac aaatttcact tatacctgct atcagcagct agaaaaacat 360
ntnnttttta natcaaagta ttttgtgttt ggaantgtnn aaatgaaatc tgaatgtggg 420
ttcnatctta ttttttcccn gacnactant tnctttttta gggnctattc tganccatc 479

<210> 98
<211> 461
<212> DNA
<213> Homo sapien

<400> 98
agtgacttgt cctccaacaa aacccсttga tcaagtttgt ggcactgaca atcagaccta 60
tgctagttcc tgtcatctat tcgctactaa atgcagactg gaggggacca aaaaggggca 120
tcaactccag ctggattatt ttggagcctg caaatctatt cctacttgta cggactttga 180
agtgattcag tttcctctac ggatgagaga ctggctcaag aatatcctca tgcagcttta 240
tgaagccact ctgaacacgc tggttatcta gatgagaaca gagaaataaa gtcagaaaat 300
ttacctggag aaaagaggct ttggctgggg accatcccat tgaaccttct cttaaggact 360
ttaagaaaaa ctaccacatg ttgtgtatcc tggtgccggc cgtttatgaa ctgaccaccc 420
tttggaataa tcttgacgct cctgaacttg ctcctctgcg a 461

<210> 99
<211> 171
<212> DNA
<213> Homo sapien

<400> 99
gtggccgcgc gcaggtgttt cctcgtaccg cagggccccc tcccttcccc aggcgtccct 60
cggcgcctct gcgggcccga ggaggagcgg ctggcgggtg gggggagtgt gacccaccct 120
cggtgagaaa agccttctct agcgatctga gaggcgtgcc ttgggggtac c 171

<210> 100
<211> 269
<212> DNA
<213> Homo sapien

<400> 100
cggccgcaag tgcaactcca gctggggccg tgcggacgaa gattctgcca gcagttggtc 60
cgactgcgac gacggcggcg gcgacagtcg caggtgcagc gcgggcgcct ggggtcttgc 120
aaggctgagc tgacgccgca gaggtcgtgt cacgtcccac gaccttgacg ccgtcgggga 180
cagccggaac agagcccggt gaagcgggag gcctcgggga gcccctcggg aagggcggcc 240
cgagagatac gcaggtgcag gtggccgcc 269

<210> 101
<211> 405
<212> DNA
<213> Homo sapien

<400> 101
tttttttttt ttttggaatc tactgcgagc acagcaggtc agcaacaagt ttattttgca 60
gctagcaagg taacagggta gggcatggtt acatgttcag gtcaacttcc tttgtcgtgg 120
ttgattggtt tgtctttatg ggggcggggt ggggtagggg aaacgaagca aataacatgg 180
agtgggtgca ccctccctgt agaacctggt tacaaagctt ggggcagttc acctggtctg 240
tgaccgtcat tttcttgaca tcaatgttat tagaagtcag gatatctttt agagagtcca 300
ctgttctgga gggagattag ggtttcttgc caaatccaac aaaatccact gaaaaagttg 360
gatgatcagt acgaataccg aggcatattc tcatatcggt ggcca 405

<210> 102
<211> 470
<212> DNA
<213> Homo sapien

<400> 102
tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 60
ggcacttaat ccatttttat ttcaaaatgt ctacaaattt aatcccatta tacggtattt 120
tcaaaatcta aattattcaa attagccaaa tccttaccaa ataataccca aaaatcaaaa 180
atatacttct ttcagcaaac ttgttacata aattaaaaaa atatatacgg ctggtgtttt 240
caaagtacaa ttatcttaac actgcaaaca ttttaaggaa ctaaaataaa aaaaaacact 300
ccgcaaaggt taaagggaac aacaaattct tttacaacac cattataaaa atcatatctc 360
aaatcttagg ggaatatata cttcacacgg gatcttaact tttactcact ttgtttattt 420
ttttaaacca ttgtttgggc ccaacacaat ggaatccccc ctggactagt 470

<210> 103
<211> 581
<212> DNA
<213> Homo sapien

<400> 103
tttttttttt tttttttgga cccccctctt ataaaaaaca agttaccatt ttattttact 60
tacacatatt tattttataa ttggtattag atattcaaaa ggcagctttt aaaatcaaac 120
taaatggaaa ctgccttaga tacataattc ttaggaatta gcttaaaatc tgcctaaagt 180
gaaaatcttc tctagctctt ttgactgtaa atttttgact cttgtaaaac atccaaattc 240
atttttcttg tctttaaaat tatctaatct ttccattttt tccctattcc aagtcaattt 300
gcttctctag cctcatttcc tagctcttat ctactattag taagtggctt ttttcctaaa 360
agggaaaaca ggaagagaaa tggcacacaa aacaaacatt ttatattcat atttctacct 420
acgttaataa aatagcattt tgtgaagcca gctcaaaaga aggcttagat ccttttatgt 480
ccattttagt cactaaacga tatcaaagtg ccagaatgca aaaggtttgt gaacatttat 540
tcaaaagcta atataagata tttcacatac tcatctttct g 581

<210> 104
<211> 578
<212> DNA
<213> Homo sapien

<400> 104
ttttttttt ttttttttt tttttctctt cttttttttt gaaatgagga tcgagttttt 60
cactctctag atagggcatg aagaaaactc atctttccag ctttaaaata acaatcaaat 120
ctcttatgct atatcatatt ttaagttaaa ctaatgagtc actggcttat cttctcctga 180
aggaaatctg ttcattcttc tcattcatat agttatatca agtactacct tgcatattga 240
gaggtttttc ttctctattt acacatatat ttccatgtga atttgtatca aacctttatt 300
ttcatgcaaa ctagaaaata atgtttcttt tgcataagag aagagaacaa tatagcatta 360
caaaactgct caaattgttt gttaagttat ccattataat tagttggcag gagctaatac 420
aaatcacatt tacgacagca ataataaaac tgaagtacca gttaaatatc caaaataatt 480
aaaggaacat ttttagcctg ggtataatta gctaattcac tttacaagca tttattagaa 540
tgaattcaca tgttattatt cctagcccaa cacaatgg 578

<210> 105
<211> 538
<212> DNA
<213> Homo sapien

<400> 105
ttttttttt tttttcagta ataatcagaa caatatttat ttttatattt aaaattcata 60
gaaaagtgcc ttacatttaa taaaagtttg tttctcaaag tgatcagagg aattagatat 120
gtcttgaaca ccaatattaa tttgaggaaa atacaccaaa atacattaag taaattattt 180
aagatcatag agcttgtaag tgaaaagata aaatttgacc tcagaaactc tgagcattaa 240
aaatccacta ttagcaaata aattactatg gacttcttgc tttaattttg tgatgaatat 300
ggggtgtcac tggtaaacca acacattctg aaggatacat tacttagtga tagattctta 360
tgtactttgc taatacgtgg atatgagttg acaagtttct ctttcttcaa tcttttaagg 420
ggcgagaaat gaggaagaaa agaaaaggat tacgcatact gttctttcta tggaaggatt 480
agatatgttt cctttgccaa tattaaaaaa ataataatgt ttactactag tgaaaccc 538

<210> 106
<211> 473
<212> DNA
<213> Homo sapien

<400> 106
ttttttttt ttttttagtc aagtttctat ttttattata attaaagtct tggtcatttc 60
atttattagc tctgcaactt acatatttaa attaaagaaa cgttttagac aactgtacaa 120
tttataaatg taaggtgcca ttattgagta atatattcct ccaagagtgg atgtgtccct 180
tctcccacca actaatgaac agcaacatta gtttaatttt attagtagat atacactgct 240
gcaaacgcta attctcttct ccatccccat gtgatattgt gtatatgtgt gagttggtag 300
aatgcatcac aatctacaat caacagcaag atgaagctag gctgggcttt cggtgaaaat 360
agactgtgtc tgtctgaatc aaatgatctg acctatcctc ggtggcaaga actcttcgaa 420
ccgcttcctc aaaggcgctg ccacatttgt ggctctttgc acttgtttca aaa 473

<210> 107
<211> 1621
<212> DNA
<213> Homo sapien

<400> 107
cgccatggca ctgcagggca tctcggtcat ggagctgtcc ggcctggccc cgggcccgtt 60
ctgtgctatg gtcctggctg acttcggggc gcgtgtggta cgcgtggacc ggcccggctc 120
ccgctacgac gtgagccgct tgggccgggg caagcgctcg ctagtgctgg acctgaagca 180
gccgcgggga gccgccgtgc tgcggcgtct gtgcaagcgg tcggatgtgc tgctggagcc 240

```
cttccgccgc ggtgtcatgg agaaactcca gctgggccca gagattctgc agcgggaaaa     300
tccaaggctt atttatgcca ggctgagtgg atttggccag tcaggaagct tctgccggtt     360
agctggccac gatatcaact atttggcttt gtcaggtgtt ctctcaaaaa ttggcagaag     420
tggtgagaat ccgtatgccc cgctgaatct cctggctgac tttgctggtg gtggccttat     480
gtgtgcactg ggcattataa tggctctttt tgaccgcaca cgcactgaca agggtcaggt     540
cattgatgca aatatggtgg aaggaacagc atatttaagt tctttctgt ggaaaactca      600
gaaatcgagt ctgtgggaag cacctcgagg acagaacatg ttggatggtg gagcaccttt     660
ctatacgact tacaggacag cagatgggga attcatggct gttggagcaa tagaacccca     720
gttctacgag ctgctgatca aaggacttgg actaaagtct gatgaacttc ccaatcagat     780
gagcatggat gattggccag aaatgaagaa gaagtttgca gatgtatttg caaagaagac     840
gaaggcagag tggtgtcaaa tctttgacgg cacagatgcc tgtgtgactc cggttctgac     900
ttttgaggag gttgttcatc atgatcacaa caaggaacgg ggctcgttta tcaccagtga     960
ggagcaggac gtgagccccc gccctgcacc tctgctgtta aacaccccag ccatcccttc    1020
tttcaaaagg gatcctttca taggagaaca cactgaggag atacttgaag aatttggatt    1080
cagccgcgaa gagatttatc agcttaactc agataaaatc attgaaagta ataaggtaaa    1140
agctagtctc taacttccag gcccacggct caagtgaatt tgaatactgc atttacagtg    1200
tagagtaaca cataacattg tatgcatgga aacatggagg aacagtatta cagtgtccta    1260
ccactctaat caagaaaaga attacagact ctgattctac agtgatgatt gaattctaaa    1320
aatggttatc attagggctt ttgatttata aaactttggg tacttatact aaattatggt    1380
agttattctg ccttccagtt tgcttgatat atttgttgat attaagattc ttgacttata    1440
ttttgaatgg gttctagtga aaaaggaatg atatattctt gaagacatcg atatacattt    1500
atttacactc ttgattctac aatgtagaaa atgaggaaat gccacaaatt gtatggtgat    1560
aaaagtcacg tgaaacaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa    1620
a                                                                    1621
```

<210> 108
<211> 382
<212> PRT
<213> Homo sapien

<400> 108

```
Met Ala Leu Gln Gly Ile Ser Val Met Glu Leu Ser Gly Leu Ala Pro
 1               5                  10                  15
Gly Pro Phe Cys Ala Met Val Leu Ala Asp Phe Gly Ala Arg Val Val
            20                  25                  30
Arg Val Asp Arg Pro Gly Ser Arg Tyr Asp Val Ser Arg Leu Gly Arg
        35                  40                  45
Gly Lys Arg Ser Leu Val Leu Asp Leu Lys Gln Pro Arg Gly Ala Ala
    50                  55                  60
Val Leu Arg Arg Leu Cys Lys Arg Ser Asp Val Leu Leu Glu Pro Phe
65                  70                  75                  80
Arg Arg Gly Val Met Glu Lys Leu Gln Leu Gly Pro Glu Ile Leu Gln
                85                  90                  95
Arg Glu Asn Pro Arg Leu Ile Tyr Ala Arg Leu Ser Gly Phe Gly Gln
            100                 105                 110
Ser Gly Ser Phe Cys Arg Leu Ala Gly His Asp Ile Asn Tyr Leu Ala
        115                 120                 125
Leu Ser Gly Val Leu Ser Lys Ile Gly Arg Ser Gly Glu Asn Pro Tyr
    130                 135                 140
Ala Pro Leu Asn Leu Leu Ala Asp Phe Ala Gly Gly Gly Leu Met Cys
145                 150                 155                 160
Ala Leu Gly Ile Ile Met Ala Leu Phe Asp Arg Thr Arg Thr Asp Lys
                165                 170                 175
Gly Gln Val Ile Asp Ala Asn Met Val Glu Gly Thr Ala Tyr Leu Ser
            180                 185                 190
Ser Phe Leu Trp Lys Thr Gln Lys Ser Ser Leu Trp Glu Ala Pro Arg
        195                 200                 205
Gly Gln Asn Met Leu Asp Gly Gly Ala Pro Phe Tyr Thr Thr Tyr Arg
```

```
    210                 215                 220
Thr Ala Asp Gly Glu Phe Met Ala Val Gly Ala Ile Glu Pro Gln Phe
225                 230                 235                 240
Tyr Glu Leu Leu Ile Lys Gly Leu Gly Leu Lys Ser Asp Glu Leu Pro
                245                 250                 255
Asn Gln Met Ser Met Asp Asp Trp Pro Glu Met Lys Lys Lys Phe Ala
            260                 265                 270
Asp Val Phe Ala Lys Lys Thr Lys Ala Glu Trp Cys Gln Ile Phe Asp
        275                 280                 285
Gly Thr Asp Ala Cys Val Thr Pro Val Leu Thr Phe Glu Glu Val Val
    290                 295                 300
His His Asp His Asn Lys Glu Arg Gly Ser Phe Ile Thr Ser Glu Glu
305                 310                 315                 320
Gln Asp Val Ser Pro Arg Pro Ala Pro Leu Leu Leu Asn Thr Pro Ala
                325                 330                 335
Ile Pro Ser Phe Lys Arg Asp Pro Phe Ile Gly Glu His Thr Glu Glu
            340                 345                 350
Ile Leu Glu Glu Phe Gly Phe Ser Arg Glu Glu Ile Tyr Gln Leu Asn
        355                 360                 365
Ser Asp Lys Ile Ile Glu Ser Asn Lys Val Lys Ala Ser Leu
    370                 375                 380
```

<210> 109
<211> 1524
<212> DNA
<213> Homo sapien

<400> 109

```
ggcacgaggc tgcgccaggg cctgagcgga ggcgggggca gcctcgccag cggggggcccc     60
gggcctggcc atgcctcact gagccagcgc ctgcgcctct acctcgccga cagctggaac    120
cagtgcgacc tagtggctct cacctgcttc ctcctgggcg tgggctgccg gctgaccccg    180
ggtttgtacc acctgggccg cactgtcctc tgcatcgact tcatggtttt cacggtgcgg    240
ctgcttcaca tcttcacggt caacaaacag ctggggccca agatcgtcat cgtgagcaag    300
atgatgaagg acgtgttctt cttcctcttc ttcctcggcg tgtggctggt agcctatggc    360
gtggccacgg aggggctcct gaggccacgg gacagtgact tcccaagtat cctgcgccgc    420
gtcttctacc gtccctacct gcagatcttc gggcagattc cccaggagga catggacgtg    480
gccctcatgg agcacagcaa ctgctcgtcg gagcccggct tctgggcaca ccctcctggg    540
gcccaggcgg gcacctgcgt ctcccagtat gccaactggc tggtggtgct gctcctcgtc    600
atcttcctgc tcgtggccaa catcctgctg gtcaacttgc tcattgccat gttcagttac    660
acattcggca aagtacaggg caacagcgat ctctactgga aggcgcagcg ttaccgcctc    720
atccgggaat tccactctcg gcccgcgctg gccccgccct ttatcgtcat ctcccacttg    780
cgcctcctgc tcaggcaatt gtgcaggcga ccccggagcc cccagccgtc ctccccggcc    840
ctcgagcatt tccgggttta cctttctaag gaagccgagc ggaagctgct aacgtgggaa    900
tcggtgcata aggagaactt tctgctggca cgcgctaggg acaagcggga gagcgactcc    960
gagcgtctga agcgcacgtc ccagaaggtg gacttggcac tgaaacagct gggacacatc   1020
cgcgagtacg aacagcgcct gaaagtgctg gagcgggagg tccagcagtg tagccgcgtc   1080
ctggggtggg tggccgaggc cctgagccgc tctgccttgc tgccccccagg tgggccgcca   1140
ccccctgacc tgcctgggtc caaagactga gccctgctgg cggacttcaa ggagaagccc   1200
ccacagggga ttttgctcct agagtaaggc tcatctgggc ctcggccccc gcacctggtg   1260
gccttgtcct tgaggtgagc cccatgtcca tctgggccac tgtcaggacc acctttggga   1320
gtgtcatcct tacaaaccac agcatgcccg gctcctccca gaaccagtcc cagcctggga   1380
ggatcaaggc ctggatcccg ggccgttatc catctggagg ctgcagggtc cttggggtaa   1440
cagggaccac agacccctca ccactcacag attcctcaca ctggggaaat aaagccattt   1500
cagaggaaaa aaaaaaaaaa aaaa                                          1524
```

<210> 110
<211> 3410
<212> DNA

<213> Homo sapien

<400> 110

```
gggaaccagc ctgcacgcgc tggctccggg tgacagccgc gcgcctcggc caggatctga 60
gtgatgagac gtgtccccac tgaggtgccc cacagcagca ggtgttgagc atgggctgag 120
aagctggacc ggcaccaaag ggctggcaga aatgggcgcc tggctgattc ctaggcagtt 180
ggcggcagca aggaggagag gccgcagctt ctggagcaga gccgagacga agcagttctg 240
gagtgcctga acggccccct gagccctacc cgcctggccc actatggtcc agaggctgtg 300
ggtgagccgc ctgctgcggc accggaaagc ccagctcttg ctggtcaacc tgctaacctt 360
tggcctggag gtgtgtttgg ccgcaggcat cacctatgtg ccgcctctgc tgctggaagt 420
gggggtagag gagaagttca tgaccatggt gctgggcatt ggtccagtgc tgggcctggt 480
ctgtgtcccg ctcctaggct cagccagtga ccactggcgt ggacgctatg gccgccgccg 540
gcccttcatc tgggcactgt ccttgggcat cctgctgagc ctctttctca tcccaagggc 600
cggctggcta gcagggctgc tgtgcccgga tcccaggccc ctggagctgg cactgctcat 660
cctgggcgtg gggctgctgg acttctgtgg ccaggtgtgc ttcactccac tggaggccct 720
gctctctgac ctcttccggg acccggacca ctgtcgccag gcctactctg tctatgcctt 780
catgatcagt cttgggggct gcctgggcta cctcctgcct gccattgact gggacaccag 840
tgccctggcc ccctacctgg gcacccagga ggagtgcctc tttggcctgc tcaccctcat 900
cttcctcacc tgcgtagcag ccacactgct ggtggctgag gaggcagcgc tgggccccac 960
cgagccagca gaagggctgt cggcccccte cttgtcgccc cactgctgtc catgccgggc 1020
ccgcttggct ttccggaacc tgggcgccct gcttccccgg ctgcaccagc tgtgctgccg 1080
catgccccgc accctgcgcc ggctcttcgt ggctgagctg tgcagctgga tggcactcat 1140
gaccttcacg ctgttttaca cggatttcgt gggcgagggg ctgtaccagg gcgtgcccag 1200
agctgagccg ggcaccgagg cccggagaca ctatgatgaa ggcgttcgga tggcagcct 1260
ggggctgttc ctgcagtgcg ccatctccct ggtcttctct ctggtcatgg accggctggt 1320
gcagcgattc ggcactcgag cagtctattt ggccagtgtg gcagctttcc ctgtggctgc 1380
cggtgccaca tgcctgtccc acagtgtggc cgtggtgaca gcttcagccg ccctcaccgg 1440
gttcaccttc tcagccctgc agatcctgcc ctacacactg gcctccctct accaccggga 1500
gaagcaggtg ttcctgccca aataccgagg ggacactgga ggtgctagca gtgaggacag 1560
cctgatgacc agcttcctgc caggccctaa gcctggagct cccttcccta atggacacgt 1620
gggtgctgga ggcagtggcc tgctcccacc tccacccgcg ctctgcgggg cctctgcctg 1680
tgatgtctcc gtacgtgtgg tggtgggtga gcccaccgag gccagggtgg ttccgggccg 1740
gggcatctgc ctggacctcg ccatcctgga tagtgccttc ctgctgtccc aggtggcccc 1800
atccctgttt atgggctcca ttgtccagct cagccagtct gtcactgcct atatggtgtc 1860
tgccgcaggc ctgggtctgg tcgccattta ctttgctaca caggtagtat ttgacaagag 1920
cgacttggcc aaatactcag cgtagaaaac ttccagcaca ttggggtgga gggcctgcct 1980
cactgggtcc cagctccccg ctcctgttag ccccatgggg ctgccgggct ggccgccagt 2040
ttctgttgct gccaaagtaa tgtggctctc tgctgccacc ctgtgctgct gaggtgcgta 2100
gctgcacagc tgggggctgg ggcgtccctc tcctctctcc ccagtctcta gggctgcctg 2160
actggaggcc ttccaagggg gtttcagtct ggacttatac agggaggcca gaagggctcc 2220
atgcactgga atgcggggac tctgcaggtg gattacccag gctcagggtt aacagctagc 2280
ctcctagttg agacacacct agagaagggt ttttgggagc tgaataaact cagtcacctg 2340
gtttcccatc tctaagcccc ttaacctgca gcttcgttta atgtagctct tgcatgggag 2400
tttctaggat gaaacactcc tccatgggat ttgaacatat gacttatttg taggggaaga 2460
gtcctgaggg gcaacacaca agaaccaggt cccctcagcc cacagcactg tctttttgct 2520
gatccacccc cctcttacct tttatcagga tgtggcctgt tggtccttct gttgccatca 2580
cagagacaca ggcatttaaa tatttaactt atttatttaa caaagtagaa gggaatccat 2640
tgctagcttt tctgtgttgg tgtctaatat ttgggtaggg tgggggatcc ccaacaatca 2700
ggtcccctga gatagctggt cattgggctg atcattgcca gaatcttctt ctcctggggt 2760
ctggcccccc aaaatgccta acccaggacc ttggaaattc tactcatccc aaatgataat 2820
tccaaatgct gttacccaag gttagggtgt tgaaggaagg tagagggtgg ggcttcaggt 2880
ctcaacggct tccctaacca cccctcttct cttggcccag cctggttccc cccacttcca 2940
ctcccctcta ctctctctag gactgggctg atgaaggcac tgcccaaaat ttcccctacc 3000
cccaactttc ccctaccccc aactttcccc accagctcca caaccctgtt tggagctact 3060
gcaggaccag aagcacaaag tgcggtttcc caagcctttg tccatctcag cccccagagt 3120
atatctgtgc ttggggaatc tcacacagaa actcaggagc accccctgcc tgagctaagg 3180
gaggtcttat ctctcagggg gggtttaagt gccgtttgca ataatgtcgt cttatttatt 3240
tagcggggtg aatattttat actgtaagtg agcaatcaga gtataatgtt tatggtgaca 3300
```

```
aaattaaagg ctttcttata tgtttaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa    3360
aaaaaaaara aaaaaaaaaa aaaaaaaaaa aaaaaaataa aaaaaaaaaa               3410

      <210> 111
      <211> 1289
      <212> DNA
      <213> Homo sapien

      <400> 111
agccaggcgt ccctctgcct gcccactcag tggcaacacc cgggagctgt tttgtccttt      60
gtggagcctc agcagttccc tctttcagaa ctcactgcca agagccctga acaggagcca     120
ccatgcagtg cttcagcttc attaagacca tgatgatcct cttcaatttg ctcatctttc     180
tgtgtggtgc agccctgttg gcagtgggca tctgggtgtc aatcgatggg gcatcctttc     240
tgaagatctt cgggccactg tcgtccagtg ccatgcagtt tgtcaacgtg ggctacttcc     300
tcatcgcagc cggcgttgtg gtctttgctc ttggtttcct gggctgctat ggtgctaaga     360
ctgagagcaa gtgtgccctc gtgacgttct tcttcatcct cctcctcatc ttcattgctg     420
aggttgcagc tgctgtggtc gccttggtgt acaccacaat ggctgagcac ttcctgacgt     480
tgctggtagt gcctgccatc aagaaagatt atggttccca ggaagacttc actcaagtgt     540
ggaacaccac catgaaaggg ctcaagtgct gtggcttcac caactatacg gattttgagg     600
actcacccta cttcaaagag aacagtgcct ttccccccatt ctgttgcaat gacaacgtca     660
ccaacacagc caatgaaacc tgcaccaagc aaaaggctca cgaccaaaaa gtagagggtt     720
gcttcaatca gcttttgtat gacatccgaa ctaatgcagt caccgtgggt ggtgtggcag     780
ctggaattgg gggcctcgag ctggctgcca tgattgtgtc catgtatctg tactgcaatc     840
tacaataagt ccacttctgc ctctgccact actgctgcca catgggaact gtgaagaggc     900
accctggcaa gcagcagtga ttgggggagg ggacaggatc taacaatgtc acttgggcca     960
gaatggacct gccctttctg ctccagactt ggggctagat agggaccact cctttagcg     1020
atgcctgact ttccttccat tggtgggtgg atgggtgggg ggcattccag agcctctaag    1080
gtagccagtt ctgttgccca ttcccccagt ctattaaacc cttgatatgc ccccctaggcc    1140
tagtggtgat cccagtgctc tactgggggga tgagagaaag gcattttata gcctgggcat    1200
aagtgaaatc agcagagcct ctgggtggat gtgtagaagg cacttcaaaa tgcataaacc    1260
tgttacaatg ttaaaaaaaa aaaaaaaaa                                      1289

      <210> 112
      <211> 315
      <212> PRT
      <213> Homo sapien

      <400> 112
Met Val Phe Thr Val Arg Leu Leu His Ile Phe Thr Val Asn Lys Gln
 1               5                  10                  15
Leu Gly Pro Lys Ile Val Ile Val Ser Lys Met Met Lys Asp Val Phe
            20                  25                  30
Phe Phe Leu Phe Phe Leu Gly Val Trp Leu Val Ala Tyr Gly Val Ala
        35                  40                  45
Thr Glu Gly Leu Leu Arg Pro Arg Asp Ser Asp Phe Pro Ser Ile Leu
    50                  55                  60
Arg Arg Val Phe Tyr Arg Pro Tyr Leu Gln Ile Phe Gly Gln Ile Pro
65                  70                  75                  80
Gln Glu Asp Met Asp Val Ala Leu Met Glu His Ser Asn Cys Ser Ser
                85                  90                  95
Glu Pro Gly Phe Trp Ala His Pro Pro Gly Ala Gln Ala Gly Thr Cys
            100                 105                 110
Val Ser Gln Tyr Ala Asn Trp Leu Val Val Leu Leu Leu Val Ile Phe
        115                 120                 125
Leu Leu Val Ala Asn Ile Leu Leu Val Asn Leu Leu Ile Ala Met Phe
    130                 135                 140
Ser Tyr Thr Phe Gly Lys Val Gln Gly Asn Ser Asp Leu Tyr Trp Lys
145                 150                 155                 160
```

```
Ala Gln Arg Tyr Arg Leu Ile Arg Glu Phe His Ser Arg Pro Ala Leu
                165                 170                 175
Ala Pro Pro Phe Ile Val Ile Ser His Leu Arg Leu Leu Leu Arg Gln
            180                 185                 190
Leu Cys Arg Arg Pro Arg Ser Pro Gln Pro Ser Ser Pro Ala Leu Glu
        195                 200                 205
His Phe Arg Val Tyr Leu Ser Lys Glu Ala Glu Arg Lys Leu Leu Thr
    210                 215                 220
Trp Glu Ser Val His Lys Glu Asn Phe Leu Leu Ala Arg Ala Arg Asp
225                 230                 235                 240
Lys Arg Glu Ser Asp Ser Glu Arg Leu Lys Arg Thr Ser Gln Lys Val
                245                 250                 255
Asp Leu Ala Leu Lys Gln Leu Gly His Ile Arg Glu Tyr Glu Gln Arg
            260                 265                 270
Leu Lys Val Leu Glu Arg Glu Val Gln Gln Cys Ser Arg Val Leu Gly
        275                 280                 285
Trp Val Ala Glu Ala Leu Ser Arg Ser Ala Leu Leu Pro Pro Gly Gly
    290                 295                 300
Pro Pro Pro Pro Asp Leu Pro Gly Ser Lys Asp
305                 310                 315

      <210> 113
      <211> 553
      <212> PRT
      <213> Homo sapien

      <400> 113
Met Val Gln Arg Leu Trp Val Ser Arg Leu Leu Arg His Arg Lys Ala
 1               5                  10                  15
Gln Leu Leu Leu Val Asn Leu Leu Thr Phe Gly Leu Glu Val Cys Leu
            20                  25                  30
Ala Ala Gly Ile Thr Tyr Val Pro Pro Leu Leu Leu Glu Val Gly Val
        35                  40                  45
Glu Glu Lys Phe Met Thr Met Val Leu Gly Ile Gly Pro Val Leu Gly
    50                  55                  60
Leu Val Cys Val Pro Leu Leu Gly Ser Ala Ser Asp His Trp Arg Gly
65                  70                  75                  80
Arg Tyr Gly Arg Arg Arg Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile
                85                  90                  95
Leu Leu Ser Leu Phe Leu Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu
            100                 105                 110
Leu Cys Pro Asp Pro Arg Pro Leu Glu Leu Ala Leu Leu Ile Leu Gly
        115                 120                 125
Val Gly Leu Leu Asp Phe Cys Gly Gln Val Cys Phe Thr Pro Leu Glu
    130                 135                 140
Ala Leu Leu Ser Asp Leu Phe Arg Asp Pro Asp His Cys Arg Gln Ala
145                 150                 155                 160
Tyr Ser Val Tyr Ala Phe Met Ile Ser Leu Gly Gly Cys Leu Gly Tyr
                165                 170                 175
Leu Leu Pro Ala Ile Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu
            180                 185                 190
Gly Thr Gln Glu Glu Cys Leu Phe Gly Leu Leu Thr Leu Ile Phe Leu
        195                 200                 205
Thr Cys Val Ala Ala Thr Leu Leu Val Ala Glu Glu Ala Ala Leu Gly
    210                 215                 220
Pro Thr Glu Pro Ala Glu Gly Leu Ser Ala Pro Ser Leu Ser Pro His
225                 230                 235                 240
Cys Cys Pro Cys Arg Ala Arg Leu Ala Phe Arg Asn Leu Gly Ala Leu
```

```
                    245                     250                     255
Leu Pro Arg Leu His Gln Leu Cys Cys Arg Met Pro Arg Thr Leu Arg
            260                     265                     270
Arg Leu Phe Val Ala Glu Leu Cys Ser Trp Met Ala Leu Met Thr Phe
        275                     280                     285
Thr Leu Phe Tyr Thr Asp Phe Val Gly Glu Gly Leu Tyr Gln Gly Val
    290                     295                     300
Pro Arg Ala Glu Pro Gly Thr Glu Ala Arg Arg His Tyr Asp Glu Gly
305                     310                     315                     320
Val Arg Met Gly Ser Leu Gly Leu Phe Leu Gln Cys Ala Ile Ser Leu
                    325                     330                     335
Val Phe Ser Leu Val Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg
            340                     345                     350
Ala Val Tyr Leu Ala Ser Val Ala Ala Phe Pro Val Ala Ala Gly Ala
        355                     360                     365
Thr Cys Leu Ser His Ser Val Ala Val Val Thr Ala Ser Ala Ala Leu
    370                     375                     380
Thr Gly Phe Thr Phe Ser Ala Leu Gln Ile Leu Pro Tyr Thr Leu Ala
385                     390                     395                     400
Ser Leu Tyr His Arg Glu Lys Gln Val Phe Leu Pro Lys Tyr Arg Gly
                    405                     410                     415
Asp Thr Gly Gly Ala Ser Ser Glu Asp Ser Leu Met Thr Ser Phe Leu
            420                     425                     430
Pro Gly Pro Lys Pro Gly Ala Pro Phe Pro Asn Gly His Val Gly Ala
        435                     440                     445
Gly Gly Ser Gly Leu Leu Pro Pro Pro Pro Ala Leu Cys Gly Ala Ser
    450                     455                     460
Ala Cys Asp Val Ser Val Arg Val Val Val Gly Glu Pro Thr Glu Ala
465                     470                     475                     480
Arg Val Val Pro Gly Arg Gly Ile Cys Leu Asp Leu Ala Ile Leu Asp
                    485                     490                     495
Ser Ala Phe Leu Leu Ser Gln Val Ala Pro Ser Leu Phe Met Gly Ser
            500                     505                     510
Ile Val Gln Leu Ser Gln Ser Val Thr Ala Tyr Met Val Ser Ala Ala
        515                     520                     525
Gly Leu Gly Leu Val Ala Ile Tyr Phe Ala Thr Gln Val Val Phe Asp
    530                     535                     540
Lys Ser Asp Leu Ala Lys Tyr Ser Ala
545                     550

      <210> 114
      <211> 241
      <212> PRT
      <213> Homo sapien

      <400> 114
Met Gln Cys Phe Ser Phe Ile Lys Thr Met Met Ile Leu Phe Asn Leu
 1               5                  10                  15
Leu Ile Phe Leu Cys Gly Ala Ala Leu Leu Ala Val Gly Ile Trp Val
            20                  25                  30
Ser Ile Asp Gly Ala Ser Phe Leu Lys Ile Phe Gly Pro Leu Ser Ser
        35                  40                  45
Ser Ala Met Gln Phe Val Asn Val Gly Tyr Phe Leu Ile Ala Ala Gly
    50                  55                  60
Val Val Val Phe Ala Leu Gly Phe Leu Gly Cys Tyr Gly Ala Lys Thr
65                  70                  75                  80
Glu Ser Lys Cys Ala Leu Val Thr Phe Phe Phe Ile Leu Leu Leu Ile
                85                  90                  95
```

Phe Ile Ala Glu Val Ala Ala Ala Val Val Ala Leu Val Tyr Thr Thr
100 105 110
Met Ala Glu His Phe Leu Thr Leu Leu Val Val Pro Ala Ile Lys Lys
115 120 125
Asp Tyr Gly Ser Gln Glu Asp Phe Thr Gln Val Trp Asn Thr Thr Met
130 135 140
Lys Gly Leu Lys Cys Cys Gly Phe Thr Asn Tyr Thr Asp Phe Glu Asp
145 150 155 160
Ser Pro Tyr Phe Lys Glu Asn Ser Ala Phe Pro Pro Phe Cys Cys Asn
165 170 175
Asp Asn Val Thr Asn Thr Ala Asn Glu Thr Cys Thr Lys Gln Lys Ala
180 185 190
His Asp Gln Lys Val Glu Gly Cys Phe Asn Gln Leu Leu Tyr Asp Ile
195 200 205
Arg Thr Asn Ala Val Thr Val Gly Gly Val Ala Ala Gly Ile Gly Gly
210 215 220
Leu Glu Leu Ala Ala Met Ile Val Ser Met Tyr Leu Tyr Cys Asn Leu
225 230 235 240
Gln

<210> 115
<211> 366
<212> DNA
<213> Homo sapien

<400> 115
gctctttctc tcccctcctc tgaatttaat tctttcaact tgcaatttgc aaggattaca 60
catttcactg tgatgtatat tgtgttgcaa aaaaaaaaaa gtgtctttgt ttaaaattac 120
ttggtttgtg aatccatctt gctttttccc cattggaact agtcattaac ccatctctga 180
actggtagaa aaacatctga agagctagtc tatcagcatc tgacaggtga attggatggt 240
tctcagaacc atttcaccca gacagcctgt ttctatcctg tttaataaat tagtttgggt 300
tctctacatg cataacaaac cctgctccaa tctgtcacat aaaagtctgt gacttgaagt 360
ttagtc 366

<210> 116
<211> 282
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(282)
<223> n = A,T,C or G

<400> 116
acaaagatga accatttcct atattatagc aaaattaaaa tctacccgta ttctaatatt 60
gagaaatgag atnaaacaca atnttataaa gtctacttag agaagatcaa gtgacctcaa 120
agactttact attttcatat tttaagacac atgatttatc ctattttagt aacctggttc 180
atacgttaaa caaaggataa tgtgaacagc agagaggatt tgttggcaga aaatctatgt 240
tcaatctnga actatctana tcacagacat ttctattcct tt 282

<210> 117
<211> 305
<212> DNA
<213> Homo sapien

<220>

<221> misc_feature
<222> (1)...(305)
<223> n = A,T,C or G

<400> 117
acacatgtcg cttcactgcc ttcttagatg cttctggtca acatanagga acagggacca 60
tatttatcct ccctcctgaa acaattgcaa aataanacaa aatatatgaa acaattgcaa 120
aataaggcaa aatatatgaa acaacaggtc tcgagatatt ggaaatcagt caatgaagga 180
tactgatccc tgatcactgt cctaatgcag gatgtgggaa acagatgagg tcacctctgt 240
gactgcccca gcttactgcc tgtagagagt ttctangctg cagttcagac agggagaaat 300
tgggt 305

<210> 118
<211> 71
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(71)
<223> n = A,T,C or G

<400> 118
accaaggtgt ntgaatctct gacgtgggga tctctgattc ccgcacaatc tgagtggaaa 60
aantcctggg t 71

<210> 119
<211> 212
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(212)
<223> n = A,T,C or G

<400> 119
actccggttg gtgtcagcag cacgtggcat tgaacatngc aatgtggagc ccaaaccaca 60
gaaaatgggg tgaaattggc caactttcta tnaacttatg ttggcaantt tgccaccaac 120
agtaagctgg cccttctaat aaaagaaaat tgaaaggttt ctcactaanc ggaattaant 180
aatggantca aganactccc aggcctcagc gt 212

<210> 120
<211> 90
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(90)
<223> n = A,T,C or G

<400> 120
actcgttgca natcaggggc cccccagagt caccgttgca ggagtccttc tggtcttgcc 60
ctccgccggc gcagaacatg ctggggtggt 90

<210> 121
<211> 218

<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(218)
<223> n = A,T,C or G

<400> 121
```
tgtancgtga anacgacaga nagggttgtc aaaaatggag aanccttgaa gtcattttga     60
gaataagatt tgctaaaaga tttggggcta aaacatggtt attgggagac atttctgaag    120
atatncangt aaattangga atgaattcat ggttcttttg ggaattcctt tacgatngcc    180
agcatanact tcatgtgggg atancagcta cccttgta                            218
```

<210> 122
<211> 171
<212> DNA
<213> Homo sapien

<400> 122
```
taggggtgta tgcaactgta aggacaaaaa ttgagactca actggcttaa ccaataaagg     60
catttgttag ctcatggaac aggaagtcgg atggtggggc atcttcagtg ctgcatgagt    120
caccaccccg gcggggtcat ctgtgccaca ggtccctgtt gacagtgcgg t             171
```

<210> 123
<211> 76
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(76)
<223> n = A,T,C or G

<400> 123
```
tgtagcgtga agacnacaga atggtgtgtg ctgtgctatc caggaacaca tttattatca     60
ttatcaanta ttgtgt                                                     76
```

<210> 124
<211> 131
<212> DNA
<213> Homo sapien

<400> 124
```
acctttcccc aaggccaatg tcctgtgtgc taactggccg gctgcaggac agctgcaatt     60
caatgtgctg ggtcatatgg aggggaggag actctaaaat agccaatttt attctcttgg    120
ttaagatttg t                                                         131
```

<210> 125
<211> 432
<212> DNA
<213> Homo sapien

<400> 125
```
actttatcta ctggctatga aatagatggt ggaaaattgc gttaccaact ataccactgg     60
cttgaaaaag aggtgatagc tcttcagagg acttgtgact tttgctcaga tgctgaagaa    120
ctacagtctg catttggcag aaatgaagat gaatttggat taaatgagga tgctgaagat    180
ttgcctcacc aaacaaaagt gaaacaactg agagaaaatt ttcaggaaaa aagacagtgg    240
```

```
ctcttgaagt atcagtcact tttgagaatg tttcttagtt actgcatact tcatggatcc     300
catggtgggg gtcttgcatc tgtaagaatg gaattgattt tgcttttgca agaatctcag     360
caggaaacat cagaaccact atttctagc cctctgtcag agcaaacctc agtgcctctc      420
ctctttgctt gt                                                         432

      <210> 126
      <211> 112
      <212> DNA
      <213> Homo sapien

      <400> 126
acacaacttg aatagtaaaa tagaaactga gctgaaattt ctaattcact ttctaaccat      60
agtaagaatg atatttcccc ccagggatca ccaaatattt ataaaaattt gt             112

      <210> 127
      <211> 54
      <212> DNA
      <213> Homo sapien

      <400> 127
accacgaaac cacaaacaag atggaagcat caatccactt gccaagcaca gcag            54

      <210> 128
      <211> 323
      <212> DNA
      <213> Homo sapien

      <400> 128
acctcattag taattgtttt gttgtttcat tttttctaa tgtctcccct ctaccagctc       60
acctgagata acagaatgaa aatggaagga cagccagatt tctcctttgc tctctgctca     120
ttctctctga agtctaggtt acccattttg gggacccatt ataggcaata aacacagttc     180
ccaaagcatt tggacagttt cttgttgtgt tttagaatgg ttttcctttt tcttagcctt     240
ttcctgcaaa aggctcactc agtcccttgc ttgctcagtg gactgggctc cccagggcct     300
aggctgcctt cttttccatg tcc                                            323

      <210> 129
      <211> 192
      <212> DNA
      <213> Homo sapien

      <220>
      <221> misc_feature
      <222> (1)...(192)
      <223> n = A,T,C or G

      <400> 129
acatacatgt gtgtatattt ttaaatatca cttttgtatc actctgactt tttagcatac      60
tgaaaacaca ctaacataat ttntgtgaac catgatcaga tacaacccaa atcattcatc     120
tagcacattc atctgtgata naaagatagg tgagtttcat ttccttcacg ttggccaatg     180
gataaacaaa gt                                                         192

      <210> 130
      <211> 362
      <212> DNA
      <213> Homo sapien

      <220>
      <221> misc_feature
```

<222> (1)...(362)
<223> n = A,T,C or G

<400> 130
cccttttta tggaatgagt agactgtatg tttgaanatt tanccacaac ctctttgaca 60
tataatgacg caacaaaaag gtgctgttta gtcctatggt tcagtttatg cccctgacaa 120
gtttccattg tgttttgccg atcttctggc taatcgtggt atcctccatg ttattagtaa 180
ttctgtattc catttttgtta acgcctggta gatgtaacct gctangaggc taactttata 240
cttatttaaa agctcttatt ttgtggtcat taaaatggca atttatgtgc agcactttat 300
tgcagcagga agcacgtgtg ggttggttgt aaagctcttt gctaatctta aaaagtaatg 360
gg 362

<210> 131
<211> 332
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(332)
<223> n = A,T,C or G

<400> 131
ctttttgaaa gatcgtgtcc actcctgtgg acatcttgtt ttaatggagt ttcccatgca 60
gtangactgg tatggttgca gctgtccaga taaaaacatt tgaagagctc caaaatgaga 120
gttctcccag gttcgccctg ctgctccaag tctcagcagc agcctctttt aggaggcatc 180
ttctgaacta gattaaggca gcttgtaaat ctgatgtgat ttggtttatt atccaactaa 240
cttccatctg ttatcactgg agaaagccca gactccccan gacnggtacg gattgtgggc 300
atanaaggat tgggtgaagc tggcgttgtg gt 332

<210> 132
<211> 322
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(322)
<223> n = A,T,C or G

<400> 132
acttttgcca ttttgtatat ataaacaatc ttgggacatt ctcctgaaaa ctaggtgtcc 60
agtggctaag agaactcgat ttcaagcaat tctgaaagga aaaccagcat gacacagaat 120
ctcaaattcc caaacagggg ctctgtggga aaaatgaggg aggacctttg tatctcgggt 180
tttagcaagt taaaatgaan atgacaggaa aggcttattt atcaacaaag agaagagttg 240
ggatgcttct aaaaaaaact ttggtagaga aaataggaat gctnaatcct agggaagcct 300
gtaacaatct acaattggtc ca 322

<210> 133
<211> 278
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(278)
<223> n = A,T,C or G

<400> 133
acaagccttc acaagtttaa ctaaattggg attaatcttt ctgtanttat ctgcataatt 60
cttgtttttc tttccatctg gctcctgggt tgacaatttg tggaaacaac tctattgcta 120
ctatttaaaa aaaatcacaa atctttccct ttaagctatg ttnaattcaa actattcctg 180
ctattcctgt tttgtcaaag aaattatatt tttcaaaata tgtntatttg tttgatgggt 240
cccacgaaac actaataaaa accacagaga ccagcctg 278

<210> 134
<211> 121
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(121)
<223> n = A,T,C or G

<400> 134
gtttanaaaa cttgtttagc tccatagagg aaagaatgtt aaactttgta ttttaaaaca 60
tgattctctg aggttaaact tggttttcaa atgttatttt tacttgtatt ttgcttttgg 120
t 121

<210> 135
<211> 350
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(350)
<223> n = A,T,C or G

<400> 135
acttanaacc atgcctagca catcagaatc cctcaaagaa catcagtata atcctatacc 60
atancaagtg gtgactggtt aagcgtgcga caaaggtcag ctggcacatt acttgtgtgc 120
aaacttgata ctttgttct aagtaggaac tagtatacag tncctaggan tggtactcca 180
gggtgccccc caactcctgc agccgctcct ctgtgccagn ccctgnaagg aactttcgct 240
ccacctcaat caagccctgg gccatgctac ctgcaattgg ctgaacaaac gtttgctgag 300
ttcccaagga tgcaaagcct ggtgctcaac tcctggggcg tcaactcagt 350

<210> 136
<211> 399
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(399)
<223> n = A,T,C or G

<400> 136
tgtaccgtga agacgacaga agttgcatgg cagggacagg gcagggccga ggccagggtt 60
gctgtgattg tatccgaata ntcctcgtga gaaaagataa tgagatgacg tgagcagcct 120
gcagacttgt gtctgccttc aanaagccag acaggaaggc cctgcctgcc ttggctctga 180
cctggcggcc agccagccag ccacaggtgg gcttcttcct tttgtggtga caacnccaag 240
aaaactgcag aggcccaggg tcaggtgtna gtgggtangt gaccataaaa caccaggtgc 300
tcccaggaac ccgggcaaag gccatcccca cctacagcca gcatgcccac tggcgtgatg 360
ggtgcagang gatgaagcag ccagntgttc tgctgtggt 399

<210> 137
<211> 165
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(165)
<223> n = A,T,C or G

<400> 137
actggtgtgg tnggggggtga tgctggtggt anaagttgan gtgacttcan gatggtgtgt 60
ggaggaagtg tgtgaacgta gggatgtaga ngttttggcc gtgctaaatg agcttcggga 120
ttggctggtc ccactggtgg tcactgtcat tggtggggtt cctgt 165

<210> 138
<211> 338
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(338)
<223> n = A,T,C or G

<400> 138
actcactgga atgccacatt cacaacagaa tcagaggtct gtgaaaacat taatggctcc 60
ttaacttctc cagtaagaat cagggacttg aaatggaaac gttaacagcc acatgcccaa 120
tgctgggcag tctcccatgc cttccacagt gaaagggctt gagaaaaatc acatccaatg 180
tcatgtgttt ccagccacac caaaaggtgc ttggggtgga gggctggggg catananggt 240
cangcctcag gaagcctcaa gttccattca gctttgccac tgtacattcc ccatntttaa 300
aaaaactgat gccttttttt tttttttttg taaaattc 338

<210> 139
<211> 382
<212> DNA
<213> Homo sapien

<400> 139
gggaatcttg gtttttggca tctggtttgc ctatagccga ggccactttg acagaacaaa 60
gaaagggact tcgagtaaga aggtgattta cagccagcct agtgcccgaa gtgaaggaga 120
attcaaacag acctcgtcat tcctggtgtg agcctggtcg gctcaccgcc tatcatctgc 180
atttgcctta ctcaggtgct accggactct ggcccctgat gtctgtagtt tcacaggatg 240
ccttatttgt cttctacacc ccacagggcc ccctacttct tcggatgtgt ttttaataat 300
gtcagctatg tgccccatcc tccttcatgc cctccctccc tttcctacca ctgctgagtg 360
gcctggaact tgtttaaagt gt 382

<210> 140
<211> 200
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(200)
<223> n = A,T,C or G

<400> 140
accaaanctt ctttctgttg tgttngattt tactataggg gtttngcttn ttctaaanat 60
acttttcatt taacanctt tgttaagtgt caggctgcac tttgctccat anaattattg 120
ttttcacatt tcaacttgta tgtgtttgtc tcttanagca ttggtgaaat cacatatttt 180
atattcagca taaaggagaa 200

<210> 141
<211> 335
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(335)
<223> n = A,T,C or G

<400> 141
actttatttt caaaacactc atatgttgca aaaaacacat agaaaaataa agtttggtgg 60
gggtgctgac taaacttcaa gtcacagact tttatgtgac agattggagc agggtttgtt 120
atgcatgtag agaacccaaa ctaatttatt aaacaggata gaaacaggct gtctgggtga 180
aatggttctg agaaccatcc aattcacctg tcagatgctg atanactagc tcttcagatg 240
tttttctacc agttcagaga tnggttaatg actanttcca atggggaaaa agcaagatgg 300
attcacaaac caagtaattt taaacaaaga cactt 335

<210> 142
<211> 459
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(459)
<223> n = A,T,C or G

<400> 142
accaggttaa tattgccaca tatatccttt ccaattgcgg gctaaacaga cgtgtattta 60
gggttgttta aagacaaccc agcttaatat caagagaaat tgtgaccttt catggagtat 120
ctgatggaga aaacactgag ttttgacaaa tcttatttta ttcagatagc agtctgatca 180
cacatggtcc aacaacactc aaataataaa tcaaatatna tcagatgtta aagattggtc 240
ttcaaacatc atagccaatg atgccccgct tgcctataat ctctccgaca taaaaccaca 300
tcaacacctc agtggccacc aaaccattca gcacagcttc cttaactgtg agctgtttga 360
agctaccagt ctgagcacta ttgactatnt ttttcangct ctgaatagct ctagggatct 420
cagcangggt gggaggaacc agctcaacct tggcgtant 459

<210> 143
<211> 140
<212> DNA
<213> Homo sapien

<400> 143
acatttcctt ccaccaagtc aggactcctg gcttctgtgg gagttcttat cacctgaggg 60
aaatccaaac agtctctcct agaaaggaat agtgtcacca accccaccca tctccctgag 120
accatccgac ttccctgtgt 140

<210> 144
<211> 164
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(164)
<223> n = A,T,C or G

<400> 144
acttcagtaa caacatacaa taacaacatt aagtgtatat tgccatcttt gtcattttct 60
atctatacca ctctcccttc tgaaaacaan aatcactanc caatcactta tacaaatttg 120
aggcaattaa tccatatttg ttttcaataa ggaaaaaaag atgt 164

<210> 145
<211> 303
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(303)
<223> n = A,T,C or G

<400> 145
acgtagacca tccaactttg tatttgtaat ggcaaacatc cagnagcaat tcctaaacaa 60
actggagggt atttataccc aattatccca ttcattaaca tgccctcctc ctcaggctat 120
gcaggacagc tatcataagt cggcccaggc atccagatac taccatttgt ataaacttca 180
gtaggggagt ccatccaagt gacaggtcta atcaaaggag gaaatggaac ataagcccag 240
tagtaaaatn ttgcttagct gaaacagcca caaaagactt accgccgtgg tgattaccat 300
caa 303

<210> 146
<211> 327
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(327)
<223> n = A,T,C or G

<400> 146
actgcagctc aattagaagt ggtctctgac tttcatcanc ttctccctgg gctccatgac 60
actggcctgg agtgactcat tgctctggtt ggttgagaga gctcctttgc caacaggcct 120
ccaagtcagg gctgggattt gtttcctttc cacattctag caacaatatg ctggccactt 180
cctgaacagg gagggtggga ggagccagca tggaacaagc tgccactttc taaagtagcc 240
agacttgccc ctgggcctgt cacacctact gatgaccttc tgtgcctgca ggatggaatg 300
taggggtgag ctgtgtgact ctatggt 327

<210> 147
<211> 173
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(173)
<223> n = A,T,C or G

<400> 147

```
acattgtttt tttgagataa agcattgana gagctctcct taacgtgaca caatggaagg      60
actggaacac atacccacat ctttgttctg agggataatt ttctgataaa gtcttgctgt     120
atattcaagc acatatgtta tatattattc agttccatgt ttatagccta gtt            173

      <210> 148
      <211> 477
      <212> DNA
      <213> Homo sapien

      <220>
      <221> misc_feature
      <222> (1)...(477)
      <223> n = A,T,C or G

      <400> 148
acaaccactt tatctcatcg aatttttaac ccaaactcac tcactgtgcc tttctatcct      60
atgggatata ttatttgatg ctccatttca tcacacatat atgaataata cactcatact     120
gccctactac ctgctgcaat aatcacattc ccttcctgtc ctgaccctga agccattggg     180
gtggtcctag tggccatcag tccangcctg caccttgagc ccttgagctc cattgctcac     240
nccancccac ctcaccgacc ccatcctctt acacagctac ctccttgctc tctaacccca     300
tagattatnt ccaaattcag tcaattaagt tactattaac actctacccg acatgtccag     360
caccactggt aagccttctc cagccaacac acacacacac acacncacac acacacatat     420
ccaggcacag gctacctcat cttcacaatc accccttttaa ttaccatgct atggtgg       477

      <210> 149
      <211> 207
      <212> DNA
      <213> Homo sapien

      <400> 149
acagttgtat tataatatca agaaataaac ttgcaatgag agcatttaag agggaagaac      60
taacgtattt tagagagcca aggaaggttt ctgtggggag tgggatgtaa ggtggggcct     120
gatgataaat aagagtcagc caggtaagtg ggtggtgtgg tatgggcaca gtgaagaaca     180
tttcaggcag agggaacagc agtgaaa                                         207

      <210> 150
      <211> 111
      <212> DNA
      <213> Homo sapien

      <220>
      <221> misc_feature
      <222> (1)...(111)
      <223> n = A,T,C or G

      <400> 150
accttgattt cattgctgct ctgatggaaa cccaactatc taatttagct aaaacatggg      60
cacttaaatg tggtcagtgt ttggacttgt taactantgg catctttggg t             111

      <210> 151
      <211> 196
      <212> DNA
      <213> Homo sapien

      <400> 151
agcgcggcag gtcatattga acattccaga tacctatcat tactcgatgc tgttgataac      60
agcaagatgg ctttgaactc agggtcacca ccagctattg gaccttacta tgaaaaccat     120
ggataccaac cggaaaaccc ctatcccgca cagcccactg tggtccccac tgtctacgag     180
```

gtgcatccgg ctcagt 196

<210> 152
<211> 132
<212> DNA
<213> Homo sapien

<400> 152
acagcacttt cacatgtaag aagggagaaa ttcctaaatg taggagaaag ataacagaac 60
cttccccttt tcatctagtg gtggaaacct gatgctttat gttgacagga atagaaccag 120
gagggagttt gt 132

<210> 153
<211> 285
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(285)
<223> n = A,T,C or G

<400> 153
acaanaccca nganaggcca ctggccgtgg tgtcatggcc tccaaacatg aaagtgtcag 60
cttctgctct tatgtcctca tctgacaact ctttaccatt tttatcctcg ctcagcagga 120
gcacatcaat aaagtccaaa gtcttggact tggccttggc ttggaggaag tcatcaacac 180
cctggctagt gagggtgcgg cgccgctcct ggatgacggc atctgtgaag tcgtgcacca 240
gtctgcaggc cctgtggaag cgccgtccac acggagtnag gaatt 285

<210> 154
<211> 333
<212> DNA
<213> Homo sapien

<400> 154
accacagtcc tgttgggcca gggcttcatg accctttctg tgaaaagcca tattatcacc 60
accccaaatt tttccttaaa tatctttaac tgaaggggtc agcctcttga ctgcaaagac 120
cctaagccgg ttacacagct aactcccact ggccctgatt tgtgaaattg ctgctgcctg 180
attggcacag gagtcgaagg tgttcagctc ccctcctccg tggaacgaga ctctgatttg 240
agtttcacaa attctcgggc cacctcgtca ttgctcctct gaaataaaat ccggagaatg 300
gtcaggcctg tctcatccat atggatcttc cgg 333

<210> 155
<211> 308
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(308)
<223> n = A,T,C or G

<400> 155
actggaaata ataaaaccca catcacagtg ttgtgtcaaa gatcatcagg gcatggatgg 60
gaaagtgctt tgggaactgt aaagtgccta acacatgatc gatgattttt gttataatat 120
ttgaatcacg gtgcatacaa actctcctgc ctgctcctcc tgggccccag ccccagcccc 180
atcacagctc actgctctgt tcatccaggc ccagcatgta gtggctgatt cttcttggct 240
gcttttagcc tccanaagtt tctctgaagc caaccaaacc tctangtgta aggcatgctg 300

gccctggt 308

<210> 156
<211> 295
<212> DNA
<213> Homo sapien

<400> 156
accttgctcg gtgcttggaa catattagga actcaaaata tgagatgata acagtgccta 60
ttattgatta ctgagagaac tgttagacat ttagttgaag attttctaca caggaactga 120
gaataggaga ttatgtttgg ccctcatatt ctctcctatc ctccttgcct cattctatgt 180
ctaatatatt ctcaatcaaa taaggttagc ataatcagga aatcgaccaa ataccaatat 240
aaaaccagat gtctatcctt aagattttca aatagaaaac aaattaacag actat 295

<210> 157
<211> 126
<212> DNA
<213> Homo sapien

<400> 157
acaagtttaa atagtgctgt cactgtgcat gtgctgaaat gtgaaatcca ccacatttct 60
gaagagcaaa acaaattctg tcatgtaatc tctatcttgg gtcgtgggta tatctgtccc 120
cttagt 126

<210> 158
<211> 442
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(442)
<223> n = A,T,C or G

<400> 158
acccactggt cttggaaaca cccatcctta atacgatgat ttttctgtcg tgtgaaaatg 60
aanccagcag gctgccccta gtcagtcctt ccttccagag aaaaagagat ttgagaaagt 120
gcctgggtaa ttcaccatta atttcctccc ccaaactctc tgagtcttcc cttaatattt 180
ctggtggttc tgaccaaagc aggtcatggt ttgttgagca tttgggatcc cagtgaagta 240
natgtttgta gccttgcata cttagccctt cccacgcaca aacggagtgg cagagtggtg 300
ccaaccctgt tttcccagtc cacgtagaca gattcacagt gcggaattct ggaagctgga 360
nacagacggg ctctttgcag agccgggact ctgagangga catgagggcc tctgcctctg 420
tgttcattct ctgatgtcct gt 442

<210> 159
<211> 498
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(498)
<223> n = A,T,C or G

<400> 159
acttccaggt aacgttgttg tttccgttga gcctgaactg atgggtgacg ttgtaggttc 60
tccaacaaga actgaggttg cagagcgggt agggaagagt gctgttccag ttgcacctgg 120
gctgctgtgg actgttgttg attcctcact acggcccaag gttgtggaac tggcanaaag 180

gtgtgttgtt gganttgagc tcgggcggct gtggtaggtt gtgggctctt caacaggggc 240
tgctgtggtg ccgggangtg aangtgttgt gtcacttgag cttggccagc tctggaaagt 300
antanattct tcctgaaggc cagcgcttgt ggagctggca ngggtcantg ttgtgtgtaa 360
cgaaccagtg ctgctgtggg tgggtgtana tcctccacaa agcctgaagt tatggtgtcn 420
tcaggtaana atgtggtttc agtgtccctg ggcngctgtg gaaggttgta nattgtcacc 480
aagggaataa gctgtggt 498

<210> 160
<211> 380
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(380)
<223> n = A,T,C or G

<400> 160
acctgcatcc agcttccctg ccaaactcac aaggagacat caacctctag acagggaaac 60
agcttcagga tacttccagg agacagagcc accagcagca aaacaaatat tcccatgcct 120
ggagcatggc atagaggaag ctganaaatg tggggtctga ggaagccatt tgagtctggc 180
cactagacat ctcatcagcc acttgtgtga agagatgccc catgacccca gatgcctctc 240
ccacccttac ctccatctca cacacttgag ctttccactc tgtataattc taacatcctg 300
gagaaaaatg gcagtttgac cgaacctgtt cacaacggta gaggctgatt tctaacgaaa 360
cttgtagaat gaagcctgga 380

<210> 161
<211> 114
<212> DNA
<213> Homo sapien

<400> 161
actccacatc cctctgagc aggcggttgt cgttcaaggt gtatttggcc ttgcctgtca 60
cactgtccac tggcccctta tccacttggt gcttaatccc tcgaaagagc atgt 114

<210> 162
<211> 177
<212> DNA
<213> Homo sapien

<400> 162
actttctgaa tcgaatcaaa tgatacttag tgtagtttta atatcctcat atatatcaaa 60
gttttactac tctgataatt ttgtaaacca ggtaaccaga acatccagtc atacagcttt 120
tggtgatata taacttggca ataacccagt ctggtgatac ataaaactac tcactgt 177

<210> 163
<211> 137
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(137)
<223> n = A,T,C or G

<400> 163
catttataca gacaggcgtg aagacattca cgacaaaaac gcgaaattct atcccgtgac 60
canagaaggc agctacggct actcctacat cctggcgtgg gtggccttcg cctgcacctt 120

catcagcggc atgatgt 137

<210> 164
<211> 469
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(469)
<223> n = A,T,C or G

<400> 164
cttatcacaa tgaatgttct cctgggcagc gttgtgatct ttgccacctt cgtgacttta 60
tgcaatgcat catgctattt catacctaat gagggagttc caggagattc aaccaggaaa 120
tgcatggatc tcaaaggaaa caaacaccca ataaactcgg agtggcagac tgacaactgt 180
gagacatgca cttgctacga aacagaaatt tcatgttgca cccttgtttc tacacctgtg 240
ggttatgaca aagacaactg ccaaagaatc ttcaagaagg aggactgcaa gtatatcgtg 300
gtggagaaga aggacccaaa aaagacctgt tctgtcagtg aatggataat ctaatgtgct 360
tctagtaggc acagggctcc caggccaggc ctcattctcc tctggcctct aatagtcaat 420
gattgtgtag ccatgcctat cagtaaaaag atntttgagc aaacacttt 469

<210> 165
<211> 195
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(195)
<223> n = A,T,C or G

<400> 165
acagtttttt atanatatcg acattgccgg cacttgtgtt cagtttcata aagctggtgg 60
atccgctgtc atccactatt ccttggctag agtaaaaatt attcttatag cccatgtccc 120
tgcaggccgc ccgcccgtag ttctcgttcc agtcgtcttg gcacacaggg tgccaggact 180
tcctctgaga tgagt 195

<210> 166
<211> 383
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(383)
<223> n = A,T,C or G

<400> 166
acatcttagt agtgtggcac atcagggggc catcagggtc acagtcactc atagcctcgc 60
cgaggtcgga gtccacacca ccggtgtagg tgtgctcaat cttgggcttg gcgcccacct 120
ttggagaagg gatatgctgc acacacatgt ccacaaagcc tgtgaactcg ccaaagaatt 180
tttgcagacc agcctgagca aggggcggat gttcagcttc agctcctcct tcgtcaggtg 240
gatgccaacc tcgtctangg tccgtgggaa gctggtgtcc acntcaccta caacctgggc 300
gangatctta taaagaggct ccnagataaa ctccacgaaa cttctctggg agctgctagt 360
nggggccttt ttggtgaact ttc 383

<210> 167

<211> 247
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(247)
<223> n = A,T,C or G

<400> 167
acagagccag accttggcca taaatgaanc agagattaag actaaacccc aagtcganat 60
tggagcagaa actggagcaa gaagtgggcc tggggctgaa gtagagacca aggccactgc 120
tatanccata cacagagcca actctcaggc caaggcnatg gttggggcag anccagagac 180
tcaatctgan tccaaagtgg tggctggaac actggtcatg acanaggcag tgactctgac 240
tgangtc 247

<210> 168
<211> 273
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(273)
<223> n = A,T,C or G

<400> 168
acttctaagt tttctagaag tggaaggatt gtantcatcc tgaaaatggg tttacttcaa 60
aatccctcan ccttgttctt cacnactgtc tatactgana gtgtcatgtt tccacaaagg 120
gctgacacct gagcctgnat tttcactcat ccctgagaag ccctttccag tagggtgggc 180
aattcccaac ttccttgcca caagcttccc aggctttctc ccctggaaaa ctccagcttg 240
agtcccagat acactcatgg gctgccctgg gca 273

<210> 169
<211> 431
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(431)
<223> n = A,T,C or G

<400> 169
acagccttgg cttccccaaa ctccacagtc tcagtgcaga aagatcatct tccagcagtc 60
agctcagacc agggtcaaag gatgtgacat caacagtttc tggtttcaga acaggttcta 120
ctactgtcaa atgacccccc atacttcctc aaaggctgtg gtaagttttg cacaggtgag 180
ggcagcagaa agggggtant tactgatgga caccatcttc tctgtatact ccacactgac 240
cttgccatgg gcaaaggccc ctaccacaaa aacaatagga tcactgctgg gcaccagctc 300
acgcacatca ctgacaaccg ggatggaaaa agaantgcca actttcatac atccaactgg 360
aaagtgatct gatactggat tcttaattac cttcaaaagc ttctgggggc catcagctgc 420
tcgaacactg a 431

<210> 170
<211> 266
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(266)
<223> n = A,T,C or G

<400> 170
acctgtgggc tgggctgtta tgcctgtgcc ggctgctgaa agggagttca gaggtggagc 60
tcaaggagct ctgcaggcat tttgccaanc ctctccanag canagggagc aacctacact 120
ccccgctaga aagacaccag attggagtcc tgggaggggg agttggggtg ggcatttgat 180
gtatacttgt cacctgaatg aangagccag agaggaanga gacgaanatg anattggcct 240
tcaaagctag ggtctggca ggtgga 266

<210> 171
<211> 1248
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(1248)
<223> n = A,T,C or G

<400> 171
ggcagccaaa tcataaacgg cgaggactgc agcccgcact cgcagccctg gcaggcggca 60
ctggtcatgg aaaacgaatt gttctgctcg ggcgtcctgg tgcatccgca gtgggtgctg 120
tcagccgcac actgtttcca gaagtgagtg cagagctcct acaccatcgg gctgggcctg 180
cacagtcttg aggccgacca agagccaggg agccagatgg tggaggccag cctctccgta 240
cggcacccag agtacaacag acccttgctc gctaacgacc tcatgctcat caagttggac 300
gaatccgtgt ccgagtctga caccatccgg agcatcagca ttgcttcgca gtgccctacc 360
gcggggaact cttgcctcgt ttctggctgg ggtctgctgg cgaacggcag aatgcctacc 420
gtgctgcagt gcgtgaacgt gtcggtggtg tctgaggagg tctgcagtaa gctctatgac 480
ccgctgtacc accccagcat gttctgcgcc ggcggagggc aagaccagaa ggactcctgc 540
aacggtgact ctgggggggcc cctgatctgc aacgggtact tgcagggcct tgtgtctttc 600
ggaaaagccc cgtgtggcca agttggcgtg ccaggtgtct acaccaacct ctgcaaattc 660
actgagtgga tagagaaaac cgtccaggcc agttaactct ggggactggg aacccatgaa 720
attgaccccc aaatacatcc tgcggaagga attcaggaat atctgttccc agcccctcct 780
ccctcaggcc caggagtcca ggcccccagc ccctcctccc tcaaaccaag ggtacagatc 840
cccagcccct cctccctcag acccaggagt ccagaccccc cagcccctcc tccctcagac 900
ccaggagtcc agcccctcct ccctcagacc caggagtcca gaccccccag cccctcctcc 960
ctcagaccca ggggtccagg cccccaaccc ctcctccctc agactcagag gtccaagccc 1020
ccaacccntc attccccaga cccagaggtc caggtcccag cccctcntcc ctcagaccca 1080
gcggtccaat gccacctaga ctntccctgt acacagtgcc ccttgtggc acgttgaccc 1140
aaccttacca gttggttttt catttttngt ccctttcccc tagatccaga aataaagttt 1200
aagagaagng caaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 1248

<210> 172
<211> 159
<212> PRT
<213> Homo sapien

<220>
<221> VARIANT
<222> (1)...(159)
<223> Xaa = Any Amino Acid

<400> 172
Met Val Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro
1 5 10 15

```
Leu Leu Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser
            20                  25                  30
Glu Ser Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr
        35                  40                  45
Ala Gly Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly
    50                  55                  60
Arg Met Pro Thr Val Leu Gln Cys Val Asn Val Ser Val Val Ser Glu
65                  70                  75                  80
Glu Val Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe
                85                  90                  95
Cys Ala Gly Gly Gly Gln Xaa Gln Xaa Asp Ser Cys Asn Gly Asp Ser
            100                 105                 110
Gly Gly Pro Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe
        115                 120                 125
Gly Lys Ala Pro Cys Gly Gln Val Gly Val Pro Gly Val Tyr Thr Asn
    130                 135                 140
Leu Cys Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Ala Ser
145                 150                 155
```

<210> 173
<211> 1265
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(1265)
<223> n = A,T,C or G

<400> 173

```
ggcagcccgc actcgcagcc ctggcaggcg gcactggtca tggaaaacga attgttctgc     60
tcgggcgtcc tggtgcatcc gcagtgggtg ctgtcagccg cacactgttt ccagaactcc    120
tacaccatcg ggctgggcct gcacagtctt gaggccgacc aagagccagg gagccagatg    180
gtggaggcca gcctctccgt acggcaccca gagtacaaca gacccttgct cgctaacgac    240
ctcatgctca tcaagttgga cgaatccgtg tccgagtctg acaccatccg gagcatcagc    300
attgcttcgc agtgccctac cgcggggaac tcttgcctcg tttctggctg gggtctgctg    360
gcgaacggtg agctcacggg tgtgtgtctg ccctcttcaa ggaggtcctc tgcccagtcg    420
cgggggctga cccagagctc tgcgtcccag gcagaatgcc taccgtgctg cagtgcgtga    480
acgtgtcggt ggtgtctgag gaggtctgca gtaagctcta tgacccgctg taccacccca    540
gcatgttctg cgccggcgga gggcaagacc agaaggactc ctgcaacggt gactctgggg    600
ggcccctgat ctgcaacggg tacttgcagg gccttgtgtc tttcggaaaa gccccgtgtg    660
gccaagttgg cgtgccaggt gtctacacca acctctgcaa attcactgag tggatagaga    720
aaaccgtcca ggccagttaa ctctggggac tgggaaccca tgaaattgac cccaaatac     780
atcctgcgga aggaattcag gaatatctgt tcccagcccc tcctccctca ggcccaggag    840
tccaggcccc cagcccctcc tccctcaaac caagggtaca gatccccagc ccctcctccc    900
tcagacccag gagtccagac cccccagccc ctcctccctc agacccagga gtccagcccc    960
tcctccntca gacccaggag tccagacccc ccagcccctc ctccctcaga cccaggggtt   1020
gaggccccca acccctcctc cttcagagtc agaggtccaa gcccccaacc cctcgttccc   1080
cagacccaga ggtnnaggtc ccagcccctc ttccntcaga cccagnggtc caatgccacc   1140
tagattttcc ctgnacacag tgcccccttg tggnangttg acccaacctt accagttggt   1200
ttttcatttt tngtcccttt cccctagatc cagaaataaa gtttaagaga ngngcaaaaa   1260
aaaaa                                                                1265
```

<210> 174
<211> 1459
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(1459)
<223> n = A,T,C or G

<400> 174
```
ggtcagccgc acactgtttc cagaagtgag tgcagagctc ctacaccatc gggctgggcc     60
tgcacagtct tgaggccgac caagagccag ggagccagat ggtggaggcc agcctctccg    120
tacggcaccc agagtacaac agacccttgc tcgctaacga cctcatgctc atcaagttgg    180
acgaatccgt gtccgagtct gacaccatcc ggagcatcag cattgcttcg cagtgcccta    240
ccgcggggaa ctcttgcctc gtttctggct ggggtctgct ggcgaacggt gagctcacgg    300
gtgtgtgtct gccctcttca aggaggtcct ctgcccagtc gcgggggctg acccagagct    360
ctgcgtccca ggcagaatgc ctaccgtgct gcagtgcgtg aacgtgtcgg tggtgtctga    420
ngaggtctgc antaagctct atgacccgct gtaccacccc ancatgttct gcgccggcgg    480
agggcaagac cagaaggact cctgcaacgt gagagagggg aaaggggagg gcaggcgact    540
cagggaaggg tggagaaggg ggagacagag acacacaggg ccgcatggcg agatgcagag    600
atggagagac acacagggag acagtgacaa ctagagagag aaactgagag aaacagagaa    660
ataaacacag gaataaagag aagcaaagga agagagaaac agaaacagac atggggaggc    720
agaaacacac acacatagaa atgcagttga ccttccaaca gcatggggcc tgagggcggt    780
gacctccacc caatagaaaa tcctcttata acttttgact ccccaaaaac ctgactagaa    840
atagcctact gttgacgggg agccttacca ataacataaa tagtcgattt atgcatacgt    900
tttatgcatt catgatatac ctttgttgga atttttttgat atttctaagc tacacagttc    960
gtctgtgaat ttttttaaat tgttgcaact ctcctaaaat ttttctgatg tgtttattga   1020
aaaaatccaa gtataagtgg acttgtgcat tcaaaccagg gttgttcaag ggtcaactgt   1080
gtacccagag ggaaacagtg acacagattc atagaggtga aacacgaaga gaaacaggaa   1140
aaatcaagac tctacaaaga ggctgggcag ggtggctcat gcctgtaatc ccagcacttt   1200
gggaggcgag gcaggcagat cacttgaggt aaggagttca agaccagcct ggccaaaatg   1260
gtgaaatcct gtctgtacta aaaatacaaa agttagctgg atatggtggc aggcgcctgt   1320
aatcccagct acttgggagg ctgaggcagg agaattgctt gaatatggga ggcagaggtt   1380
gaagtgagtt gagatcacac cactatactc cagctggggc aacagagtaa gactctgtct   1440
caaaaaaaaa aaaaaaaaa                                                1459
```

<210> 175
<211> 1167
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(1167)
<223> n = A,T,C or G

<400> 175
```
gcgcagccct ggcaggcggc actggtcatg gaaaacgaat tgttctgctc gggcgtcctg     60
gtgcatccgc agtgggtgct gtcagccgca cactgtttcc agaactccta caccatcggg    120
ctgggcctgc acagtcttga ggccgaccaa gagccaggga gccagatggt ggaggccagc    180
ctctccgtac ggcacccaga gtacaacaga ctcttgctcg ctaacgacct catgctcatc    240
aagttggacg aatccgtgtc cgagtctgac accatccgga gcatcagcat tgcttcgcag    300
tgccctaccg cggggaactc ttgcctcgtn tctggctggg gtctgctggc gaacggcaga    360
atgcctaccg tgctgcactg cgtgaacgtg tcggtggtgt ctgaggangt ctgcagtaag    420
ctctatgacc cgctgtacca ccccagcatg ttctgcgccg gcggagggca agaccagaag    480
gactcctgca acggtgactc tgggggggccc ctgatctgca acgggtactt gcagggcctt    540
gtgtctttcg gaaaagcccc gtgtggccaa cttggcgtgc caggtgtcta caccaacctc    600
tgcaaattca ctgagtggat agagaaaacc gtccagncca gttaactctg gggactggga    660
acccatgaaa ttgaccccca aatacatcct gcggaangaa ttcaggaata tctgttccca    720
gcccctcctc cctcaggccc aggagtccag gcccccagcc cctcctccct caaaccaagg    780
gtacagatcc ccagcccctc ctccctcaga cccaggagtc cagacccccc agcccctcnt    840
ccntcagacc caggagtcca gcccctcctc cntcagacgc aggagtccag accccccagc    900
```

```
ccntcntccg tcagacccag gggtgcaggc ccccaacccc tcntccntca gagtcagagg    960
tccaagcccc caacccctcg ttccccagac ccagaggtnc aggtcccagc ccctcctccc   1020
tcagacccag cggtccaatg ccacctagan tntccctgta cacagtgccc ccttgtggca   1080
ngttgaccca accttaccag ttggttttc atttttgtc cctttcccct agatccagaa     1140
ataaagtnta agagaagcgc aaaaaaa                                         1167

<210> 176
<211> 205
<212> PRT
<213> Homo sapien

<220>
<221> VARIANT
<222> (1)...(205)
<223> Xaa = Any Amino Acid

<400> 176
Met Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln Trp
 1               5                   10                  15
Val Leu Ser Ala Ala His Cys Phe Gln Asn Ser Tyr Thr Ile Gly Leu
            20                  25                  30
Gly Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met Val
        35                  40                  45
Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Leu Leu Leu
    50                  55                  60
Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu Ser
65                  70                  75                  80
Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala Gly
                85                  90                  95
Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly Arg Met
            100                 105                 110
Pro Thr Val Leu His Cys Val Asn Val Ser Val Val Ser Glu Xaa Val
        115                 120                 125
Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe Cys Ala
    130                 135                 140
Gly Gly Gly Gln Asp Gln Lys Asp Ser Cys Asn Gly Asp Ser Gly Gly
145                 150                 155                 160
Pro Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe Gly Lys
                165                 170                 175
Ala Pro Cys Gly Gln Leu Gly Val Pro Gly Val Tyr Thr Asn Leu Cys
            180                 185                 190
Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Xaa Ser
        195                 200                 205

<210> 177
<211> 1119
<212> DNA
<213> Homo sapien

<400> 177
gcgcactcgc agccctggca ggcggcactg gtcatggaaa acgaattgtt ctgctcgggc     60
gtcctggtgc atccgcagtg ggtgctgtca gccgcacact gtttccagaa ctcctacacc    120
atcgggctgg gcctgcacag tcttgaggcc gaccaagagc cagggagcca gatggtggag    180
gccagcctct ccgtacggca cccagagtac aacagaccct tgctcgctaa cgacctcatg    240
ctcatcaagt tggacgaatc cgtgtccgag tctgacacca tccggagcat cagcattgct    300
tcgcagtgcc ctaccgcggg gaactcttgc ctcgtttctg gctggggtct gctggcgaac    360
gatgctgtga ttgccatcca gtcccagact gtgggaggct gggagtgtga gaagctttcc    420
caaccctggc agggttgtac catttcggca acttccagtg caaggacgtc ctgctgcatc    480
```

```
ctcactgggt gctcactact gctcactgca tcacccggaa cactgtgatc aactagccag      540
caccatagtt ctccgaagtc agactatcat gattactgtg ttgactgtgc tgtctattgt      600
actaaccatg ccgatgttta ggtgaaatta gcgtcacttg gcctcaacca tcttggtatc      660
cagttatcct cactgaattg agatttcctg cttcagtgtc agccattccc acataatttc      720
tgacctacag aggtgaggga tcatatagct cttcaaggat gctggtactc ccctcacaaa      780
ttcatttctc ctgttgtagt gaaaggtgcg ccctctggag cctcccaggg tgggtgtgca      840
ggtcacaatg atgaatgtat gatcgtgttc ccattaccca aagcctttaa atccctcatg      900
ctcagtacac cagggcaggt ctagcatttc ttcatttagt gtatgctgtc cattcatgca      960
accacctcag gactcctgga ttctctgcct agttgagctc ctgcatgctg cctccttggg     1020
gaggtgaggg agagggccca tggttcaatg ggatctgtgc agttgtaaca cattaggtgc     1080
ttaataaaca gaagctgtga tgttaaaaaa aaaaaaaaa                            1119
```

<210> 178
<211> 164
<212> PRT
<213> Homo sapien

<220>
<221> VARIANT
<222> (1)...(164)
<223> Xaa = Any Amino Acid

<400> 178

```
Met Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln Trp
 1               5                  10                  15
Val Leu Ser Ala Ala His Cys Phe Gln Asn Ser Tyr Thr Ile Gly Leu
            20                  25                  30
Gly Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met Val
        35                  40                  45
Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro Leu Leu
    50                  55                  60
Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu Ser
65                  70                  75                  80
Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala Gly
                85                  90                  95
Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Asp Ala Val
            100                 105                 110
Ile Ala Ile Gln Ser Xaa Thr Val Gly Gly Trp Glu Cys Glu Lys Leu
        115                 120                 125
Ser Gln Pro Trp Gln Gly Cys Thr Ile Ser Ala Thr Ser Ser Ala Arg
    130                 135                 140
Thr Ser Cys Cys Ile Leu Thr Gly Cys Ser Leu Leu Leu Thr Ala Ser
145                 150                 155                 160
Pro Gly Thr Leu
```

<210> 179
<211> 250
<212> DNA
<213> Homo sapien

<400> 179

```
ctggagtgcc ttggtgtttc aagcccctgc aggaagcaga atgcaccttc tgaggcacct       60
ccagctgccc ccggccgggg gatgcgaggc tcggagcacc cttgcccggc tgtgattgct      120
gccaggcact gttcatctca gcttttctgt ccctttgctc ccggcaagcg cttctgctga      180
aagttcatat ctggagcctg atgtcttaac gaataaaggt cccatgctcc acccgaaaaa      240
aaaaaaaaaa                                                            250
```

<210> 180
<211> 202
<212> DNA
<213> Homo sapien

<400> 180
actagtccag tgtggtggaa ttccattgtg ttgggcccaa cacaatggct acctttaaca 60
tcacccagac cccgcccctg cccgtgcccc acgctgctgc taacgacagt atgatgctta 120
ctctgctact cggaaactat ttttatgtaa ttaatgtatg ctttcttgtt tataaatgcc 180
tgatttaaaa aaaaaaaaaa aa 202

<210> 181
<211> 558
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(558)
<223> n = A,T,C or G

<400> 181
tccytttgkt naggtttkkg agacamccck agacctwaan ctgtgtcaca gacttcyngg 60
aatgtttagg cagtgctagt aatttcytcg taatgattct gttattactt tcctnattct 120
ttattcctct ttcttctgaa gattaatgaa gttgaaaatt gaggtggata aatacaaaaa 180
ggtagtgtga tagtataagt atctaagtgc agatgaaagt gtgttatata tatccattca 240
aaattatgca agttagtaat tactcagggt taactaaatt actttaatat gctgttgaac 300
ctactctgtt ccttggctag aaaaaattat aaacaggact ttgttagttt gggaagccaa 360
attgataata ttctatgttc taaaagttgg gctatacata aattattaag aaatatggaw 420
ttttattccc aggaatatgg kgttcatttt atgaatatta cscrggatag awgtwtgagt 480
aaaaycagtt ttggtwaata ygtwaatatg tcmtaaataa acaakgcttt gacttatttc 540
caaaaaaaaa aaaaaaaa 558

<210> 182
<211> 479
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(479)
<223> n = A,T,C or G

<400> 182
acagggwttk grggatgcta agsccccrga rwtygtttga tccaacccctg gcttwttttc 60
agaggggaaa atggggccta gaagttacag mscatytagy tggtgcgmtg gcacccctgg 120
cstcacacag astcccgagt agctgggact acaggcacac agtcactgaa gcaggccctg 180
ttwgcaattc acgttgccac ctccaactta aacattcttc atatgtgatg tccttagtca 240
ctaaggttaa actttcccac ccagaaaagg caacttagat aaaatcttag agtactttca 300
tactmttcta agtcctcttc cagcctcact kkgagtcctm cytgggggtt gataggaant 360
ntctcttggc tttctcaata aartctctat ycatctcatg tttaatttgg tacgcatara 420
awtgstgara aaattaaaat gttctggtty mactttaaaa araaaaaaaa aaaaaaaaa 479

<210> 183
<211> 384
<212> DNA
<213> Homo sapien

<400> 183
aggcgggagc agaagctaaa gccaaagccc aagaagagtg gcagtgccag cactggtgcc 60
agtaccagta ccaataacag tgccagtgcc agtgccagca ccagtggtgg cttcagtgct 120
ggtgccagcc tgaccgccac tctcacattt gggctcttcg ctggccttgg tggagctggt 180
gccagcacca gtggcagctc tggtgcctgt ggtttctcct acaagtgaga ttttagatat 240
tgttaatcct gccagtcttt ctcttcaagc cagggtgcat cctcagaaac ctactcaaca 300
cagcactcta ggcagccact atcaatcaat tgaagttgac actctgcatt aratctattt 360
gccatttcaa aaaaaaaaaa aaaa 384

<210> 184
<211> 496
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(496)
<223> n = A,T,C or G

<400> 184
accgaattgg gaccgctggc ttataagcga tcatgtyynt ccrgtatkac ctcaacgagc 60
agggagatcg agtctatacg ctgaagaaat ttgacccgat gggacaacag acctgctcag 120
cccatcctgc tcggttctcc ccagatgaca aatactctsg acaccgaatc accatcaaga 180
aacgcttcaa ggtgctcatg acccagcaac cgcgccctgt cctctgaggg tcccttaaac 240
tgatgtcttt tctgccacct gttacccctc ggagactccg taaccaaact cttcggactg 300
tgagccctga tgccttttg ccagccatac tctttggcat ccagtctctc gtggcgattg 360
attatgcttg tgtgaggcaa tcatggtggc atcacccata aagggaacac atttgacttt 420
tttttctcat atttaaatt actacmagaw tattwmagaw waaatgawtt gaaaaactst 480
taaaaaaaaa aaaaaa 496

<210> 185
<211> 384
<212> DNA
<213> Homo sapien

<400> 185
gctggtagcc tatggcgkgg cccacggagg ggctcctgag gccacggrac agtgacttcc 60
caagtatcyt gcgcsgcgtc ttctaccgtc cctacctgca gatcttcggg cagattcccc 120
aggaggacat ggacgtggcc ctcatggagc acagcaactg ytcgtcggag cccggcttct 180
gggcacaccc tcctgggggcc caggcgggca cctgcgtctc ccagtatgcc aactggctgg 240
tggtgctgct cctcgtcatc ttcctgctcg tggccaacat cctgctggtc aacttgctca 300
ttgccatgtt cagttacaca ttcggcaaag tacagggcaa cagcgatctc tactgggaag 360
gcgcagcgtt accgcctcat ccgg 384

<210> 186
<211> 577
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(577)
<223> n = A,T,C or G

<400> 186
gagttagctc ctccacaacc ttgatgaggt cgtctgcagt ggcctctcgc ttcataccgc 60
tnccatcgtc atactgtagg tttgccacca cytcctggca tcttggggcg gcntaatatt 120
ccaggaaact ctcaatcaag tcaccgtcga tgaaacctgt gggctggttc tgtcttccgc 180

```
tcggtgtgaa aggatctccc agaaggagtg ctcgatcttc cccacacttt tgatgacttt     240
attgagtcga ttctgcatgt ccagcaggag gttgtaccag ctctctgaca gtgaggtcac     300
cagccctatc atgccgttga mcgtgccgaa garcaccgag ccttgtgtgg gggkkgaagt     360
ctcacccaga ttctgcatta ccagagagcc gtggcaaaag acattgacaa actcgcccag     420
gtggaaaaag amcamctcct ggargtgctn gccgctcctc gtcmgttggt ggcagcgctw     480
tcctttgac acacaaacaa gttaaaggca ttttcagccc ccagaaantt gtcatcatcc     540
aagatntcgc acagcactna tccagttggg attaaat                              577
```

```
<210> 187
<211> 534
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(534)
<223> n = A,T,C or G

<400> 187
aacatcttcc tgtataatgc tgtgtaatat cgatccgatn ttgtctgstg agaatycatw      60
actkggaaaa gmaacattaa agcctggaca ctggtattaa aattcacaat atgcaacact     120
ttaaacagtg tgtcaatctg ctcccyynac tttgtcatca ccagtctggg aakaagggta     180
tgccctattc acacctgtta aaagggcgct aagcattttt gattcaacat cttttttttt     240
gacacaagtc cgaaaaaagc aaaagtaaac agttatyaat ttgttagcca attcactttc     300
ttcatgggac agagccatyt gatttaaaaa gcaaattgca taatattgag cttygggagc     360
tgatatttga gcggaagagt agcctttcta cttcaccaga cacaactccc tttcatattg     420
ggatgttnac naaagtwatg tctctwacag atgggatgct tttgtggcaa ttctgttctg     480
aggatctccc agtttattta ccacttgcac aagaaggcgt tttcttcctc aggc           534
```

```
<210> 188
<211> 761
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(761)
<223> n = A,T,C or G

<400> 188
agaaaccagt atctctnaaa acaacctctc ataccttgtg gacctaattt tgtgtgcgtg      60
tgtgtgtgcg cgcatattat atagacaggc acatcttttt tacttttgta aaagcttatg     120
cctctttggt atctatatct gtgaaagttt taatgatctg ccataatgtc ttggggacct     180
ttgtcttctg tgtaaatggt actagagaaa acacctatnt tatgagtcaa tctagttngt     240
tttattcgac atgaaggaaa tttccagatn acaacactna caaactctcc ctkgackarg     300
ggggacaaag aaaagcaaaa ctgamcataa raaacaatwa cctggtgaga arttgcataa     360
acagaaatwr ggtagtatat tgaarnacag catcattaaa rmgttwtktt wttctccctt     420
gcaaaaaaca tgtacngact tcccgttgag taatgccaag ttgttttttt tatnataaaa     480
cttgcccttc attacatgtt tnaaagtggt gtggtgggcc aaaatattga aatgatggaa     540
ctgactgata aagctgtaca aataagcagt gtgcctaaca agcaacacag taatgttgac     600
atgcttaatt cacaaatgct aatttcatta taaatgtttg ctaaaataca ctttgaacta     660
tttttctgtn ttcccagagc tgagatntta gattttatgt agtatnaagt gaaaaantac     720
gaaaataata acattgaaga aaaananaaa aaanaaaaaa a                         761
```

```
<210> 189
<211> 482
<212> DNA
<213> Homo sapien
```

<220>
<221> misc_feature
<222> (1)...(482)
<223> n = A,T,C or G

<400> 189
```
ttttttttt tttgccgatn ctactatttt attgcaggan gtgggggtgt atgcaccgca      60
caccggggct atnagaagca agaaggaagg agggagggca cagccccttg ctgagcaaca    120
aagccgcctg ctgccttctc tgtctgtctc ctggtgcagg cacatgggga gaccttcccc    180
aaggcagggg ccaccagtcc aggggtggga atacaggggg tgggangtgt gcataagaag    240
tgataggcac aggccacccg gtacagaccc ctcggctcct gacaggtnga tttcgaccag    300
gtcattgtgc cctgcccagg cacagcgtan atctggaaaa gacagaatgc tttccttttc    360
aaatttggct ngtcatngaa ngggcanttt tccaanttng gctnggtctt ggtacncttg    420
gttcggccca gctccncgtc caaaaantat tcacccnnct ccnaattgct tgcnggnccc    480
cc                                                                   482
```

<210> 190
<211> 471
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(471)
<223> n = A,T,C or G

<400> 190
```
ttttttttt ttttaaaaca gtttttcaca acaaaattta ttagaagaat agtggttttg      60
aaaactctcg catccagtga gaactaccat acaccacatt acagctngga atgtnctcca    120
aatgtctggt caaatgatac aatggaacca ttcaatctta cacatgcacg aaagaacaag    180
cgcttttgac atacaatgca caaaaaaaaa aggggggggg gaccacatgg attaaaattt    240
taagtactca tcacatacat taagacacag ttctagtcca gtcnaaaatc agaactgcnt    300
tgaaaaattt catgtatgca atccaaccaa agaacttnat tggtgatcat gantnctcta    360
ctacatcnac cttgatcatt gccaggaacn aaaagttnaa ancacncngt acaaaaanaa    420
tctgtaattn anttcaacct ccgtacngaa aaatnttnnt tatacactcc c             471
```

<210> 191
<211> 402
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(402)
<223> n = A,T,C or G

<400> 191
```
gagggattga aggtctgttc tastgtcggm ctgttcagcc accaactcta acaagttgct      60
gtcttccact cactgtctgt aagcttttta acccagacwg tatcttcata aatagaacaa    120
attcttcacc agtcacatct tctaggacct ttttggattc agttagtata agctcttcca    180
cttcctttgt taagacttca tctggtaaag tcttaagttt tgtagaaagg aattyaattg    240
ctcgttctct aacaatgtcc tctccttgaa gtatttggct gaacaaccca cctaaagtcc    300
ctttgtgcat ccattttaaa tatacttaat agggcattgk tncactaggt taaattctgc    360
aagagtcatc tgtctgcaaa agttgcgtta gtatatctgc ca                       402
```

<210> 192
<211> 601

<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(601)
<223> n = A,T,C or G

<400> 192
gagctcggat ccaataatct ttgtctgagg gcagcacaca tatncagtgc catggnaact 60
ggtctacccc acatgggagc agcatgccgt agntatataa ggtcattccc tgagtcagac 120
atgcytyttt gaytaccgtg tgccaagtgc tggtgattct yaacacacyt ccatcccgyt 180
cttttgtgga aaaactggca cttktctgga actagcarga catcacttac aaattcaccc 240
acgagacact tgaaaggtgt aacaaagcga ytcttgcatt gctttttgtc cctccggcac 300
cagttgtcaa tactaacccg ctggtttgcc tccatcacat ttgtgatctg tagctctgga 360
tacatctcct gacagtactg aagaacttct tcttttgttt caaaagcarc tcttggtgcc 420
tgttggatca ggttcccatt tcccagtcyg aatgttcaca tggcatattt wacttcccac 480
aaaacattgc gatttgaggc tcagcaacag caaatcctgt tccggcattg gctgcaagag 540
cctcgatgta gccggccagc gccaaggcag gcgccgtgag ccccaccagc agcagaagca 600
g 601

<210> 193
<211> 608
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(608)
<223> n = A,T,C or G

<400> 193
atacagccca natcccacca cgaagatgcg cttgttgact gagaacctga tgcggtcact 60
ggtcccgctg tagccccagc gactctccac ctgctggaag cggttgatgc tgcactcytt 120
cccaacgcag gcagmagcgg gsccggtcaa tgaactccay tcgtggcttg gggtkgacgg 180
tkaagtgcag gaagaggctg accacctcgc ggtccaccag gatgcccgac tgtgcgggac 240
ctgcagcgaa actcctcgat ggtcatgagc gggaagcgaa tgaggcccag ggccttgccc 300
agaaccttcc gcctgttctc tggcgtcacc tgcagctgct gccgctgaca ctcggcctcg 360
gaccagcgga caaacggcrt tgaacagccg cacctcacgg atgcccagtg tgtcgcgctc 420
caggammgsc accagcgtgt ccaggtcaat gtcggtgaag ccctccgcgg gtratggcgt 480
ctgcagtgtt tttgtcgatg ttctccaggc acaggctggc cagctgcggt tcatcgaaga 540
gtcgcgcctg cgtgagcagc atgaaggcgt tgtcggctcg cagttcttct tcaggaactc 600
cacgcaat 608

<210> 194
<211> 392
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(392)
<223> n = A,T,C or G

<400> 194
gaacggctgg accttgcctc gcattgtgct tgctggcagg gaataccttg gcaagcagyt 60
ccagtccgag cagccccaga ccgctgccgc ccgaagctaa gcctgcctct ggccttcccc 120
tccgcctcaa tgcagaacca gtagtgggag cactgtgttt agagttaaga gtgaacactg 180

```
tttgatttta cttgggaatt tcctctgtta tatagctttt cccaatgcta atttccaaac     240
aacaacaaca aaataacatg tttgcctgtt aagttgtata aaagtaggtg attctgtatt     300
taaagaaaat attactgtta catatactgc ttgcaatttc tgtatttatt gktnctstgg     360
aaataaatat agttattaaa ggttgtcant cc                                   392

      <210> 195
      <211> 502
      <212> DNA
      <213> Homo sapien

      <220>
      <221> misc_feature
      <222> (1)...(502)
      <223> n = A,T,C or G

      <400> 195
ccsttkgagg ggtkaggkyc cagttyccga gtggaagaaa caggccagga gaagtgcgtg      60
ccgagctgag gcagatgttc ccacagtgac cccagagcc stgggstata gtytctgacc      120
cctcncaagg aaagaccacs ttctggggac atgggctgga gggcaggacc tagaggcacc     180
aagggaaggc cccattccgg ggstgttccc cgaggaggaa gggaaggggc tctgtgtgcc     240
ccccasgagg aagaggccct gagtcctggg atcagacacc ccttcacgtg tatccccaca     300
caaatgcaag ctcaccaagg tcccctctca gtccccttcc stacaccctg amcggccact     360
gscscacacc cacccagagc acgccacccg ccatggggar tgtgctcaag gartcgcngg     420
gcarcgtgga catctngtcc cagaaggggg cagaatctcc aatagangga ctgarcmstt     480
gctnanaaaa aaaaanaaaa aa                                              502

      <210> 196
      <211> 665
      <212> DNA
      <213> Homo sapien

      <220>
      <221> misc_feature
      <222> (1)...(665)
      <223> n = A,T,C or G

      <400> 196
ggttacttgg tttcattgcc accacttagt ggatgtcatt tagaaccatt ttgtctgctc      60
cctctggaag ccttgcgcag agcggacttt gtaattgttg gagaataact gctgaatttt     120
wagctgtttk gagttgatts gcaccactgc acccacaact tcaatatgaa aacyawttga     180
actwatttat tatcttgtga aaagtataac aatgaaaatt ttgttcatac tgtattkatc     240
aagtatgatg aaaagcaawa gatatatatt cttttattat gttaaattat gattgccatt     300
attaatcggc aaaatgtgga gtgtatgttc ttttcacagt aatatatgcc ttttgtaact     360
tcacttggtt attttattgt aaatgartta caaaattctt aatttaagar aatggtatgt     420
watatttatt tcattaattt ctttcctkgt ttacgtwaat tttgaaaaga wtgcatgatt     480
tcttgacaga aatcgatctt gatgctgtgg aagtagtttg acccacatcc ctatgagttt     540
ttcttagaat gtataaaggt tgtagcccat cnaacttcaa agaaaaaaat gaccacatac     600
tttgcaatca ggctgaaatg tggcatgctn ttctaattcc aactttataa actagcaaan     660
aagtg                                                                 665

      <210> 197
      <211> 492
      <212> DNA
      <213> Homo sapien

      <220>
      <221> misc_feature
      <222> (1)...(492)
```

<223> n = A,T,C or G

<400> 197
```
ttttnttttt ttttttttgc aggaaggatt ccatttattg tggatgcatt ttcacaatat     60
atgtttattg gagcgatcca ttatcagtga aaagtatcaa gtgtttataa natttttagg    120
aaggcagatt cacagaacat gctngtcngc ttgcagtttt acctcgtana gatnacagag    180
aattatagtc naaccagtaa acnaggaatt tacttttcaa aagattaaat ccaaactgaa    240
caaaattcta ccctgaaact tactccatcc aaatattgga ataanagtca gcagtgatac    300
attctcttct gaactttaga ttttctagaa aaatatgtaa tagtgatcag gaagagctct    360
tgttcaaaag tacaacnaag caatgttccc ttaccatagg ccttaattca aactttgatc    420
catttcactc ccatcacggg agtcaatgct acctgggaca cttgtatttt gttcatnctg    480
ancntggctt aa                                                         492
```

<210> 198
<211> 478
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(478)
<223> n = A,T,C or G

<400> 198
```
tttnttttgn atttcantct gtannaanta ttttcattat gtttattana aaaatatnaa     60
tgtntccacn acaaatcatn ttacntnagt aagaggccan ctacattgta caacatacac    120
tgagtatatt ttgaaaagga caagtttaaa gtanacncat attgccganc atancacatt    180
tatacatggc ttgattgata tttagcacag canaaactga gtgagttacc agaaanaaat    240
natatatgtc aatcngattt aagatacaaa acagatccta tggtacatan catcntgtag    300
gagttgtggc tttatgttta ctgaaagtca atgcagttcc tgtacaaaga gatggccgta    360
agcattctag tacctctact ccatggttaa gaatcgtaca cttatgttta catatgtnca    420
gggtaagaat tgtgttaagt naanttatgg agaggtccan gagaaaaatt tgatncaa      478
```

<210> 199
<211> 482
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(482)
<223> n = A,T,C or G

<400> 199
```
agtgacttgt cctccaacaa aacccсttga tcaagtttgt ggcactgaca atcagaccta     60
tgctagttcc tgtcatctat tcgctactaa atgcagactg gaggggacca aaaaggggca    120
tcaactccag ctggattatt ttggagcctg caaatctatt cctacttgta cggactttga    180
agtgattcag tttcctctac ggatgagaga ctggctcaag aatatcctca tgcagcttta    240
tgaagccnac tctgaacacg ctggttatct nagatgagaa ncagagaaat aaagtcnaga    300
aaatttacct ggangaaaag aggctttngg ctggggacca tcccattgaa ccttctctta    360
anggacttta agaanaaact accacatgtn tgtngtatcc tggtgccngg ccgtttantg    420
aacntngacn ncacccttnt ggaatanant cttgacngcn tcctgaactt gctcctctgc    480
ga                                                                    482
```

<210> 200
<211> 270
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(270)
<223> n = A,T,C or G

<400> 200
cggccgcaag tgcaactcca gctggggccg tgcggacgaa gattctgcca gcagttggtc 60
cgactgcgac gacggcggcg gcgacagtcg caggtgcagc gcgggcgcct ggggtcttgc 120
aaggctgagc tgacgccgca gaggtcgtgt cacgtcccac gaccttgacg ccgtcgggga 180
cagccggaac agagcccggt gaangcggga ggcctcgggg agcccctcgg gaagggcggc 240
ccgagagata cgcaggtgca ggtggccgcc 270

<210> 201
<211> 419
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(419)
<223> n = A,T,C or G

<400> 201
tttttttttt ttttggaatc tactgcgagc acagcaggtc agcaacaagt ttattttgca 60
gctagcaagg taacagggta gggcatggtt acatgttcag gtcaacttcc tttgtcgtgg 120
ttgattggtt tgtctttatg gggcggggt ggggtagggg aaancgaagc anaantaaca 180
tggagtgggt gcaccctccc tgtagaacct ggttacnaaa gcttggggca gttcacctgg 240
tctgtgaccg tcattttctt gacatcaatg ttattagaag tcaggatatc ttttagagag 300
tccactgtnt ctggagggag attagggttt cttgccaana tccaancaaa atccacntga 360
aaaagttgga tgatncangt acngaatacc ganggcatan ttctcatant cggtggcca 419

<210> 202
<211> 509
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(509)
<223> n = A,T,C or G

<400> 202
tttntttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 60
tggcacttaa tccattttta tttcaaaatg tctacaaant ttnaatncnc cattatacng 120
gtnattttnc aaaatctaaa nnttattcaa atntnagcca aantccttac ncaaatnnaa 180
tacncncaaa aatcaaaaat atacntntct ttcagcaaac ttngttacat aaattaaaaa 240
aatatatacg gctggtgttt tcaaagtaca attatcttaa cactgcaaac atntttnnaa 300
ggaactaaaa taaaaaaaaa cactnccgca aaggttaaag ggaacaacaa attcntttta 360
caacancnnc nattataaaa atcatatctc aaatcttagg ggaatatata cttcacacng 420
ggatcttaac ttttactnca ctttgtttat ttttttanaa ccattgtntt gggcccaaca 480
caatggnaat nccnccncnc tggactagt 509

<210> 203
<211> 583
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(583)
<223> n = A,T,C or G

<400> 203
```
ttttttttt tttttttga ccccctctt ataaaaaca agttaccatt ttattttact 60
tacacatatt tattttataa ttggtattag atattcaaaa ggcagctttt aaaatcaaac 120
taaatggaaa ctgccttaga tacataattc ttaggaatta gcttaaaatc tgcctaaagt 180
gaaaatcttc tctagctctt ttgactgtaa atttttgact cttgtaaaac atccaaattc 240
atttttcttg tctttaaaat tatctaatct ttccattttt tccctattcc aagtcaattt 300
gcttctctag cctcatttcc tagctcttat ctactattag taagtggctt ttttcctaaa 360
agggaaaaca ggaagagana atggcacaca aaacaaacat tttatattca tatttctacc 420
tacgttaata aaatagcatt ttgtgaagcc agctcaaaag aaggcttaga tcctttttatg 480
tccattttag tcactaaacg atatcnaaag tgccagaatg caaaaggttt gtgaacattt 540
attcaaaagc taatataaga tatttcacat actcatcttt ctg 583
```

<210> 204
<211> 589
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(589)
<223> n = A,T,C or G

<400> 204
```
ttttttttnt tttttttttt tttttttnctc ttctttttttt ttganaatga ggatcgagtt 60
tttcactctc tagatagggc atgaagaaaa ctcatctttc cagctttaaa ataacaatca 120
aatctcttat gctatatcat attttaagtt aaactaatga gtcactggct tatcttctcc 180
tgaaggaaat ctgttcattc ttctcattca tatagttata tcaagtacta ccttgcatat 240
tgagaggttt ttcttctcta tttacacata tatttccatg tgaatttgta tcaaaccttt 300
attttcatgc aaactagaaa ataatgtntt cttttgcata agagaagaga acaatatnag 360
cattacaaaa ctgctcaaat tgtttgttaa gnttatccat tataattagt tnggcaggag 420
ctaatacaaa tcacatttac ngacnagcaa taataaaact gaagtaccag ttaaatatcc 480
aaaataatta aaggaacatt tttagcctgg gtataattag ctaattcact ttacaagcat 540
ttattnagaa tgaattcaca tgttattatt ccntagccca acacaatgg 589
```

<210> 205
<211> 545
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(545)
<223> n = A,T,C or G

<400> 205
```
tttttntttt ttttttcagt aataatcaga acaatattta tttttatatt taaaattcat 60
agaaaagtgc cttacattta ataaaagttt gtttctcaaa gtgatcagag gaattagata 120
tngtcttgaa caccaatatt aatttgagga aaatacacca aaatacatta agtaaattat 180
ttaagatcat agagcttgta agtgaaaaga taaaatttga cctcagaaac tctgagcatt 240
aaaaatccac tattagcaaa taaattacta tggacttctt gctttaattt tgtgatgaat 300
atggggtgtc actggtaaac caacacattc tgaaggatac attacttagt gatagattct 360
tatgtacttt gctanatnac gtggatatga gttgacaagt ttctctttct tcaatctttt 420
aaggggcnga ngaaatgagg aagaaaagaa aaggattacg catactgttc tttctatngg 480
```

aaggattaga tatgtttcct ttgccaatat taaaaaaata ataatgttta ctactagtga 540
aaccc 545

<210> 206
<211> 487
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(487)
<223> n = A,T,C or G

<400> 206
tttttttttt tttttagtc aagtttctna tttttattat aattaaagtc ttggtcattt 60
catttattag ctctgcaact tacatattta aattaaagaa acgttnttag acaactgtna 120
caatttataa atgtaaggtg ccattattga gtanatatat tcctccaaga gtggatgtgt 180
cccttctccc accaactaat gaancagcaa cattagttta attttattag tagatnatac 240
actgctgcaa acgctaattc tcttctccat ccccatgtng atattgtgta tatgtgtgag 300
ttggtnagaa tgcatcanca atctnacaat caacagcaag atgaagctag gcntgggctt 360
tcggtgaaaa tagactgtgt ctgtctgaat caaatgatct gacctatcct cggtggcaag 420
aactcttcga accgcttcct caaaggcngc tgccacattt gtggcntctn ttgcacttgt 480
ttcaaaa 487

<210> 207
<211> 332
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(332)
<223> n = A,T,C or G

<400> 207
tgaattggct aaaagactgc atttttanaa ctagcaactc ttatttcttt cctttaaaaa 60
tacatagcat taaatcccaa atcctattta aagacctgac agcttgagaa ggtcactact 120
gcatttatag gaccttctgg tggttctgct gttacntttg aantctgaca atccttgana 180
atctttgcat gcagaggagg taaaaggtat tggattttca cagaggaana acacagcgca 240
gaaatgaagg ggccaggctt actgagcttg tccactggag ggctcatggg tgggacatgg 300
aaaagaaggc agcctaggcc ctggggagcc ca 332

<210> 208
<211> 524
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(524)
<223> n = A,T,C or G

<400> 208
agggcgtggt gcggagggcg ttactgtttt gtctcagtaa caataaatac aaaaagactg 60
gttgtgttcc ggccccatcc aaccacgaag ttgatttctc ttgtgtgcag agtgactgat 120
tttaaaggac atggagcttg tcacaatgtc acaatgtcac agtgtgaagg gcacactcac 180
tcccgcgtga ttcacattta gcaaccaaca atagctcatg agtccatact tgtaaatact 240
tttggcagaa tacttnttga aacttgcaga tgataactaa gatccaagat atttcccaaa 300

gtaaatagaa gtgggtcata atattaatta cctgttcaca tcagcttcca tttacaagtc 360
atgagcccag acactgacat caaactaagc ccacttagac tcctcaccac cagtctgtcc 420
tgtcatcaga caggaggctg tcaccttgac caaattctca ccagtcaatc atctatccaa 480
aaaccattac ctgatccact tccggtaatg caccaccttg gtga 524

<210> 209
<211> 159
<212> DNA
<213> Homo sapien

<400> 209
gggtgaggaa atccagagtt gccatggaga aaattccagt gtcagcattc ttgctccttg 60
tggccctctc ctacactctg gccagagata ccacagtcaa acctggagcc aaaaaggaca 120
caaaggactc tcgacccaaa ctgccccaga ccctctcca 159

<210> 210
<211> 256
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(256)
<223> n = A,T,C or G

<400> 210
actccctggc agacaaaggc agaggagaga gctctgttag ttctgtgttg ttgaactgcc 60
actgaatttc tttccacttg gactattaca tgccanttga gggactaatg gaaaaacgta 120
tggggagatt ttanccaatt tangtntgta aatggggaga ctggggcagg cgggagagat 180
ttgcagggtg naaatgggan ggctggtttg ttanatgaac agggacatag gaggtaggca 240
ccaggatgct aaatca 256

<210> 211
<211> 264
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(264)
<223> n = A,T,C or G

<400> 211
acattgtttt tttgagataa agcattgaga gagctctcct taacgtgaca caatggaagg 60
actggaacac atacccacat ctttgttctg agggataatt ttctgataaa gtcttgctgt 120
atattcaagc acatatgtta tatattattc agttccatgt ttatagccta gttaaggaga 180
ggggagatac attcngaaag aggactgaaa gaaatactca agtnggaaaa cagaaaaaga 240
aaaaaaggag caaatgagaa gcct 264

<210> 212
<211> 328
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(328)
<223> n = A,T,C or G

<400> 212
acccaaaaat ccaatgctga atatttggct tcattattcc canattcttt gattgtcaaa 60
ggatttaatg ttgtctcagc ttgggcactt cagttaggac ctaaggatgc cagccggcag 120
gtttatatat gcagcaacaa tattcaagcg cgacaacagg ttattgaact tgcccgccag 180
ttnaatttca ttcccattga cttgggatcc ttatcatcag ccagagagat tgaaaattta 240
cccctacnac tctttactct ctgganaggg ccagtggtgg tagctataag cttggccaca 300
tttttttttc ctttattcct ttgtcaga 328

<210> 213
<211> 250
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(250)
<223> n = A,T,C or G

<400> 213
acttatgagc agagcgacat atccnagtgt agactgaata aaactgaatt ctctccagtt 60
taaagcattg ctcactgaag ggatagaagt gactgccagg agggaaagta agccaaggct 120
cattatgcca aagganatat acatttcaat tctccaaact tcttcctcat tccaagagtt 180
ttcaatattt gcatgaacct gctgataanc catgttaana aacaaatatc tctctnacct 240
tctcatcggt 250

<210> 214
<211> 444
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(444)
<223> n = A,T,C or G

<400> 214
acccagaatc caatgctgaa tatttggctt cattattccc agattctttg attgtcaaag 60
gatttaatgt tgtctcagct tgggcacttc agttaggacc taaggatgcc agccggcagg 120
tttatatatg cagcaacaat attcaagcgc gacaacaggt tattgaactt gcccgccagt 180
tgaatttcat tcccattgac ttgggatcct tatcatcagc canagagatt gaaaatttac 240
ccctacgact ctttactctc tggagagggc cagtggtggt agctataagc ttggccacat 300
ttttttttcc tttattcctt tgtcagagat gcgattcatc catatgctan aaaccaacag 360
agtgactttt acaaaattcc tataganatt gtgaataaaa ccttacctat agttgccatt 420
actttgctct ccctaatata cctc 444

<210> 215
<211> 366
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(366)
<223> n = A,T,C or G

<400> 215
acttatgagc agagcgacat atccaagtgt anactgaata aaactgaatt ctctccagtt 60

taaagcattg ctcactgaag ggatagaagt gactgccagg agggaaagta agccaaggct 120
cattatgcca aagganatat acatttcaat tctccaaact tcttcctcat tccaagagtt 180
ttcaatattt gcatgaacct gctgataagc catgttgaga aacaaatatc tctctgacct 240
tctcatcggt aagcagaggc tgtaggcaac atggaccata gcgaanaaaa aacttagtaa 300
tccaagctgt tttctacact gtaaccaggt ttccaaccaa ggtggaaatc tcctatactt 360
ggtgcc 366

<210> 216
<211> 260
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(260)
<223> n = A,T,C or G

<400> 216
ctgtataaac agaactccac tgcangaggg agggccgggc caggagaatc tccgcttgtc 60
caagacaggg gcctaaggag ggtctccaca ctgctnntaa gggctnttnc atttttttat 120
taataaaaag tnnaaaaggc ctcttctcaa ctttttttccc ttnggctgga aaatttaaaa 180
atcaaaaatt tcctnaagtt ntcaagctat catatatact ntatcctgaa aaagcaacat 240
aattcttcct tccctccttt 260

<210> 217
<211> 262
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(262)
<223> n = A,T,C or G

<400> 217
acctacgtgg gtaagtttan aaatgttata atttcaggaa naggaacgca tataattgta 60
tcttgcctat aatttctat tttaataagg aaatagcaaa ttggggtggg gggaatgtag 120
ggcattctac agtttgagca aaatgcaatt aaatgtggaa ggacagcact gaaaaatttt 180
atgaataatc tgtatgatta tatgtctcta gagtagattt ataattagcc acttacccta 240
atatccttca tgcttgtaaa gt 262

<210> 218
<211> 205
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(205)
<223> n = A,T,C or G

<400> 218
accaaggtgg tgcattaccg gaantggatc aangacacca tcgtggccaa cccctgagca 60
cccctatcaa ctcccttttg tagtaaactt ggaaccttgg aaatgaccag gccaagactc 120
aggcctcccc agttctactg acctttgtcc ttangtntna ngtccagggt tgctaggaaa 180
anaaatcagc agacacaggt gtaaa 205

<210> 219

<211> 114
<212> DNA
<213> Homo sapien

<400> 219
tactgttttg tctcagtaac aataaataca aaaagactgg ttgtgttccg gccccatcca 60
accacgaagt tgatttctct tgtgtgcaga gtgactgatt ttaaaggaca tgga 114

<210> 220
<211> 93
<212> DNA
<213> Homo sapien

<400> 220
actagccagc acaaaaggca gggtagcctg aattgctttc tgctctttac atttctttta 60
aaataagcat ttagtgctca gtccctactg agt 93

<210> 221
<211> 167
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(167)
<223> n = A,T,C or G

<400> 221
actangtgca ggtgcgcaca aatatttgtc gatattccct tcatcttgga ttccatgagg 60
tcttttgccc agcctgtggc tctactgtag taagtttctg ctgatgagga gccagnatgc 120
cccccactac cttccctgac gctccccana aatcacccaa cctctgt 167

<210> 222
<211> 351
<212> DNA
<213> Homo sapien

<400> 222
agggcgtggt gcggagggcg gtactgacct cattagtagg aggatgcatt ctggcacccc 60
gttcttcacc tgtcccccaa tccttaaaag gccatactgc ataaagtcaa caacagataa 120
atgtttgctg aattaaagga tggatgaaaa aaattaataa tgaatttttg cataatccaa 180
ttttctcttt tatatttcta gaagaagttt ctttgagcct attagatccc gggaatcttt 240
taggtgagca tgattagaga gcttgtaggt tgcttttaca tatatctggc atatttgagt 300
ctcgtatcaa aacaatagat tggtaaaggt ggtattattg tattgataag t 351

<210> 223
<211> 383
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(383)
<223> n = A,T,C or G

<400> 223
aaaacaaaca aacaaaaaaa acaattcttc attcagaaaa attatcttag ggactgatat 60
tggtaattat ggtcaattta atwrtrttkt ggggcatttc cttacattgt cttgacaaga 120

ttaaaatgtc tgtgccaaaa ttttgtattt tatttggaga cttcttatca aaagtaatgc 180
tgccaaagga agtctaagga attagtagtg ttcccmtcac ttgtttggag tgtgctattc 240
taaaagattt tgatttcctg gaatgacaat tatattttaa ctttggtggg ggaaanagtt 300
ataggaccac agtcttcact tctgatactt gtaaattaat cttttattgc acttgttttg 360
accattaagc tatatgttta aaa 383

<210> 224
<211> 320
<212> DNA
<213> Homo sapien

<400> 224
cccctgaagg cttcttgtta gaaaatagta cagttacaac caataggaac aacaaaaaga 60
aaaagtttgt gacattgtag tagggagtgt gtacccctta ctccccatca aaaaaaaaat 120
ggatacatgg ttaaaggata raagggcaat attttatcat atgttctaaa agagaaggaa 180
gagaaaatac tactttctcr aaatggaagc ccttaaaggt gctttgatac tgaaggacac 240
aaatgtggcc gtccatcctc ctttaragtt gcatgacttg gacacggtaa ctgttgcagt 300
tttaractcm gcattgtgac 320

<210> 225
<211> 1214
<212> DNA
<213> Homo sapien

<400> 225
gaggactgca gcccgcactc gcagccctgg caggcggcac tggtcatgga aaacgaattg 60
ttctgctcgg gcgtcctggt gcatccgcag tgggtgctgt cagccgcaca ctgtttccag 120
aactcctaca ccatcgggct gggcctgcac agtcttgagg ccgaccaaga gccagggagc 180
cagatggtgg aggccagcct ctccgtacgg cacccagagt acaacagacc cttgctcgct 240
aacgacctca tgctcatcaa gttggacgaa tccgtgtccg agtctgacac catccggagc 300
atcagcattg cttcgcagtg ccctaccgcg gggaactctt gcctcgtttc tggctggggt 360
ctgctggcga acggcagaat gcctaccgtg ctgcagtgcg tgaacgtgtc ggtggtgtct 420
gaggaggtct gcagtaagct ctatgacccg ctgtaccacc ccagcatgtt ctgcgccggc 480
ggagggcaag accagaagga ctcctgcaac ggtgactctg gggggcccct gatctgcaac 540
gggtacttgc agggccttgt gtctttcgga aaagccccgt gtggccaagt tggcgtgcca 600
ggtgtctaca ccaacctctg caaattcact gagtggatag agaaaaccgt ccaggccagt 660
taactctggg gactgggaac ccatgaaatt gaccccccaaa tacatcctgc ggaaggaatt 720
caggaatatc tgttcccagc ccctcctccc tcaggcccag gagtccaggc ccccagcccc 780
tcctccctca aaccaagggt acagatcccc agcccctcct ccctcagacc caggagtcca 840
gaccccccag cccctcctcc ctcagaccca ggagtccagc ccctcctccc tcagacccag 900
gagtccagac cccccagccc ctcctccctc agacccaggg gtccaggccc ccaacccctc 960
ctccctcaga ctcagaggtc caagccccca acccctcctt ccccagaccc agaggtccag 1020
gtcccagccc ctcctccctc agacccagcg gtccaatgcc acctagactc tccctgtaca 1080
cagtgccccc ttgtggcacg ttgacccaac cttaccagtt ggtttttcat tttttgtccc 1140
tttcccctag atccagaaat aaagtctaag agaagcgcaa aaaaaaaaaa aaaaaaaaaa 1200
aaaaaaaaaa aaaa 1214

<210> 226
<211> 119
<212> DNA
<213> Homo sapien

<400> 226
acccagtatg tgcagggaga cggaacccca tgtgacagcc cactccacca gggttcccaa 60
agaacctggc ccagtcataa tcattcatcc tgacagtggc aataatcacg ataaccagt 119

<210> 227
<211> 818

<212> DNA
<213> Homo sapien

<400> 227
acaattcata gggacgacca atgaggacag ggaatgaacc cggctctccc ccagccctga 60
tttttgctac atatggggtc ccttttcatt ctttgcaaaa acactgggtt ttctgagaac 120
acggacggtt cttagcacaa tttgtgaaat ctgtgtaraa ccgggctttg caggggagat 180
aattttcctc ctctggagga aaggtggtga ttgacaggca gggagacagt gacaaggcta 240
gagaaagcca cgctcggcct tctctgaacc aggatggaac ggcagacccc tgaaaacgaa 300
gcttgtcccc ttccaatcag ccacttctga gaacccccat ctaacttcct actggaaaag 360
agggcctcct caggagcagt ccaagagttt tcaaagataa cgtgacaact accatctaga 420
ggaaagggtg caccctcagc agagaagccg agagcttaac tctggtcgtt tccagagaca 480
acctgctggc tgtcttggga tgcgcccagc ctttgagagg ccactacccc atgaacttct 540
gccatccact ggacatgaag ctgaggacac tgggcttcaa cactgagttg tcatgagagg 600
gacaggctct gccctcaagc cggctgaggg cagcaaccac tctcctcccc tttctcacgc 660
aaagccattc ccacaaatcc agaccatacc atgaagcaac gagacccaaa cagtttggct 720
caagaggata tgaggactgt ctcagcctgg ctttgggctg acaccatgca cacacacaag 780
gtccacttct aggttttcag cctagatggg agtcgtgt 818

<210> 228
<211> 744
<212> DNA
<213> Homo sapien

<400> 228
actggagaca ctgttgaact tgatcaagac ccagaccacc ccaggtctcc ttcgtgggat 60
gtcatgacgt ttgacatacc tttggaacga gcctcctcct tggaagatgg aagaccgtgt 120
tcgtggccga cctggcctct cctggcctgt ttcttaagat gcggagtcac atttcaatgg 180
taggaaaagt ggcttcgtaa aatagaagag cagtcactgt ggaactacca aatggcgaga 240
tgctcggtgc acattggggt gctttgggat aaaagattta tgagccaact attctctggc 300
accagattct aggccagttt gttccactga agcttttccc acagcagtcc acctctgcag 360
gctggcagct gaatggcttg ccggtggctc tgtggcaaga tcacactgag atcgatgggt 420
gagaaggcta ggatgcttgt ctagtgttct tagctgtcac gttggctcct tccaggttgg 480
ccagacggtg ttggccactc ccttctaaaa cacaggcgcc ctcctggtga cagtgacccg 540
ccgtggtatg ccttggccca ttccagcagt cccagttatg catttcaagt ttggggtttg 600
ttcttttcgt taatgttcct ctgtgttgtc agctgtcttc atttcctggg ctaagcagca 660
ttgggagatg tggaccagag atccactcct taagaaccag tggcgaaaga cactttcttt 720
cttcactctg aagtagctgg tggt 744

<210> 229
<211> 300
<212> DNA
<213> Homo sapien

<400> 229
cgagtctggg ttttgtctat aaagtttgat ccctcctttt ctcatccaaa tcatgtgaac 60
cattacacat cgaaataaaa gaaaggtggc agacttgccc aacgccaggc tgacatgtgc 120
tgcaggttg ttgtttttta attattattg ttagaaacgt cacccacagt ccctgttaat 180
ttgtatgtga cagccaactc tgagaaggtc ctatttttcc acctgcagag gatccagtct 240
cactaggctc ctccttgccc tcacactgga gtctccgcca gtgtgggtgc ccactgacat 300

<210> 230
<211> 301
<212> DNA
<213> Homo sapien

<400> 230
cagcagaaca aatacaaata tgaagagtgc aaagatctca taaaatctat gctgaggaat 60

gagcgacagt tcaaggagga gaagcttgca gagcagctca agcaagctga ggagctcagg 120
caatataaag tcctggttca cactcaggaa cgagagctga cccagttaag ggagaagttg 180
cgggaaggga gagatgcctc cctctcattg aatgagcatc tccaggccct cctcactccg 240
gatgaaccgg acaagtccca ggggcaggac ctccaagaaa cagacctcgg ccgcgaccac 300
g 301

<210> 231
<211> 301
<212> DNA
<213> Homo sapien

<400> 231
gcaagcacgc tggcaaatct ctgtcaggtc agctccagag aagccattag tcattttagc 60
caggaactcc aagtccacat ccttggcaac tggggacttg cgcaggttag ccttgaggat 120
ggcaacacgg gacttctcat caggaagtgg gatgtagatg agctgatcaa gacggccagg 180
tctgaggatg gcaggatcaa tgatgtcagg ccggttggta ccgccaatga tgaacacatt 240
tttttttgtg gacatgccat ccatttctgt caggatctgg ttgatgactc ggtcagcagc 300
c 301

<210> 232
<211> 301
<212> DNA
<213> Homo sapien

<400> 232
agtaggtatt tcgtgagaag ttcaacacca aaactggaac atagttctcc ttcaagtgtt 60
ggcgacagcg gggcttcctg attctggaat ataactttgt gtaaattaac agccacctat 120
agaagagtcc atctgctgtg aaggagagac agagaactct gggttccgtc gtcctgtcca 180
cgtgctgtac caagtgctgg tgccagcctg ttacctgttc tcactgaaaa tctggctaat 240
gctcttgtgt atcacttctg attctgacaa tcaatcaatc aatggcctag agcactgact 300
g 301

<210> 233
<211> 301
<212> DNA
<213> Homo sapien

<400> 233
atgactgact tcccagtaag gctctctaag gggtaagtag gaggatccac aggatttgag 60
atgctaaggc cccagagatc gtttgatcca accctcttat tttcagaggg gaaaatgggg 120
cctagaagtt acagagcatc tagctggtgc gctggcaccc ctggcctcac acagactccc 180
gagtagctgg gactacaggc acacagtcac tgaagcaggc cctgttagca attctatgcg 240
tacaaattaa catgagatga gtagagactt tattgagaaa gcaagagaaa atcctatcaa 300
c 301

<210> 234
<211> 301
<212> DNA
<213> Homo sapien

<400> 234
aggtcctaca catcgagact catccatgat tgatatgaat ttaaaaatta caagcaaaga 60
cattttattc atcatgatgc tttcttttgt ttcttctttt cgttttcttc tttttctttt 120
tcaatttcag caacatactt ctcaatttct tcaggattta aaatcttgag ggattgatct 180
cgcctcatga cagcaagttc aatgtttttg ccacctgact gaaccacttc caggagtgcc 240
ttgatcacca gcttaatggt cagatcatct gcttcaatgg cttcgtcagt atagttcttc 300
t 301

<210> 235
<211> 283
<212> DNA
<213> Homo sapien

<400> 235
tggggctgtg catcaggcgg gtttgagaaa tattcaattc tcagcagaag ccagaatttg 60
aattccctca tcttttaggg aatcatttac caggtttgga gaggattcag acagctcagg 120
tgctttcact aatgtctctg aacttctgtc cctctttgtt catggatagt ccaataaata 180
atgttatctt tgaactgatg ctcataggag agaatataag aactctgagt gatatcaaca 240
ttagggattc aaagaatat tagatttaag ctcacactgg tca 283

<210> 236
<211> 301
<212> DNA
<213> Homo sapien

<400> 236
aggtcctcca ccaactgcct gaagcacggt taaaattggg aagaagtata gtgcagcata 60
aatactttta aatcgatcag atttccctaa cccacatgca atcttcttca ccagaagagg 120
tcggagcagc atcattaata ccaagcagaa tgcgtaatag ataaatacaa tggtatatag 180
tgggtagacg gcttcatgag tacagtgtac tgtggtatcg taatctggac ttgggttgta 240
aagcatcgtg taccagtcag aaagcatcaa tactcgacat gaacgaatat aaagaacacc 300
a 301

<210> 237
<211> 301
<212> DNA
<213> Homo sapien

<400> 237
cagtggtagt ggtggtggac gtggcgttgg tcgtggtgcc tttttggtg cccgtcacaa 60
actcaatttt tgttcgctcc tttttggcct tttccaattt gtccatctca attttctggg 120
ccttggctaa tgcctcatag taggagtcct cagaccagcc atggggatca aacatatcct 180
ttgggtagtt ggtgccaagc tcgtcaatgg cacagaatgg atcagcttct cgtaaatcta 240
gggttccgaa attctttctt cctttggata atgtagttca tatccattcc ctcctttatc 300
t 301

<210> 238
<211> 301
<212> DNA
<213> Homo sapien

<400> 238
gggcaggttt tttttttttt ttttttgatg gtgcagaccc ttgctttatt tgtctgactt 60
gttcacagtt cagccccctg ctcagaaaac caacgggcca gctaaggaga ggaggaggca 120
ccttgagact tccggagtcg aggctctcca gggttcccca gcccatcaat cattttctgc 180
accccctgcc tgggaagcag ctccctgggg ggtgggaatg ggtgactaga agggatttca 240
gtgtgggacc cagggtctgt tcttcacagt aggaggtgga agggatgact aatttcttta 300
t 301

<210> 239
<211> 239
<212> DNA
<213> Homo sapien

<400> 239
ataagcagct agggaattct ttatttagta atgtcctaac ataaaagttc acataactgc 60

ttctgtcaaa ccatgatact gagctttgtg acaacccaga aataactaag agaaggcaaa 120
cataatacct tagagatcaa gaaacattta cacagttcaa ctgtttaaaa atagctcaac 180
attcagccag tgagtagagt gtgaatgcca gcatacacag tatacaggtc cttcaggga 239

<210> 240
<211> 300
<212> DNA
<213> Homo sapien

<400> 240
ggtcctaatg aagcagcagc ttccacattt taacgcaggt ttacggtgat actgtccttt 60
gggatctgcc ctccagtgga accttttaag gaagaagtgg gcccaagcta agttccacat 120
gctgggtgag ccagatgact tctgttccct ggtcactttc ttcaatgggg cgaatggggg 180
ctgccaggtt tttaaaatca tgcttcatct tgaagcacac ggtcacttca ccctcctcac 240
gctgtgggtg tactttgatg aaaataccca ctttgttggc ctttctgaag ctataatgtc 300

<210> 241
<211> 301
<212> DNA
<213> Homo sapien

<400> 241
gaggtctggt gctgaggtct ctgggctagg aagaggagtt ctgtggagct ggaagccaga 60
cctctttgga ggaaactcca gcagctatgt tggtgtctct gagggaatgc aacaaggctg 120
ctcctccatg tattggaaaa ctgcaaactg gactcaactg gaaggaagtg ctgctgccag 180
tgtgaagaac cagcctgagg tgacagaaac ggaagcaaac aggaacagcc agtcttttct 240
tcctcctcct gtcatacggt ctctctcaag catcctttgt tgtcaggggc ctaaaggga 300
g 301

<210> 242
<211> 301
<212> DNA
<213> Homo sapien

<400> 242
ccgaggtcct gggatgcaac caatcactct gtttcacgtg acttttatca ccatacaatt 60
tgtggcattt cctcattttc tacattgtag aatcaagagt gtaaataaat gtatatcgat 120
gtcttcaaga atatatcatt cctttttcac tagaacccat tcaaaatata agtcaagaat 180
cttaatatca acaaatatat caagcaaact ggaaggcaga ataactacca taatttagta 240
taagtaccca aagttttata aatcaaaagc cctaatgata accattttta gaattcaatc 300
a 301

<210> 243
<211> 301
<212> DNA
<213> Homo sapien

<400> 243
aggtaagtcc cagtttgaag ctcaaaagat ctggtatgag cataggctca tcgacgacat 60
ggtggcccaa gctatgaaat cagagggagg cttcatctgg gcctgtaaaa actatgatgg 120
tgacgtgcag tcggactctg tggcccaagg gtatggctct ctcggcatga tgaccagcgt 180
gctggtttgt ccagatggca agacagtaga agcagaggct gcccacggga ctgtaacccg 240
tcactaccgc atgttccaga aaggacagga gacgtccacc aatcccattg cttccatttt 300
t 301

<210> 244
<211> 300
<212> DNA

<213> Homo sapien

<400> 244
gctggtttgc aagaatgaaa tgaatgattc tacagctagg acttaacctt gaaatggaaa 60
gtcatgcaat cccatttgca ggatctgtct gtgcacatgc ctctgtagag agcagcattc 120
ccagggacct tggaaacagt tgacactgta aggtgcttgc tccccaagac acatcctaaa 180
aggtgttgta atggtgaaaa cgtcttcctt ctttattgcc ccttcttatt tatgtgaaca 240
actgtttgtc ttttgtgtat cttttttaaa ctgtaaagtt caattgtgaa aatgaatatc 300

<210> 245
<211> 301
<212> DNA
<213> Homo sapien

<400> 245
gtctgagtat ttaaaatgtt attgaaatta tccccaacca atgttagaaa agaaagaggt 60
tatatactta gataaaaaat gaggtgaatt actatccatt gaaatcatgc tcttagaatt 120
aaggccagga gatattgtca ttaatgtara cttcaggaca ctagagtata gcagccctat 180
gttttcaaag agcagagatg caattaaata ttgtttagca tcaaaaaggc cactcaatac 240
agctaataaa atgaaagacc taatttctaa agcaattctt tataatttac aaagttttaa 300
g 301

<210> 246
<211> 301
<212> DNA
<213> Homo sapien

<400> 246
ggtctgtcct acaatgcctg cttcttgaaa gaagtcggca ctttctagaa tagctaaata 60
acctgggctt attttaaaga actatttgta gctcagattg gttttcctat ggctaaaata 120
agtgcttctt gtgaaaatta aataaaacag ttaattcaaa gccttgatat atgttaccac 180
taacaatcat actaaatata ttttgaagta caaagtttga catgctctaa agtgacaacc 240
caaatgtgtc ttacaaaaca cgttcctaac aaggtatgct ttacactacc aatgcagaaa 300
c 301

<210> 247
<211> 301
<212> DNA
<213> Homo sapien

<400> 247
aggtcctttg gcagggctca tggatcagag ctcaaactgg agggaaaggc atttcgggta 60
gcctaagagg gcgactggcg gcagcacaac caaggaaggc aaggttgttt cccccacgct 120
gtgtcctgtg ttcaggtgcg acacacaatc ctcatgggaa caggatcacc catgcgctgc 180
ccttgatgat caaggttggg gcttaagtgg attaagggag gcaagttctg ggttccttgc 240
cttttcaaac catgaagtca ggctctgtat ccctcctttt cctaactgat attctaacta 300
a 301

<210> 248
<211> 301
<212> DNA
<213> Homo sapien

<400> 248
aggtccttgg agatgccatt tcagccgaag gactcttctw ttcggaagta caccctcact 60
attaggaaga ttcttagggg taatttttct gaggaaggag aactagccaa cttaagaatt 120
acaggaagaa agtggtttgg aagacagcca aagaaataaa agcagattaa attgtatcag 180
gtacattcca gcctgttggc aactccataa aaacatttca gattttaatc ccgaatttag 240

ctaatgagac tggatttttg ttttttatgt tgtgtgtcgc agagctaaaa actcagttcc 300
c 301

<210> 249
<211> 301
<212> DNA
<213> Homo sapien

<400> 249
gtccagagga agcacctggt gctgaactag gcttgccctg ctgtgaactt gcacttggag 60
ccctgacgct gctgttctcc ccgaaaaacc cgaccgacct ccgcgatctc cgtcccgccc 120
ccagggagac acagcagtga ctcagagctg gtcgcacact gtgcctccct cctcaccgcc 180
catcgtaatg aattattttg aaaattaatt ccaccatcct ttcagattct ggatggaaag 240
actgaatctt tgactcagaa ttgtttgctg aaaagaatga tgtgactttc ttagtcattt 300
a 301

<210> 250
<211> 301
<212> DNA
<213> Homo sapien

<400> 250
ggtctgtgac aaggacttgc aggctgtggg aggcaagtga cccttaacac tacacttctc 60
cttatcttta ttggcttgat aaacataatt atttctaaca ctagcttatt tccagttgcc 120
cataagcaca tcagtacttt tctctggctg gaatagtaaa ctaaagtatg gtacatctac 180
ctaaaagact actatgtgga ataatacata ctaatgaagt attacatgat ttaaagacta 240
caataaaacc aaacatgctt ataacattaa gaaaaacaat aaagatacat gattgaaacc 300
a 301

<210> 251
<211> 301
<212> DNA
<213> Homo sapien

<400> 251
gccgaggtcc tacatttggc ccagtttccc cctgcatcct ctccagggcc cctgcctcat 60
agacaacctc atagagcata ggagaactgg ttgccctggg ggcaggggga ctgtctggat 120
ggcaggggtc ctcaaaaatg ccactgtcac tgccaggaaa tgcttctgag cagtacacct 180
cattgggatc aatgaaaagc ttcaagaaat cttcaggctc actctcttga aggcccggaa 240
cctctggagg ggggcagtgg aatcccagct ccaggacgga tcctgtcgaa aagatatcct 300
c 301

<210> 252
<211> 301
<212> DNA
<213> Homo sapien

<400> 252
gcaaccaatc actctgtttc acgtgacttt tatcaccata caatttgtgg catttcctca 60
ttttctacat tgtagaatca agagtgtaaa taaatgtata tcgatgtctt caagaatata 120
tcattccttt ttcactagga acccattcaa aatataagtc aagaatctta atatcaacaa 180
atatatcaag caaactggaa ggcagaataa ctaccataat ttagtataag tacccaaagt 240
tttataaatc aaaagcccta atgataacca tttttagaat tcaatcatca ctgtagaatc 300
a 301

<210> 253
<211> 301
<212> DNA

<213> Homo sapien

<400> 253
ttccctaaga agatgttatt ttgttgggtt ttgttccccc tccatctcga ttctcgtacc 60
caactaaaaa aaaaaaataa agaaaaaatg tgctgcgttc tgaaaaataa ctccttagct 120
tggtctgatt gttttcagac cttaaaatat aaacttgttt cacaagcttt aatccatgtg 180
gatttttttt cttagagaac cacaaaacat aaaaggagca agtcggactg aatacctgtt 240
tccatagtgc ccacagggta ttcctcacat tttctccata ggaaaatgct ttttcccaag 300
g 301

<210> 254
<211> 301
<212> DNA
<213> Homo sapien

<400> 254
cgctgcgcct ttcccttggg ggagggggcaa ggccagaggg ggtccaagtg cagcacgagg 60
aacttgacca attcccttga agcgggtggg ttaaaccctg taaatgggaa caaaatcccc 120
ccaaatctct tcatcttacc ctggtggact cctgactgta gaattttttg gttgaaacaa 180
gaaaaaaata aagctttgga cttttcaagg ttgcttaaca ggtactgaaa gactggcctc 240
acttaaactg agccaggaaa agctgcagat ttattaatgg gtgtgttagt gtgcagtgcc 300
t 301

<210> 255
<211> 302
<212> DNA
<213> Homo sapien

<400> 255
agcttttttt tttttttttt tttttttttt ttcattaaaa aatagtgctc tttattataa 60
attactgaaa tgtttctttt ctgaatataa atataaatat gtgcaaagtt tgacttggat 120
tgggattttg ttgagttctt caagcatctc ctaataccct caagggcctg agtagggggg 180
aggaaaaagg actggaggtg gaatctttat aaaaaacaag agtgattgag gcagattgta 240
aacattatta aaaaacaaga aacaaacaaa aaaatagaga aaaaaaccac cccaacacac 300
aa 302

<210> 256
<211> 301
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(301)
<223> n = A,T,C or G

<400> 256
gttccagaaa acattgaagg tggcttccca aagtctaact agggataccc cctctagcct 60
aggaccctcc tccccacacc tcaatccacc aaaccatcca taatgcaccc agataggccc 120
acccccaaaa gcctggacac cttgagcaca cagttatgac caggacagac tcatctctat 180
aggcaaatag ctgctggcaa actggcatta cctggtttgt ggggatgggg gggcaagtgt 240
gtggcctctc ggcctggtta gcaagaacat tcagggtagg cctaagttan tcgtgttagt 300
t 301

<210> 257
<211> 301
<212> DNA
<213> Homo sapien

<400> 257
gttgtggagg aactctggct tgctcattaa gtcctactga ttttcactat cccctgaatt 60
tccccactta tttttgtctt tcactatcgc aggccttaga agaggtctac ctgcctccag 120
tcttacctag tccagtctac cccctggagt tagaatggcc atcctgaagt gaaaagtaat 180
gtcacattac tcccttcagt gatttcttgt agaagtgcca atccctgaat gccaccaaga 240
tcttaatctt cacatcttta atcttatctc tttgactcct ctttacaccg gagaaggctc 300
c 301

<210> 258
<211> 301
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(301)
<223> n = A,T,C or G

<400> 258
cagcagtagt agatgccgta tgccagcacg cccagcactc ccaggatcag caccagcacc 60
aggggcccag ccaccaggcg cagaagcaag ataaacagta ggctcaagac cagagccacc 120
cccagggcaa caagaatcca ataccaggac tgggcaaaat cttcaaagat cttaacactg 180
atgtctcggg cattgaggct gtcaataana cgctgatccc ctgctgtatg gtggtgtcat 240
tggtgatccc tgggagcgcc ggtggagtaa cgttggtcca tggaaagcag cgcccacaac 300
t 301

<210> 259
<211> 301
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(301)
<223> n = A,T,C or G

<400> 259
tcatatatgc aaacaaatgc agactangcc tcaggcagag actaaaggac atctcttggg 60
gtgtcctgaa gtgatttgga cccctgaggg cagacaccta agtaggaatc ccagtgggaa 120
gcaaagccat aaggaagccc aggattcctt gtgatcagga agtgggccag gaaggtctgt 180
tccagctcac atctcatctg catgcagcac ggaccggatg cgcccactgg gtcttggctt 240
ccctcccatc ttctcaagca gtgtccttgt tgagccattt gcatccttgg ctccaggtgg 300
c 301

<210> 260
<211> 301
<212> DNA
<213> Homo sapien

<400> 260
tttttttct ccctaaggaa aaagaaggaa caagtctcat aaaaccaaat aagcaatggt 60
aaggtgtctt aacttgaaaa agattaggag tcactggttt acaagttata attgaatgaa 120
agaactgtaa cagccacagt tggccatttc atgccaatgg cagcaaacaa caggattaac 180
tagggcaaaa taaataagtg tgtggaagcc ctgataagtg cttaataaac agactgattc 240
actgagacat cagtacctgc ccgggcggcc gctcgagccg aattctgcag atatccatca 300
c 301

<210> 261
<211> 301
<212> DNA
<213> Homo sapien

<400> 261
aaatattcga gcaaatcctg taactaatgt gtctccataa aaggctttga actcagtgaa 60
tctgcttcca tccacgattc tagcaatgac ctctcggaca tcaaagctcc tcttaaggtt 120
agcaccaact attccataca attcatcagc aggaaataaa ggctcttcag aaggttcaat 180
ggtgacatcc aatttcttct gataatttag attcctcaca accttcctag ttaagtgaag 240
ggcatgatga tcatccaaag cccagtggtc acttactcca gactttctgc aatgaagatc 300
a 301

<210> 262
<211> 301
<212> DNA
<213> Homo sapien

<400> 262
gaggagagcc tgttacagca tttgtaagca cagaatactc caggagtatt tgtaattgtc 60
tgtgagcttc ttgccgcaag tctctcagaa atttaaaaag atgcaaatcc ctgagtcacc 120
cctagacttc ctaaaccaga tcctctgggg ctggaacctg gcactctgca tttgtaatga 180
gggctttctg gtgcacacct aattttgtgc atctttgccc taaatcctgg attagtgccc 240
catcattacc cccacattat aatgggatag attcagagca gatactctcc agcaaagaat 300
c 301

<210> 263
<211> 301
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(301)
<223> n = A,T,C or G

<400> 263
tttagcttgt ggtaaatgac tcacaaaact gattttaaaa tcaagttaat gtgaattttg 60
aaaattacta cttaatccta attcacaata acaatggcat taaggtttga cttgagttgg 120
ttcttagtat tatttatggt aaataggctc ttaccacttg caaataactg gccacatcat 180
taatgactga cttcccagta aggctctcta aggggtaagt angaggatcc acaggatttg 240
agatgctaag gccccagaga tcgtttgatc caaccctctt attttcagag gggaaaatgg 300
g 301

<210> 264
<211> 301
<212> DNA
<213> Homo sapien

<400> 264
aaagacgtta aaccactcta ctaccacttg tggaactctc aaagggtaaa tgacaaascc 60
aatgaatgac tctaaaaaca atatttacat ttaatggttt gtagacaata aaaaaacaag 120
gtggatagat ctagaattgt aacattttaa gaaaaccata scatttgaca gatgagaaag 180
ctcaattata gatgcaaagt tataactaaa ctactatagt agtaaagaaa tacatttcac 240
acccttcata taaattcact atcttggctt gaggcactcc ataaaatgta tcacgtgcat 300
a 301

<210> 265

<211> 301
<212> DNA
<213> Homo sapien

<400> 265
tgcccaagtt atgtgtaagt gtatccgcac ccagaggtaa aactacactg tcatctttgt 60
cttcttgtga cgcagtattt cttctctggg gagaagccgg gaagtcttct cctggctcta 120
catattcttg gaagtctcta atcaactttt gttccatttg tttcatttct tcaggaggga 180
ttttcagttt gtcaacatgt tctctaacaa cacttgccca tttctgtaaa gaatccaaag 240
cagtccaagg ctttgacatg tcaacaacca gcataactag agtatccttc agagatacgg 300
c 301

<210> 266
<211> 301
<212> DNA
<213> Homo sapien

<400> 266
taccgtctgc ccttcctccc atccaggcca tctgcgaatc tacatgggtc ctcctattcg 60
acaccagatc actctttcct ctacccacag gcttgctatg agcaagagac acaacctcct 120
ctcttctgtg ttccagcttc ttttcctgtt cttcccaccc cttaagttct attcctgggg 180
atagagacac caatacccat aacctctctc ctaagcctcc ttataaccca gggtgcacag 240
cacagactcc tgacaactgg taaggccaat gaactgggag ctcacagctg gctgtgcctg 300
a 301

<210> 267
<211> 301
<212> DNA
<213> Homo sapien

<400> 267
aaagagcaca ggccagctca gcctgccctg gccatctaga ctcagcctgg ctccatgggg 60
gttctcagtg ctgagtccat ccaggaaaag ctcacctaga ccttctgagg ctgaatcttc 120
atcctcacag gcagcttctg agagcctgat attcctagcc ttgatggtct ggagtaaagc 180
ctcattctga ttcctctcct tcttttcttt caagttggct ttcctcacat ccctctgttc 240
aattcgcttc agcttgtctg ctttagccct catttccaga agcttcttct ctttggcatc 300
t 301

<210> 268
<211> 301
<212> DNA
<213> Homo sapien

<400> 268
aatgtctcac tcaactactt cccagcctac cgtggcctaa ttctgggagt tttcttctta 60
gatcttggga gagctggttc ttctaaggag aaggaggaag gacagatgta actttggatc 120
tcgaagagga agtctaatgg aagtaattag tcaacggtcc ttgtttagac tcttggaata 180
tgctgggtgg ctcagtgagc ccttttggag aaagcaagta ttattcttaa ggagtaacca 240
cttcccattg ttctactttc taccatcatc aattgtatat tatgtattct ttggagaact 300
a 301

<210> 269
<211> 301
<212> DNA
<213> Homo sapien

<400> 269
taacaatata cactagctat ctttttaact gtccatcatt agcaccaatg aagattcaat 60

aaaattacct ttattcacac atctcaaaac aattctgcaa attcttagtg aagtttaact 120
atagtcacag accttaaata ttcacattgt tttctatgtc tactgaaaat aagttcacta 180
cttttctgga tattctttac aaaatcttat taaaattcct ggtattatca cccccaatta 240
tacagtagca caaccacctt atgtagtttt tacatgatag ctctgtagaa gtttcacatc 300
t 301

<210> 270
<211> 301
<212> DNA
<213> Homo sapien

<400> 270
cattgaagag cttttgcgaa acatcagaac acaagtgctt ataaaattaa ttaagcctta 60
cacaagaata catattcctt ttatttctaa ggagttaaac atagatgtag ctgatgtgga 120
gagcttgctg gtgcagtgca tattggataa cactattcat ggccgaattg atcaagtcaa 180
ccaactcctt gaactggatc atcagaagaa gggtggtgca cgatatactg cactagataa 240
tggaccaacc aactaaattc tctcaccagg ctgtatcagt aaactggctt aacagaaaac 300
a 301

<210> 271
<211> 301
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(301)
<223> n = A,T,C or G

<400> 271
aaaaggttct cataagatta acaatttaaa taaatatttg atagaacatt ctttctcatt 60
tttatagctc atctttaggg ttgatattca gttcatgctt cccttgctgt tcttgatcca 120
gaattgcaat cacttcatca gcctgtattc gctccaattc tctataaagt gggtccaagg 180
tgaaccacag agccacagca cacctctttc ccttggtgac tgccttcacc ccatganggt 240
tctctcctcc agatganaac tgatcatgcg cccacatttt gggttttata gaagcagtca 300
c 301

<210> 272
<211> 301
<212> DNA
<213> Homo sapien

<400> 272
taaattgcta agccacagat aacaccaatc aaatggaaca aatcactgtc ttcaaatgtc 60
ttatcagaaa accaaatgag cctggaatct tcataatacc taaacatgcc gtatttagga 120
tccaataatt ccctcatgat gagcaagaaa aattctttgc gcacccctcc tgcatccaca 180
gcatcttctc caacaaatat aaccttgagt ggcttcttgt aatctatgtt ctttgttttc 240
ctaaggactt ccattgcatc tcctacaata ttttctctac gcaccactag aattaagcag 300
g 301

<210> 273
<211> 301
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(301)

<223> n = A,T,C or G

<400> 273
acatgtgtgt atgtgtatct ttgggaaaan aanaagacat cttgtttayt attttttgg 60
agagangctg ggacatggat aatcacwtaa tttgctayta tyactttaat ctgactygaa 120
gaaccgtcta aaaataaaat ttaccatgtc dtatattcct tatagtatgc ttatttcacc 180
ttytttctgt ccagagagag tatcagtgac ananatttma gggtgaamac atgmattggt 240
gggacttnty tttacngagm accctgcccg sgcgccctcg makcngantt ccgcsananc 300
t 301

<210> 274
<211> 301
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(301)
<223> n = A,T,C or G

<400> 274
cttatatact ctttctcaga ggcaaaagag gagatgggta atgtagacaa ttctttgagg 60
aacagtaaat gattattaga gagaangaat ggaccaagga gacagaaatt aacttgtaaa 120
tgattctctt tggaatctga atgagatcaa gaggccagct ttagcttgtg gaaaagtcca 180
tctaggtatg gttgcattct cgtcttcttt tctgcagtag ataatgaggt aaccgaaggc 240
aattgtgctt cttttgataa gaagctttct tggtcatatc aggaaattcc aganaaagtc 300
c 301

<210> 275
<211> 301
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(301)
<223> n = A,T,C or G

<400> 275
tcggtgtcag cagcacgtgg cattgaacat tgcaatgtgg agcccaaacc acagaaaatg 60
gggtgaaatt ggccaacttt ctattaactt atgttggcaa ttttgccacc aacagtaagc 120
tggcccttct aataaaagaa aattgaaagg tttctcacta aacggaatta agtagtggag 180
tcaagagact cccaggcctc agcgtacctg cccgggcggc cgctcgaagc cgaattctgc 240
agatatccat cacactggcg gncgctcgan catgcatcta gaaggnccaa ttcgccctat 300
a 301

<210> 276
<211> 301
<212> DNA
<213> Homo sapien

<400> 276
tgtacacata ctcaataaat aaatgactgc attgtggtat tattactata ctgattatat 60
ttatcatgtg acttctaatt agaaaatgta tccaaaagca aaacagcaga tatacaaaat 120
taaagagaca gaagatagac attaacagat aaggcaactt atacattgag aatccaaatc 180
caatacattt aaacatttgg gaaatgaggg ggacaaatgg aagccagatc aaatttgtgt 240
aaaactattc agtatgtttc ccttgcttca tgtctgagaa ggctctcctt caatggggat 300
g 301

<210> 277
<211> 301
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(301)
<223> n = A,T,C or G

<400> 277
tttgttgatg tcagtatttt attacttgcg ttatgagtgc tcacctggga aattctaaag 60
atacagagga cttggaggaa gcagagcaac tgaatttaat ttaaaagaag gaaaacattg 120
gaatcatggc actcctgata ctttcccaaa tcaacactct caatgcccca ccctcgtcct 180
caccatagtg ggagactaa agtggccacg gatttgcctt angtgtgcag tgcgttctga 240
gttcnctgtc gattacatct gaccagtctc ctttttccga agtccntccg ttcaatcttg 300
c 301

<210> 278
<211> 301
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(301)
<223> n = A,T,C or G

<400> 278
taccactaca ctccagcctg ggcaacagag caagacctgt ctcaaagcat aaaatggaat 60
aacatatcaa atgaaacagg gaaaatgaag ctgacaattt atggaagcca gggcttgtca 120
cagtctctac tgttattatg cattacctgg gaatttatat aagcccttaa taataatgcc 180
aatgaacatc tcatgtgtgc tcacaatgtt ctggcactat tataagtgct tcacaggttt 240
tatgtgttct tcgtaacttt atggantagg tactcggccg cgaacacgct aagccgaatt 300
c 301

<210> 279
<211> 301
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(301)
<223> n = A,T,C or G

<400> 279
aaagcaggaa tgacaaagct tgcttttctg gtatgttcta ggtgtattgt gacttttact 60
gttatattaa ttgccaatat aagtaaatat agattatata tgtatagtgt ttcacaaagc 120
ttagaccttt accttccagc caccccacag tgcttgatat ttcagagtca gtcattggtt 180
atacatgtgt agttccaaag cacataagct agaanaanaa atatttctag ggagcactac 240
catctgtttt cacatgaaat gccacacaca tagaactcca acatcaattt cattgcacag 300
a 301

<210> 280
<211> 301
<212> DNA

<213> Homo sapien

<400> 280
ggtactggag ttttcctccc ctgtgaaaac gtaactactg ttgggagtga attgaggatg 60
tagaaaggtg gtggaaccaa attgtggtca atggaaatag gagaatatgg ttctcactct 120
tgagaaaaaa acctaagatt agcccaggta gttgcctgta acttcagttt ttctgcctgg 180
gtttgatata gtttagggtt ggggttagat taagatctaa attacatcag gacaaagaga 240
cagactatta actccacagt taattaagga ggtatgttcc atgtttattt gttaaagcag 300
t 301

<210> 281
<211> 301
<212> DNA
<213> Homo sapien

<400> 281
aggtacaaga aggggaatgg gaaagagctg ctgctgtggc attgttcaac ttggatattc 60
gccgagcaat ccaaatcctg aatgaagggg catcttctga aaaaggagat ctgaatctca 120
atgtggtagc aatggcttta tcgggttata cggatgagaa gaactccctt tggagagaaa 180
tgtgtagcac actgcgatta cagctaaata acccgtattt gtgtgtcatg tttgcatttc 240
tgacaagtga aacaggatct tacgatggag ttttgtatga aaacaaagtt gcagtacctc 300
g 301

<210> 282
<211> 301
<212> DNA
<213> Homo sapien

<400> 282
caggtactac agaattaaaa tactgacaag caagtagttt cttggcgtgc acgaattgca 60
tccagaaccc aaaaattaag aaattcaaaa agacattttg tgggcacctg ctagcacaga 120
agcgcagaag caaagcccag gcagaaccat gctaacctta cagctcagcc tgcacagaag 180
cgcagaagca aagcccaggc agaaccatgc taaccttaca gctcagcctg cacagaagcg 240
cagaagcaaa gcccaggcag aacatgctaa ccttacagct cagcctgcac agaagcacag 300
a 301

<210> 283
<211> 301
<212> DNA
<213> Homo sapien

<400> 283
atctgtatac ggcagacaaa ctttatarag tgtagagagg tgagcgaaag gatgcaaaag 60
cactttgagg gctttataat aatatgctgc ttgaaaaaaa aaatgtgtag ttgatactca 120
gtgcatctcc agacatagta aggggttgct ctgaccaatc aggtgatcat tttttctatc 180
acttcccagg ttttatgcaa aaattttgtt aaattctata atggtgatat gcatctttta 240
ggaaacatat acatttttaa aaatctattt tatgtaagaa ctgacagacg aatttgcttt 300
g 301

<210> 284
<211> 301
<212> DNA
<213> Homo sapien

<400> 284
caggtacaaa acgctattaa gtggcttaga atttgaacat ttgtggtctt tatttacttt 60
gcttcgtgtg tgggcaaagc aacatcttcc ctaaatatat attaccaaga aaagcaagaa 120
gcagattagg tttttgacaa aacaaacagg ccaaaagggg gctgacctgg agcagagcat 180

ggtgagaggc aaggcatgag agggcaagtt tgttgtggac agatctgtgc ctactttatt 240
actggagtaa aagaaaacaa agttcattga tgtcgaagga tatatacagt gttagaaatt 300
a 301

<210> 285
<211> 301
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(301)
<223> n = A,T,C or G

<400> 285
acatcaccat gatcggatcc cccacccatt atacgttgta tgtttacata aatactcttc 60
aatgatcatt agtgttttaa aaaaaatact gaaaactcct tctgcatccc aatctctaac 120
caggaaagca aatgctattt acagacctgc aagccctccc tcaaacnaaa ctatttctgg 180
attaaatatg tctgacttct tttgaggtca cacgactagg caaatgctat ttacgatctg 240
caaaagctgt ttgaagagtc aaagccccca tgtgaacacg atttctggac cctgtaacag 300
t 301

<210> 286
<211> 301
<212> DNA
<213> Homo sapien

<400> 286
taccactgca ttccagcctg ggtgacagag tgagactccg tctccaaaaa aaactttgct 60
tgtatattat ttttgcctta cagtggatca ttctagtagg aaaggacagt aagatttttt 120
atcaaaatgt gtcatgccag taagagatgt tatattcttt tctcatttct tccccaccca 180
aaaataagct accatatagc ttataagtct caaattttg cctttacta aaatgtgatt 240
gtttctgttc attgtgtatg cttcatcacc tatattaggc aaattccatt ttttcccttg 300
t 301

<210> 287
<211> 301
<212> DNA
<213> Homo sapien

<400> 287
tacagatctg ggaactaaat attaaaaatg agtgtggctg gatatatgga gaatgttggg 60
cccagaagga acgtagagat cagatattac aacagctttg ttttgagggt tagaaatatg 120
aaatgatttg gttatgaacg cacagtttag gcagcagggc cagaatcctg accctctgcc 180
ccgtggttat ctcctcccca gcttggctgc ctcatgttat cacagtattc cattttgttt 240
gttgcatgtc ttgtgaagcc atcaagattt tctcgtctgt tttcctctca ttggtaatgc 300
t 301

<210> 288
<211> 301
<212> DNA
<213> Homo sapien

<400> 288
gtacacctaa ctgcaaggac agctgaggaa tgtaatgggc agccgctttt aaagaagtag 60
agtcaatagg aagacaaatt ccagttccag ctcagtctgg gtatctgcaa agctgcaaaa 120
gatctttaaa gacaatttca agagaatatt tccttaaagt tggcaatttg gagatcatac 180
aaaagcatct gcttttgtga tttaatttag ctcatctggc cactggaaga atccaaacag 240

tctgccttaa ttttggatga atgcatgatg gaaattcaat aatttagaaa gttaaaaaaa 300
a 301

<210> 289
<211> 301
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(301)
<223> n = A,T,C or G

<400> 289
ggtacactgt ttccatgtta tgtttctaca cattgctacc tcagtgctcc tggaaactta 60
gcttttgatg tctccaagta gtccaccttc atttaactct ttgaaactgt atcatctttg 120
ccaagtaaga gtggtggcct atttcagctg ctttgacaaa atgactggct cctgacttaa 180
cgttctataa atgaatgtgc tgaagcaaag tgcccatggt ggcggcgaan aagagaaaga 240
tgtgttttgt tttggactct ctgtggtccc ttccaatgct gtgggtttcc aaccagngga 300
a 301

<210> 290
<211> 301
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(301)
<223> n = A,T,C or G

<400> 290
acactgagct cttcttgata aatatacaga atgcttggca tatacaagat tctatactac 60
tgactgatct gttcatttct ctcacagctc ttacccccaa aagcttttcc accctaagtg 120
ttctgacctc cttttctaat cacagtaggg atagaggcag anccacctac aatgaacatg 180
gagttctatc aagaggcaga aacagcacag aatcccagtt ttaccattcg ctagcagtgc 240
tgccttgaac aaaaacattt ctccatgtct cattttcttc atgcctcaag taacagtgag 300
a 301

<210> 291
<211> 301
<212> DNA
<213> Homo sapien

<400> 291
caggtaccaa tttcttctat cctagaaaca tttcatttta tgttgttgaa acataacaac 60
tatatcagct agattttttt tctatgcttt acctgctatg gaaaatttga cacattctgc 120
tttactcttt tgtttatagg tgaatcacaa aatgtatttt tatgtattct gtagttcaat 180
agccatggct gtttacttca tttaatttat ttagcataaa gacattatga aaaggcctaa 240
acatgagctt cacttcccca ctaactaatt agcatctgtt atttcttaac cgtaatgcct 300
a 301

<210> 292
<211> 301
<212> DNA
<213> Homo sapien

<220>

<221> misc_feature
<222> (1)...(301)
<223> n = A,T,C or G

<400> 292
acctttagt agtaatgtct aataataaat aagaaatcaa ttttataagg tccatatagc 60
tgtattaaat aatttttaag tttaaaagat aaaataccat cattttaaat gttggtattc 120
aaaaccaaag natataaccg aaaggaaaaa cagatgagac ataaaatgat ttgcnagatg 180
ggaaatatag tasttyatga atgttnatta aattccagtt ataatagtgg ctacacactc 240
tcactacaca cacagacccc acagtcctat atgccacaaa cacatttcca taacttgaaa 300
a 301

<210> 293
<211> 301
<212> DNA
<213> Homo sapien

<400> 293
ggtaccaagt gctggtgcca gcctgttacc tgttctcact gaaaagtctg gctaatgctc 60
ttgtgtagtc acttctgatt ctgacaatca atcaatcaat ggcctagagc actgactgtt 120
aacacaaacg tcactagcaa agtagcaaca gctttaagtc taaatacaaa gctgttctgt 180
gtgagaattt tttaaaaggc tacttgtata ataacccttg tcatttttaa tgtacctcgg 240
ccgcgaccac gctaagccga attctgcaga tatccatcac actggcggcc gctcgagcat 300
g 301

<210> 294
<211> 301
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(301)
<223> n = A,T,C or G

<400> 294
tgacccataa caatatacac tagctatctt tttaactgtc catcattagc accaatgaag 60
attcaataaa attaccttta ttcacacatc tcaaaacaat tctgcaaatt cttagtgaag 120
tttaactata gtcacaganc ttaaatattc acattgtttt ctatgtctac tgaaaataag 180
ttcactactt ttctgggata ttctttacaa aatcttatta aaattcctgg tattatcacc 240
cccaattata cagtagcaca accaccttat gtagttttta catgatagct ctgtagaggt 300
t 301

<210> 295
<211> 305
<212> DNA
<213> Homo sapien

<400> 295
gtactctttc tctcccctcc tctgaattta attctttcaa cttgcaattt gcaaggatta 60
cacatttcac tgtgatgtat attgtgttgc aaaaaaaaaa gtgtctttgt ttaaaattac 120
ttggtttgtg aatccatctt gctttttccc cattggaact agtcattaac ccatctctga 180
actggtagaa aaacrtctga agagctagtc tatcagcatc tgacaggtga attggatggt 240
tctcagaacc atttcaccca gacagcctgt ttctatcctg tttaataaat tagtttgggt 300
tctct 305

<210> 296
<211> 301

<212> DNA
<213> Homo sapien

<400> 296
```
aggtactatg ggaagctgct aaaataatat ttgatagtaa aagtatgtaa tgtgctatct     60
cacctagtag taaactaaaa ataaactgaa actttatgga atctgaagtt attttccttg    120
attaaataga attaataaac caatatgagg aaacatgaaa ccatgcaatc tactatcaac    180
tttgaaaaag tgattgaacg aaccacttag ctttcagatg atgaacactg ataagtcatt    240
tgtcattact ataaatttta aaatctgtta ataagatggc ctatagggag gaaaaagggg    300
c                                                                    301
```

<210> 297
<211> 300
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(300)
<223> n = A,T,C or G

<400> 297
```
actgagtttt aactggacgc caagcaggca aggctggaag gttttgctct ctttgtgcta     60
aaggttttga aaaccttgaa ggagaatcat tttgacaaga agtacttaag agtctagaga    120
acaaagangt gaaccagctg aaagctctcg gggaanctt acatgtgttg ttaggcctgt    180
tccatcattg ggagtgcact ggccatccct caaaatttgt ctgggctggc ctgagtggtc    240
accgcacctc ggccgcgacc acgctaagcc gaattctgca gatatccatc acactggcgg    300
```

<210> 298
<211> 301
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(301)
<223> n = A,T,C or G

<400> 298
```
tatggggttt gtcacccaaa agctgatgct gagaaaggcc tccctggggc ccctcccgcg     60
ggcatctgag agacctggtg ttccagtgtt tctggaaatg ggtcccagtg ccgccggctg    120
tgaagctctc agatcaatca cgggaagggc ctggcggtgg tggccacctg gaaccaccct    180
gtcctgtctg tttacatttc actaycaggt tttctctggg cattacnatt tgttccccta    240
caacagtgac ctgtgcattc tgctgtggcc tgctgtgtct gcaggtggct ctcagcgagg    300
t                                                                    301
```

<210> 299
<211> 301
<212> DNA
<213> Homo sapien

<400> 299
```
gttttgagac ggagtttcac tcttgttgcc cagactggac tgcaatggca gggtctctgc     60
tcactgcacc ctctgcctcc caggttcgag caattctcct gcctcagcct cccaggtagc    120
tgggattgca ggctcacgcc accataccca gctaattttt ttgtattttt agtagagacg    180
gagtttcgcc atgttggcca gctggtctca aactcctgac ctcaagcgac ctgcctgcct    240
cggcctccca aagtgctgga attataggca tgagtcaaca cgcccagcct aaagatattt    300
t                                                                    301
```

<210> 300
<211> 301
<212> DNA
<213> Homo sapien

<400> 300
attcagtttt atttgctgcc ccagtatctg taaccaggag tgccacaaaa tcttgccaga 60
tatgtcccac acccactggg aaaggctccc acctggctac ttcctctatc agctgggtca 120
gctgcattcc acaaggttct cagcctaatg agtttcacta cctgccagtc tcaaaactta 180
gtaaagcaag accatgacat tcccccacgg aaatcagagt ttgccccacc gtcttgttac 240
tataaagcct gcctctaaca gtccttgctt cttcacacca atcccgagcg catcccccat 300
g 301

<210> 301
<211> 301
<212> DNA
<213> Homo sapien

<400> 301
ttaaattttt gagaggataa aaaggacaaa taatctagaa atgtgtcttc ttcagtctgc 60
agaggacccc aggtctccaa gcaaccacat ggtcaagggc atgaataatt aaaagttggt 120
gggaactcac aaagaccctc agagctgaga cacccacaac agtgggagct cacaaagacc 180
ctcagagctg agacacccac aacagtggga gctcacaaag accctcagag ctgagacacc 240
cacaacagca cctcgttcag ctgccacatg tgtgaataag gatgcaatgt ccagaagtgt 300
t 301

<210> 302
<211> 301
<212> DNA
<213> Homo sapien

<400> 302
aggtacacat ttagcttgtg gtaaatgact cacaaaactg attttaaaat caagttaatg 60
tgaattttga aaattactac ttaatcctaa ttcacaataa caatggcatt aaggtttgac 120
ttgagttggt tcttagtatt atttatggta aataggctct taccacttgc aaataactgg 180
ccacatcatt aatgactgac ttcccagtaa ggctctctaa ggggtaagta ggaggatcca 240
caggatttga gatgctaagg ccccagagat cgtttgatcc aaccctctta ttttcagagg 300
g 301

<210> 303
<211> 301
<212> DNA
<213> Homo sapien

<400> 303
aggtaccaac tgtggaaata ggtagaggat catttttttct ttccatatca actaagttgt 60
atattgtttt ttgacagttt aacacatctt cttctgtcag agattctttc acaatagcac 120
tggctaatgg aactaccgct tgcatgttaa aaatggtggt ttgtgaaatg atcataggcc 180
agtaacgggt atgtttttct aactgatctt ttgctcgttc caaagggacc tcaagacttc 240
catcgatttt atatctgggg tctagaaaag gagttaatct gttttccctc ataaattcac 300
c 301

<210> 304
<211> 301
<212> DNA
<213> Homo sapien

<400> 304
acatggatgt tattttgcag actgtcaacc tgaatttgta tttgcttgac attgcctaat 60
tattagtttc agtttcagct tacccacttt ttgtctgcaa catgcaraas agacagtgcc 120
ctttttagtg tatcatatca ggaatcatct cacattggtt tgtgccatta ctggtgcagt 180
gactttcagc cacttgggta aggtggagtt ggccatatgt ctccactgca aaattactga 240
ttttcctttt gtaattaata agtgtgtgtg tgaagattct ttgagatgag gtatatatct 300
c 301

<210> 305
<211> 301
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(301)
<223> n = A,T,C or G

<400> 305
gangtacagc gtggtcaagg taacaagaag aaaaaaatgt gagtggcatc ctgggatgag 60
caggggggaca gacctggaca gacacgttgt catttgctgc tgtgggtagg aaaatgggcg 120
taaaggagga gaaacagata caaaatctcc aactcagtat taaggtattc tcatgcctag 180
aatattggta gaaacaagaa tacattcata tggcaaataa ctaaccatgg tggaacaaaa 240
ttctgggatt taagttggat accaangaaa ttgtattaaa agagctgttc atggaataag 300
a 301

<210> 306
<211> 8
<212> PRT
<213> Homo sapien

<400> 306
Val Leu Gly Trp Val Ala Glu Leu
1 5

<210> 307
<211> 637
<212> DNA
<213> Homo sapien

<400> 307
acagggratg aagggaaagg gagaggatga ggaagccccc ctggggattt ggtttggtcc 60
ttgtgatcag gtggtctatg gggcttatcc ctacaaagaa gaatccagaa ataggggcac 120
attgaggaat gatacttgag cccaaagagc attcaatcat tgttttattt gccttmtttt 180
cacaccattg gtgagggagg gattaccacc ctggggttat gaagatggtt gaacacccca 240
cacatagcac cggagatatg agatcaacag tttcttagcc atagagattc acagcccaga 300
gcaggaggac gcttgcacac catgcaggat gacatggggg atgcgctcgg gattggtgtg 360
aagaagcaag gactgttaga ggcaggcttt atagtaacaa gacggtgggg caaactctga 420
tttccgtggg ggaatgtcat ggtcttgctt tactaagttt tgagactggc aggtagtgaa 480
actcattagg ctgagaacct tgtggaatgc acttgaccca sctgatagag gaagtagcca 540
ggtgggagcc tttcccagtg ggtgtgggac atatctggca agatttgtg gcactcctgg 600
ttacagatac tggggcagca aataaaactg aatcttg 637

<210> 308
<211> 647
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(647)
<223> n = A,T,C or G

<400> 308
acgattttca ttatcatgta aatcgggtca ctcaaggggc caaccacagc tggagccac 60
tgctcagggg aaggttcata tgggactttc tactgcccaa ggttctatac aggatataaa 120
ggngcctcac agtatagatc tggtagcaaa gaagaagaaa caaacactga tctctttctg 180
ccacccctct gaccctttgg aactcctctg accctttaga acaagcctac ctaatatctg 240
ctagagaaaa gaccaacaac ggcctcaaag gatctcttac catgaaggtc tcagctaatt 300
cttggctaag atgtgggttc cacattaggt tctgaatatg gggggaaggg tcaatttgct 360
cattttgtgt gtggataaag tcaggatgcc caggggccag agcagggggc tgcttgcttt 420
gggaacaatg gctgagcata taaccatagg ttatggggaa caaaacaaca tcaaagtcac 480
tgtatcaatt gccatgaaga cttgagggac ctgaatctac cgattcatct taaggcagca 540
ggaccagttt gagtggcaac aatgcagcag cagaatcaat ggaaacaaca gaatgattgc 600
aatgtccttt tttttctcct gcttctgact tgataaaagg ggaccgt 647

<210> 309
<211> 460
<212> DNA
<213> Homo sapien

<400> 309
actttatagt ttaggctgga cattggaaaa aaaaaaaagc cagaacaaca tgtgatagat 60
aatatgattg gctgcacact tccagactga tgaatgatga acgtgatgga ctattgtatg 120
gagcacatct tcagcaagag gggaaatac tcatcatttt tggccagcag ttgtttgatc 180
accaaacatc atgccagaat actcagcaaa ccttcttagc tcttgagaag tcaaagtccg 240
ggggaattta ttcctggcaa ttttaattgg actccttatg tgagagcagc ggctacccag 300
ctggggtggt ggagcgaacc cgtcactagt ggacatgcag tggcagagct cctggtaacc 360
acctagagga atacacaggc acatgtgtga tgccaagcgt gacacctgta gcactcaaat 420
ttgtcttgtt tttgtctttc ggtgtgtaag attcttaagt 460

<210> 310
<211> 539
<212> DNA
<213> Homo sapien

<400> 310
acgggactta tcaaataaag ataggaaaag aagaaaactc aaatattata ggcagaaatg 60
ctaaaggttt taaaatatgt caggattgga agaaggcatg gataaagaac aaagttcagt 120
taggaaagag aaacacagaa ggaagagaca caataaaagt cattatgtat tctgtgagaa 180
gtcagacagt aagatttgtg ggaaatgggt tggtttgttg tatggtatgt attttagcaa 240
taatctttat ggcagagaaa gctaaaatcc tttagcttgc gtgaatgatc acttgctgaa 300
ttcctcaagg taggcatgat gaaggagggt ttagaggaga cacagacaca atgaactgac 360
ctagatagaa agccttagta tactcagcta ggaatagtga ttctgagggc acactgtgac 420
atgattatgt cattacatgt atggtagtga tggggatgat aggaaggaag aacttatggc 480
atattttcac ccccacaaaa gtcagttaaa tattgggaca ctaaccatcc aggtcaaga 539

<210> 311
<211> 526
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(526)
<223> n = A,T,C or G

<400> 311
caaatttgag ccaatgacat agaattttac aaatcaagaa gcttattctg gggccatttc 60
ttttgacgtt ttctctaaac tactaaagag gcattaatga tccataaatt atattatcta 120
catttacagc atttaaaatg tgttcagcat gaaatattag ctacagggga agctaaataa 180
attaaacatg gaataaagat ttgtccttaa atataatcta caagaagact ttgatatttg 240
tttttcacaa gtgaagcatt cttataaagt gtcataacct ttttggggaa actatgggaa 300
aaaatgggga aactctgaag ggttttaagt atcttacctg aagctacaga ctccataacc 360
tctctttaca gggagctcct gcagccccta cagaaatgag tggctgagat tcttgattgc 420
acagcaagag cttctcatct aaaccctttc ccttttagt atctgtgtat caagtataaa 480
agttctataa actgtagtnt acttatttta atccccaaag cacagt 526

<210> 312
<211> 500
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(500)
<223> n = A,T,C or G

<400> 312
cctctctctc cccacccccct gactctagag aactgggttt tctcccagta ctccagcaat 60
tcatttctga aagcagttga gccactttat tccaaagtac actgcagatg ttcaaactct 120
ccatttctct ttcccttcca cctgccagtt ttgctgactc tcaacttgtc atgagtgtaa 180
gcattaagga cattatgctt cttcgattct gaagacaggc cctgctcatg gatgactctg 240
gcttcttagg aaaatatttt tcttccaaaa tcagtaggaa atctaaactt atcccctctt 300
tgcagatgtc tagcagcttc agacatttgg ttaagaaccc atgggaaaaa aaaaaatcct 360
tgctaatgtg gtttcctttg taaaccanga ttcttatttg nctggtatag aatatcagct 420
ctgaacgtgt ggtaaagatt tttgtgtttg aatataggag aaatcagttt gctgaaaagt 480
tagtcttaat tatctattgg 500

<210> 313
<211> 718
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(718)
<223> n = A,T,C or G

<400> 313
ggagatttgt gtggtttgca gccgagggag accaggaaga tctgcatggt gggaaggacc 60
tgatgataca gaggtgagaa ataagaaagg ctgctgactt taccatctga ggccacacat 120
ctgctgaaat ggagataatt aacatcacta gaaacagcaa gatgacaata taatgtctaa 180
gtagtgacat gtttttgcac atttccagcc cttttaaata tccacacaca caggaagcac 240
aaaaggaagc acagagatcc ctgggagaaa tgcccggccg ccatcttggg tcatcgatga 300
gcctcgccct gtgcctgntc ccgcttgtga gggaaggaca ttagaaaatg aattgatgtg 360
ttccttaaag gatggcagga aaacagatcc tgttgtggat atttatttga acgggattac 420
agatttgaaa tgaagtcaca aagtgagcat taccaatgag aggaaaacag acgagaaaat 480
cttgatggtt cacaagacat gcaacaaaca aaatggaata ctgtgatgac acgagcagcc 540
aactggggag gagataccac ggggcagagg tcaggattct ggccctgctg cctaactgtg 600
cgttatacca atcatttcta tttctaccct caaacaagct gtngaatatc tgacttacgg 660
ttcttntggc ccacattttc atnatccacc ccntcntttt aannttantc caaantgt 718

<210> 314

<211> 358
<212> DNA
<213> Homo sapien

<400> 314
gtttatttac attacagaaa aaacatcaag acaatgtata ctatttcaaa tatatccata 60
cataatcaaa tatagctgta gtacatgttt tcattggtgt agattaccac aaatgcaagg 120
caacatgtgt agatctcttg tcttattctt ttgtctataa tactgtattg tgtagtccaa 180
gctctcggta gtccagccac tgtgaaacat gctcccttta gattaacctc gtggacgctc 240
ttgttgtatt gctgaactgt agtgccctgt attttgcttc tgtctgtgaa ttctgttgct 300
tctggggcat ttccttgtga tgcagaggac caccacacag atgacagcaa tctgaatt 358

<210> 315
<211> 341
<212> DNA
<213> Homo sapien

<400> 315
taccacctcc ccgctggcac tgatgagccg catcaccatg gtcaccagca ccatgaaggc 60
ataggtgatg atgaggacat ggaatgggcc cccaaggatg gtctgtccaa agaagcgagt 120
gaccccccatt ctgaagatgt ctggaacctc taccagcagg atgatgatag ccccaatgac 180
agtcaccagc tccccgacca gccggatatc gtccttaggg gtcatgtagg cttcctgaag 240
tagcttctgc tgtaagaggg tgttgtcccg gggctcgtg cggttattgg tcctgggctt 300
gagggggcgg tagatgcagc acatggtgaa gcagatgatg t 341

<210> 316
<211> 151
<212> DNA
<213> Homo sapien

<400> 316
agactgggca agactcttac gccccacact gcaatttggt cttgttgccg tatccattta 60
tgtgggcctt tctcgagttt ctgattataa acaccactgg agcgatgtgt tgactggact 120
cattcaggga gctctggttg caatattagt t 151

<210> 317
<211> 151
<212> DNA
<213> Homo sapien

<400> 317
agaactagtg gatcctaatg aaatacctga aacatatatt ggcatttatc aatggctcaa 60
atcttcattt atctctggcc ttaaccctgg ctcctgaggc tgcggccagc agatcccagg 120
ccagggctct gttcttgcca cacctgcttg a 151

<210> 318
<211> 151
<212> DNA
<213> Homo sapien

<400> 318
actggtggga ggcgctgttt agttggctgt tttcagaggg gtctttcgga gggacctcct 60
gctgcaggct ggagtgtctt tattcctggc gggagaccgc acattccact gctgaggctg 120
tgggggcggt ttatcaggca gtgataaaca t 151

<210> 319
<211> 151
<212> DNA

<213> Homo sapien

<400> 319
aactagtgga tccagagcta taggtacagt gtgatctcag ctttgcaaac acattttcta 60
catagatagt actaggtatt aatagatatg taaagaaaga aatcacacca ttaataatgg 120
taagattggg tttatgtgat tttagtgggt a 151

<210> 320
<211> 150
<212> DNA
<213> Homo sapien

<400> 320
aactagtgga tccactagtc cagtgtggtg gaattccatt gtgttggggt tctagatcgc 60
gagcggctgc cctttttttt tttttttttg ggggggaatt tttttttttt aatagttatt 120
gagtgttcta cagcttacag taaataccat 150

<210> 321
<211> 151
<212> DNA
<213> Homo sapien

<400> 321
agcaactttg tttttcatcc aggttatttt aggcttagga tttcctctca cactgcagtt 60
tagggtggca ttgtaaccag ctatggcata ggtgttaacc aaaggctgag taaacatggg 120
tgcctctgag aaatcaaagt cttcatacac t 151

<210> 322
<211> 151
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(151)
<223> n = A,T,C or G

<400> 322
atccagcatc ttctcctgtt tcttgccttc ctttttcttc ttcttasatt ctgcttgagg 60
tttgggcttg gtcagtttgc cacagggctt ggagatggtg acagtcttct ggcattcggc 120
attgtgcagg gctcgcttca nacttccagt t 151

<210> 323
<211> 151
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(151)
<223> n = A,T,C or G

<400> 323
tgaggacttg tkttcttttt ctttattttt aatcctctta ckttgtaaat atattgccta 60
nagactcant tactacccag tttgtggttt twtgggagaa atgtaactgg acagttagct 120
gttcaatyaa aaagacactt ancccatgtg g 151

<210> 324

<211> 461
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(461)
<223> n = A,T,C or G

<400> 324
```
acctgtgtgg aatttcagct ttcctcatgc aaaaggattt tgtatccccg gcctacttga      60
agaagtggtc agctaaagga atccaggttg ttggttggac tgttaatacc tttgatgaaa     120
agagttacta cgaatcccat cttggttcca gctatatcac tgacagcatg gtagaagact     180
gcgaacctca cttctagact ttcacggtgg gacgaaacgg gttcagaaac tgccaggggc     240
ctcatacagg gatatcaaaa taccctttgt gctacccagg ccctggggaa tcaggtgact     300
cacacaaatg caatagttgg tcactgcatt tttacctgaa ccaaagctaa acccggtgtt     360
gccaccatgc accatggcat gccagagttc aacactgttg ctcttgaaaa ttgggtctga     420
aaaaacgcac aagagcccct gccctgccct agctgangca c                         461
```

<210> 325
<211> 400
<212> DNA
<213> Homo sapien

<400> 325
```
acactgtttc catgttatgt ttctacacat tgctacctca gtgctcctgg aaacttagct      60
tttgatgtct ccaagtagtc caccttcatt taactctttg aaactgtatc atctttgcca     120
agtaagagtg gtggcctatt tcagctgctt tgacaaaatg actggctcct gacttaacgt     180
tctataaatg aatgtgctga agcaaagtgc ccatggtggc ggcgaagaag agaaagatgt     240
gttttgtttt ggactctctg tggtcccttc caatgctgtg ggtttccaac caggggaagg     300
gtcccttttg cattgccaag tgccataacc atgagcacta cgctaccatg gttctgcctc     360
ctggccaagc aggctggttt gcaagaatga aatgaatgat                           400
```

<210> 326
<211> 1215
<212> DNA
<213> Homo sapien

<400> 326
```
ggaggactgc agcccgcact cgcagccctg gcaggcggca ctggtcatgg aaaacgaatt      60
gttctgctcg ggcgtcctgg tgcatccgca gtgggtgctg tcagccgcac actgtttcca     120
gaactcctac accatcgggc tgggcctgca cagtcttgag gccgaccaag agccagggag     180
ccagatggtg gaggccagcc tctccgtacg gcacccagag tacaacagac ccttgctcgc     240
taacgacctc atgctcatca agttggacga atccgtgtcc gagtctgaca ccatccggag     300
catcagcatt gcttcgcagt gccctaccgc ggggaactct tgcctcgttt ctggctgggg     360
tctgctggcg aacggcagaa tgcctaccgt gctgcagtgc gtgaacgtgt cggtggtgtc     420
tgaggaggtc tgcagtaagc tctatgaccc gctgtaccac cccagcatgt tctgcgccgg     480
cggaggcaa gaccagaagg actcctgcaa cggtgactct gggggcccc tgatctgcaa       540
cgggtacttg cagggccttg tgtctttcgg aaaagccccg tgtggccaag ttggcgtgcc     600
aggtgtctac accaacctct gcaaattcac tgagtggata gagaaaaccg tccaggccag     660
ttaactctgg ggactgggaa cccatgaaat tgacccccaa atacatcctg cggaaggaat     720
tcaggaatat ctgttcccag cccctcctcc ctcaggccca ggagtccagg cccccagccc     780
ctcctccctc aaaccaaggg tacagatccc cagcccctcc tccctcagac ccaggagtcc     840
agacccccca gcccctcctc cctcagaccc aggagtccag cccctcctcc ctcagaccca     900
ggagtccaga ccccccagcc cctcctccct cagacccagg ggtccaggcc cccaacccct     960
cctccctcag actcagaggt ccaagccccc aacccctcct tccccagacc cagaggtcca    1020
ggtcccagcc cctcctccct cagacccagc ggtccaatgc cacctagact ctccctgtac    1080
acagtgcccc cttgtggcac gttgacccaa ccttaccagt tggtttttca tttttttgtcc   1140
```

ctttcccta gatccagaaa taaagtctaa gagaagcgca aaaaaaaaa aaaaaaaaa 1200
aaaaaaaaaa aaaaa 1215

<210> 327
<211> 220
<212> PRT
<213> Homo sapien

<400> 327
Glu Asp Cys Ser Pro His Ser Gln Pro Trp Gln Ala Ala Leu Val Met
1 5 10 15
Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln Trp Val
20 25 30
Leu Ser Ala Ala His Cys Phe Gln Asn Ser Tyr Thr Ile Gly Leu Gly
35 40 45
Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met Val Glu
50 55 60
Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro Leu Leu Ala
65 70 75 80
Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu Ser Asp
85 90 95
Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala Gly Asn
100 105 110
Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly Arg Met Pro
115 120 125
Thr Val Leu Gln Cys Val Asn Val Ser Val Val Ser Glu Glu Val Cys
130 135 140
Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe Cys Ala Gly
145 150 155 160
Gly Gly Gln Asp Gln Lys Asp Ser Cys Asn Gly Asp Ser Gly Gly Pro
165 170 175
Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe Gly Lys Ala
180 185 190
Pro Cys Gly Gln Val Gly Val Pro Gly Val Tyr Thr Asn Leu Cys Lys
195 200 205
Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Ala Ser
210 215 220

<210> 328
<211> 234
<212> DNA
<213> Homo sapien

<400> 328
cgctcgtctc tggtagctgc agccaaatca taaacggcga ggactgcagc ccgcactcgc 60
agccctggca ggcggcactg gtcatggaaa acgaattgtt ctgctcgggc gtcctggtgc 120
atccgcagtg ggtgctgtca gccacacact gtttccagaa ctcctacacc atcgggctgg 180
gcctgcacag tcttgaggcc gaccaagagc cagggagcca gatggtggag gcca 234

<210> 329
<211> 77
<212> PRT
<213> Homo sapien

<400> 329
Leu Val Ser Gly Ser Cys Ser Gln Ile Ile Asn Gly Glu Asp Cys Ser
1 5 10 15
Pro His Ser Gln Pro Trp Gln Ala Ala Leu Val Met Glu Asn Glu Leu

                20   25   30
Phe Cys Ser Gly Val Leu Val His Pro Gln Trp Val Leu Ser Ala Thr
        35   40   45
His Cys Phe Gln Asn Ser Tyr Thr Ile Gly Leu Gly Leu His Ser Leu
    50   55   60
Glu Ala Asp Gln Glu Pro Gly Ser Gln Met Val Glu Ala
65   70   75

<210> 330
<211> 70
<212> DNA
<213> Homo sapien

<400> 330
cccaacacaa tggcccgatc ccatccctga ctccgccctc aggatcgctc gtctctggta 60
gctgcagcca 70

<210> 331
<211> 22
<212> PRT
<213> Homo sapien

<400> 331
Gln His Asn Gly Pro Ile Pro Ser Leu Thr Pro Pro Ser Gly Ser Leu
 1   5   10   15
Val Ser Gly Ser Cys Ser
            20

<210> 332
<211> 2507
<212> DNA
<213> Homo sapien

<400> 332
tggtgccgct gcagccggca gagatggttg agctcatgtt cccgctgttg ctcctccttc 60
tgcccttcct tctgtatatg gctgcgcccc aaatcaggaa aatgctgtcc agtggggtgt 120
gtacatcaac tgttcagctt cctgggaaag tagttgtggt cacaggagct aatacaggta 180
tcgggaagga gacagccaaa gagctggctc agagaggagc tcgagtatat ttagcttgcc 240
gggatgtgga aaagggggaa ttggtggcca aagagatcca gaccacgaca gggaaccagc 300
aggtgttggt gcggaaactg gacctgtctg atactaagtc tattcgagct tttgctaagg 360
gcttcttagc tgaggaaaag cacctccacg ttttgatcaa caatgcagga gtgatgatgt 420
gtccgtactc gaagacagca gatggctttg agatgcacat aggagtcaac cacttgggtc 480
acttcctcct aacccatctg ctgctagaga aactaaagga atcagcccca tcaaggatag 540
taaatgtgtc ttccctcgca catcacctgg gaaggatcca cttccataac ctgcagggcg 600
agaaattcta caatgcaggc ctggcctact gtcacagcaa gctagccaac atcctcttca 660
cccaggaact ggcccggaga ctaaaaggct ctggcgttac gacgtattct gtacaccctg 720
gcacagtcca atctgaactg gttcggcact catctttcat gagatggatg tggtggcttt 780
tctccttttt catcaagact cctcagcagg gagcccagac cagcctgcac tgtgccttaa 840
cagaaggtct tgagattcta agtgggaatc atttcagtga ctgtcatgtg gcatgggtct 900
ctgcccaagc tcgtaatgag actatagcaa ggcggctgtg ggacgtcagt tgtgacctgc 960
tgggcctccc aatagactaa caggcagtgc cagttggacc caagagaaga ctgcagcaga 1020
ctacacagta cttcttgtca aaatgattct ccttcaaggt tttcaaaacc tttagcacaa 1080
agagagcaaa accttccagc cttgcctgct tggtgtccag ttaaaactca gtgtactgcc 1140
agattcgtct aaatgtctgt catgtccaga tttactttgc ttctgttact gccagagtta 1200
ctagagatat cataatagga taagaagacc ctcatatgac ctgcacagct cattttcctt 1260
ctgaaagaaa ctactaccta ggagaatcta agctatagca gggatgattt atgcaaattt 1320
gaactagctt ctttgttcac aattcagttc ctcccaacca accagtcttc acttcaagag 1380
ggccacactg caacctcagc ttaacatgaa taacaaagac tggctcagga gcagggcttg 1440

```
cccaggcatg gtggatcacc ggaggtcagt agttcaagac cagcctggcc aacatggtga    1500
aaccccacct ctactaaaaa ttgtgtatat ctttgtgtgt cttcctgttt atgtgtgcca    1560
agggagtatt ttcacaaagt tcaaaacagc cacaataatc agagatggag caaaccagtg    1620
ccatccagtc tttatgcaaa tgaaatgctg caaagggaag cagattctgt atatgttggt    1680
aactacccac caagagcaca tgggtagcag ggaagaagta aaaaaagaga aggagaatac    1740
tggaagataa tgcacaaaat gaagggacta gttaaggatt aactagccct ttaaggatta    1800
actagttaag gattaatagc aaaagayatt aaatatgcta acatagctat ggaggaattg    1860
agggcaagca cccaggactg atgaggtctt aacaaaaacc agtgtggcaa aaaaaaaaaa    1920
aaaaaaaaaa aaaaatccta aaaacaaaca aacaaaaaaa acaattcttc attcagaaaa    1980
attatcttag ggactgatat tggtaattat ggtcaattta ataatatttt ggggcatttc    2040
cttacattgt cttgacaaga ttaaaatgtc tgtgccaaaa ttttgtattt tatttggaga    2100
cttcttatca aaagtaatgc tgccaaagga agtctaagga attagtagtg ttcccatcac    2160
ttgtttggag tgtgctattc taaaagattt tgatttcctg gaatgacaat tatattttaa    2220
ctttggtggg ggaaagagtt ataggaccac agtcttcact tctgatactt gtaaattaat    2280
cttttattgc acttgttttg accattaagc tatatgttta gaaatggtca ttttacggaa    2340
aaattagaaa aattctgata atagtgcaga ataaatgaat taatgtttta cttaatttat    2400
attgaactgt caatgacaaa taaaaattct ttttgattat tttttgtttt catttaccag    2460
aataaaaacg taagaattaa aagtttgatt acaaaaaaaa aaaaaaa                  2507
```

<210> 333
<211> 3030
<212> DNA
<213> Homo sapien

<400> 333

```
gcaggcgact tgcgagctgg gagcgattta aaacgctttg gattcccccg gcctgggtgg      60
ggagagcgag ctgggtgccc cctagattcc ccgcccccgc acctcatgag ccgaccctcg     120
gctccatgga gcccggcaat tatgccacct tggatggagc caaggatatc gaaggcttgc     180
tgggagcggg agggggcgg aatctggtcg cccactcccc tctgaccagc cacccagcgg      240
cgcctacgct gatgcctgct gtcaactatg ccccttgga tctgccaggc tcggcggagc      300
cgccaaagca atgccaccca tgccctgggg tgccccaggg gacgtcccca gctcccgtgc     360
cttatggtta ctttggaggc gggtactact cctgccgagt gtcccggagc tcgctgaaac     420
cctgtgccca ggcagccacc ctggccgcgt accccgcgga gactcccacg gccggggaag     480
agtaccccag ycgcccact gagtttgcct tctatccggg atatccggga acctaccagc      540
ctatggccag ttacctggac gtgtctgtgg tgcagactct gggtgctcct ggagaaccgc     600
gacatgactc cctgttgcct gtggacagtt accagtcttg ggctctcgct ggtggctgga     660
acagccagat gtgttgccag ggagaacaga acccaccagg tcccttttgg aaggcagcat     720
ttgcagactc cagcgggcag caccctcctg acgcctgcgc ctttcgtcgc ggccgcaaga     780
aacgcattcc gtacagcaag gggcagttgc gggagctgga gcgggagtat gcggctaaca     840
agttcatcac caaggacaag aggcgcaaga tctcggcagc caccagcctc tcggagcgcc     900
agattaccat ctggtttcag aaccgccggg tcaaagagaa gaaggttctc gccaaggtga     960
agaacagcgc taccccttaa gagatctcct tgcctgggtg ggaggagcga aagtgggggt    1020
gtcctgggga gaccaggaac ctgccaagcc caggctgggg ccaaggactc tgctgagagg    1080
cccctagaga caacaccctt cccaggccac tggctgctgg actgttcctc aggagcggcc    1140
tgggtaccca gtatgtgcag ggagacggaa ccccatgtga cagcccactc caccagggtt    1200
cccaaagaac ctggcccagt cataatcatt catcctgaca gtggcaataa tcacgataac    1260
cagtactagc tgccatgatc gttagcctca tattttctat ctagagctct gtagagcact    1320
ttagaaaccg ctttcatgaa ttgagctaat tatgaataaa tttggaaggc gatccctttg    1380
cagggaagct ttctctcaga cccccttcca ttacacctct caccctggta acagcaggaa    1440
gactgaggag aggggaacgg gcagattcgt tgtgtggctg tgatgtccgt ttagcatttt    1500
tctcagctga cagctgggta ggtggacaat tgtagaggct gtctcttcct ccctccttgt    1560
ccaccccata gggtgtaccc actggtcttg gaagcaccca tccttaatac gatgattttt    1620
ctgtcgtgtg aaaatgaagc cagcaggctg cccctagtca gtccttcctt ccagagaaaa    1680
agagatttga gaaagtgcct gggtaattca ccattaattt cctcccccaa actctctgag    1740
tcttccctta atatttctgg tggttctgac caaagcaggt catggtttgt tgagcatttg    1800
ggatcccagt gaagtagatg tttgtagcct tgcatactta gcccttccca ggcacaaacg    1860
gagtggcaga gtggtgccaa ccctgttttc ccagtccacg tagacagatt cacagtgcgg    1920
aattctggaa gctggagaca gacgggctct ttgcagagcc gggactctga gagggacatg    1980
```

agggcctctg cctctgtgtt cattctctga tgtcctgtac ctgggctcag tgcccggtgg 2040
gactcatctc ctggccgcgc agcaaagcca gcgggttcgt gctggtcctt cctgcacctt 2100
aggctggggg tgggggcct gccggcgcat tctccacgat tgagcgcaca ggcctgaagt 2160
ctggacaacc cgcagaaccg aagctccgag cagcgggtcg gtggcgagta gtggggtcgg 2220
tggcgagcag ttggtggtgg gccgcggccg ccactacctc gaggacattt ccctcccgga 2280
gccagctctc ctagaaaccc cgcggcggcc gccgcagcca agtgtttatg gcccgcggtc 2340
gggtgggatc ctagccctgt ctcctctcct gggaaggagt gagggtggga cgtgacttag 2400
acacctacaa atctatttac caaagaggag cccgggactg agggaaaagg ccaaagagtg 2460
tgagtgcatg cggactgggg gttcagggga agaggacgag gaggaggaag atgaggtcga 2520
tttcctgatt taaaaaatcg tccaagcccc gtggtccagc ttaaggtcct cggttacatg 2580
cgccgctcag agcaggtcac tttctgcctt ccacgtcctc cttcaaggaa gccccatgtg 2640
ggtagctttc aatatcgcag gttcttactc ctctgcctct ataagctcaa acccaccaac 2700
gatcgggcaa gtaaaccccc tccctcgccg acttcggaac tggcgagagt tcagcgcaga 2760
tgggcctgtg gggaggggc aagatagatg agggggagcg gcatggtgcg gggtgacccc 2820
ttggagagag gaaaaaggcc acaagagggg ctgccaccgc cactaacgga gatggccctg 2880
gtagagacct ttgggggtct ggaacctctg gactccccat gctctaactc ccacactctg 2940
ctatcagaaa cttaaacttg aggattttct ctgtttttca ctcgcaataa aytcagagca 3000
aacaaaaaaa aaaaaaaaaa aaaactcgag 3030

<210> 334
<211> 2417
<212> DNA
<213> Homo sapien

<400> 334
ggcggccgct ctagagctag tgggatcccc cgggctgcac gaattcggca cgagtgagtt 60
ggagttttac ctgtattgtt ttaatttcaa caagcctgag gactagccac aaatgtaccc 120
agtttacaaa tgaggaaaca ggtgcaaaaa ggttgttacc tgtcaaaggt cgtatgtggc 180
agagccaaga tttgagccca gttatgtctg atgaacttag cctatgctct ttaaacttct 240
gaatgctgac cattgaggat atctaaactt agatcaattg cattttccct ccaagactat 300
ttacttatca atacaataat accaccttta ccaatctatt gttttgatac gagactcaaa 360
tatgccagat atatgtaaaa gcaacctaca agctctctaa tcatgctcac ctaaaagatt 420
cccgggatct aataggctca aagaaacttc ttctagaaat ataaaagaga aaattggatt 480
atgcaaaaat tcattattaa tttttttcat ccatccttta attcagcaaa catttatctg 540
ttgttgactt tatgcagtat ggccttttaa ggattggggg acaggtgaag aacggggtgc 600
cagaatgcat cctcctacta atgaggtcag tacacatttg cattttaaaa tgccctgtcc 660
agctgggcat ggtggatcat gcctgtaatc tcaacattgg aaggccaagg caggaggatt 720
gcttcagccc aggagttcaa gaccagcctg ggcaacatag aaagacccca tctctcaatc 780
aatcaatcaa tgccctgtct ttgaaaataa aactctttaa gaaaggttta atgggcaggg 840
tgtggtagct catgcctata atacagcact ttgggaggct gaggcaggag gatcacttta 900
gcccagaagt tcaagaccag cctgggcaac aagtgacacc tcatctcaat tttttaataa 960
aatgaataca tacataagga aagataaaaa gaaaagttta atgaaagaat acagtataaa 1020
acaaatctct tggacctaaa agtatttttg ttcaagccaa atattgtgaa tcacctctct 1080
gtgttgagga tacagaatat ctaagcccag gaaactgagc agaaagttca tgtactaact 1140
aatcaacccg aggcaaggca aaaatgagac taactaatca atccgaggca aggggcaaat 1200
tagacggaac ctgactctgg tctattaagc gacaactttc cctctgttgt atttttcttt 1260
tattcaatgt aaaaggataa aaactctcta aaactaaaaa caatgtttgt caggagttac 1320
aaaccatgac caactaatta tggggaatca taaaatatga ctgtatgaga tcttgatggt 1380
ttacaaagtg tacccactgt taatcacttt aaacattaat gaacttaaaa atgaatttac 1440
ggagattgga atgtttcttt cctgttgtat tagttggctc aggctgccat aacaaaatac 1500
cacagactgg gaggcttaag taacagaaat tcatttctca cagttctggg ggctggaagt 1560
ccacgatcaa ggtgcaggaa aggcaggctt cattctgagg cccctctctt ggctcacatg 1620
tggccaccct cccactgcgt gctcacatga cctctttgtg ctcctggaaa gagggtgtgg 1680
gggacagagg gaaagagaag gagagggaac tctctggtgt ctcgtctttc aaggacccta 1740
acctgggcca ctttggccca ggcactgtgg ggtgggggt tgtggctgct ctgctctgag 1800
tggccaagat aaagcaacag aaaaatgtcc aaagctgtgc agcaaagaca agccaccgaa 1860
cagggatctg ctcatcagtg tggggacctc caagtcggcc accctggagg caagccccca 1920
cagagcccat gcaaggtggc agcagcagaa gaagggaatt gtccctgtcc ttggcacatt 1980

cctcaccgac ctggtgatgc tggacactgc gatgaatggt aatgtggatg agaatatgat 2040
ggactcccag aaaaggagac ccagctgctc aggtggctgc aaatcattac agccttcatc 2100
ctggggagga actgggggcc tggttctggg tcagagagca gcccagtgag ggtgagagct 2160
acagcctgtc ctgccagctg gatccccagt cccggtcaac cagtaatcaa ggctgagcag 2220
atcaggcttc ccggagctgg tcttgggaag ccagccctgg ggtgagttgg ctcctgctgt 2280
ggtactgaga caatattgtc ataaattcaa tgcgcccttg tatccctttt tctttttat 2340
ctgtctacat ctataatcac tatgcatact agtctttgtt agtgtttcta ttcmacttaa 2400
tagagatatg ttatact 2417

<210> 335
<211> 2984
<212> DNA
<213> Homo sapien

<400> 335
atccctcctt ccccactctc ctttccagaa ggcacttggg gtcttatctg ttggactctg 60
aaaacacttc aggcgccctt ccaaggcttc cccaaacccc taagcagccg cagaagcgct 120
cccgagctgc cttctcccac actcaggtga tcgagttgga gaggaagttc agccatcaga 180
agtacctgtc ggcccctgaa cgggcccacc tggccaagaa cctcaagctc acggagaccc 240
aagtgaagat atggttccag aacagacgct ataagactaa gcgaaagcag ctctcctcgg 300
agctgggaga cttggagaag cactcctctt tgccggccct gaaagaggag gccttctccc 360
gggcctccct ggtctccgtg tataacagct atccttacta cccatacctg tactgcgtgg 420
gcagctggag cccagctttt tggtaatgcc agctcaggtg acaaccatta tgatcaaaaa 480
ctgccttccc cagggtgtct ctatgaaaag cacaaggggc caaggtcagg gagcaagagg 540
tgtgcacacc aaagctattg gagatttgcg tggaaatctc asattcttca ctggtgagac 600
aatgaaacaa cagagacagt gaaagtttta atacctaagt cattccccca gtgcatactg 660
taggtcattt tttttgcttc tggctacctg tttgaagggg agagagggaa aatcaagtgg 720
tattttccag cactttgtat gattttggat gagctgtaca cccaaggatt ctgttctgca 780
actccatcct cctgtgtcac tgaatatcaa ctctgaaaga gcaaacctaa caggagaaag 840
gacaaccagg atgaggatgt caccaactga attaaactta agtccagaag cctcctgttg 900
gccttggaat atggccaagg ctctctctgt ccctgtaaaa gagaggggca aatagagagt 960
ctccaagaga acgccctcat gctcagcaca tatttgcatg ggaggggggag atgggtggga 1020
ggagatgaaa atatcagctt ttcttattcc tttttattcc ttttaaaatg gtatgccaac 1080
ttaagtattt acagggtggc ccaaatagaa caagatgcac tcgctgtgat tttaagacaa 1140
gctgtataaa cagaactcca ctgcaagagg gggggccggg ccaggagaat ctccgcttgt 1200
ccaagacagg ggcctaagga gggtctccac actgctgcta ggggctgttg cattttttta 1260
ttagtagaaa gtggaaaggc ctcttctcaa ctttttcccc ttgggctgga gaatttagaa 1320
tcagaagttt cctggagttt tcaggctatc atatatactg tatcctgaaa ggcaacataa 1380
ttcttccttc cctcctttta aaattttgtg ttccttttttg cagcaattac tcactaaagg 1440
gcttcatttt agtccagatt tttagtctgg ctgcacctaa cttatgcctc gcttatttag 1500
cccgagatct ggtctttttt tttttttttt tttttccgtc tccccaaagc tttatctgtc 1560
ttgacttttt aaaaaagttt gggggcagat tctgaattgg ctaaaagaca tgcattttta 1620
aaactagcaa ctcttatttc tttcctttaa aaatacatag cattaaatcc caaatcctat 1680
ttaaagacct gacagcttga gaaggtcact actgcattta taggaccttc tggtggttct 1740
gctgttacgt ttgaagtctg acaatccttg agaatctttg catgcagagg aggtaagagg 1800
tattggattt tcacagagga agaacacagc gcagaatgaa gggccaggct tactgagctg 1860
tccagtggag ggctcatggg tgggacatgg aaaagaaggc agcctaggcc ctggggagcc 1920
cagtccactg agcaagcaag ggactgagtg agcctttttgc aggaaaaggc taagaaaaag 1980
gaaaaccatt ctaaaacaca acaagaaact gtccaaatgc tttgggaact gtgtttattg 2040
cctataatgg gtccccaaaa tgggtaacct agacttcaga gagaatgagc agagagcaaa 2100
ggagaaatct ggctgtcctt ccattttcat tctgttatct caggtgagct ggtagagggg 2160
agacattaga aaaaaatgaa acaacaaaac aattactaat gaggtacgct gaggcctggg 2220
agtctcttga ctccactact taattccgtt tagtgagaaa cctttcaatt ttcttttatt 2280
agaaggcca gcttactgtt ggtggcaaaa ttgccaacat aagttaatag aaagttggcc 2340
aatttcaccc catttctgt ggtttgggct ccacattgca atgttcaatg ccacgtgctg 2400
ctgacaccga ccggagtact agccagcaca aaaggcaggg tagcctgaat tgctttctgc 2460
tctttacatt tcttttaaaa taagcattta gtgctcagtc cctactgagt actctttctc 2520
tcccctcctc tgaatttaat tctttcaact tgcaatttgc aaggattaca catttcactg 2580

```
tgatgtatat tgtgttgcaa aaaaaaaaaa aagtgtcttt gtttaaaatt acttggtttg    2640
tgaatccatc ttgcttttc cccattggaa ctagtcatta acccatctct gaactggtag    2700
aaaaacatct gaagagctag tctatcagca tctgacaggt gaattggatg gttctcagaa    2760
ccatttcacc cagacagcct gtttctatcc tgtttaataa attagtttgg gttctctaca    2820
tgcataacaa accctgctcc aatctgtcac ataaaagtct gtgacttgaa gtttagtcag    2880
cacccccacc aaactttatt tttctatgtg ttttttgcaa catatgagtg ttttgaaaat    2940
aaagtaccca tgtctttatt agaaaaaaaa aaaaaaaaaa aaaa                     2984

      <210> 336
      <211> 147
      <212> PRT
      <213> Homo sapien

      <400> 336
Pro Ser Phe Pro Thr Leu Leu Ser Arg Arg His Leu Gly Ser Tyr Leu
 1              5                   10                  15
Leu Asp Ser Glu Asn Thr Ser Gly Ala Leu Pro Arg Leu Pro Gln Thr
            20                  25                  30
Pro Lys Gln Pro Gln Lys Arg Ser Arg Ala Ala Phe Ser His Thr Gln
        35                  40                  45
Val Ile Glu Leu Glu Arg Lys Phe Ser His Gln Lys Tyr Leu Ser Ala
    50                  55                  60
Pro Glu Arg Ala His Leu Ala Lys Asn Leu Lys Leu Thr Glu Thr Gln
65                  70                  75                  80
Val Lys Ile Trp Phe Gln Asn Arg Arg Tyr Lys Thr Lys Arg Lys Gln
                85                  90                  95
Leu Ser Ser Glu Leu Gly Asp Leu Glu Lys His Ser Ser Leu Pro Ala
            100                 105                 110
Leu Lys Glu Glu Ala Phe Ser Arg Ala Ser Leu Val Ser Val Tyr Asn
        115                 120                 125
Ser Tyr Pro Tyr Tyr Pro Tyr Leu Tyr Cys Val Gly Ser Trp Ser Pro
    130                 135                 140
Ala Phe Trp
145

      <210> 337
      <211> 9
      <212> PRT
      <213> Homo sapien

      <400> 337
Ala Leu Thr Gly Phe Thr Phe Ser Ala
 1              5

      <210> 338
      <211> 9
      <212> PRT
      <213> Homo sapien

      <400> 338
Leu Leu Ala Asn Asp Leu Met Leu Ile
 1              5

      <210> 339
      <211> 318
      <212> PRT
      <213> Homo sapien
```

<400> 339
```
Met Val Glu Leu Met Phe Pro Leu Leu Leu Leu Leu Leu Pro Phe Leu
1               5                   10                  15
Leu Tyr Met Ala Ala Pro Gln Ile Arg Lys Met Leu Ser Ser Gly Val
            20                  25                  30
Cys Thr Ser Thr Val Gln Leu Pro Gly Lys Val Val Val Val Thr Gly
        35                  40                  45
Ala Asn Thr Gly Ile Gly Lys Glu Thr Ala Lys Glu Leu Ala Gln Arg
    50                  55                  60
Gly Ala Arg Val Tyr Leu Ala Cys Arg Asp Val Glu Lys Gly Glu Leu
65                  70                  75                  80
Val Ala Lys Glu Ile Gln Thr Thr Thr Gly Asn Gln Gln Val Leu Val
                85                  90                  95
Arg Lys Leu Asp Leu Ser Asp Thr Lys Ser Ile Arg Ala Phe Ala Lys
            100                 105                 110
Gly Phe Leu Ala Glu Glu Lys His Leu His Val Leu Ile Asn Asn Ala
        115                 120                 125
Gly Val Met Met Cys Pro Tyr Ser Lys Thr Ala Asp Gly Phe Glu Met
    130                 135                 140
His Ile Gly Val Asn His Leu Gly His Phe Leu Leu Thr His Leu Leu
145                 150                 155                 160
Leu Glu Lys Leu Lys Glu Ser Ala Pro Ser Arg Ile Val Asn Val Ser
                165                 170                 175
Ser Leu Ala His His Leu Gly Arg Ile His Phe His Asn Leu Gln Gly
            180                 185                 190
Glu Lys Phe Tyr Asn Ala Gly Leu Ala Tyr Cys His Ser Lys Leu Ala
        195                 200                 205
Asn Ile Leu Phe Thr Gln Glu Leu Ala Arg Arg Leu Lys Gly Ser Gly
    210                 215                 220
Val Thr Thr Tyr Ser Val His Pro Gly Thr Val Gln Ser Glu Leu Val
225                 230                 235                 240
Arg His Ser Ser Phe Met Arg Trp Met Trp Trp Leu Phe Ser Phe Phe
                245                 250                 255
Ile Lys Thr Pro Gln Gln Gly Ala Gln Thr Ser Leu His Cys Ala Leu
            260                 265                 270
Thr Glu Gly Leu Glu Ile Leu Ser Gly Asn His Phe Ser Asp Cys His
        275                 280                 285
Val Ala Trp Val Ser Ala Gln Ala Arg Asn Glu Thr Ile Ala Arg Arg
    290                 295                 300
Leu Trp Asp Val Ser Cys Asp Leu Leu Gly Leu Pro Ile Asp
305                 310                 315
```

<210> 340
<211> 483
<212> DNA
<213> Homo sapien

<400> 340
```
gccgaggtct gccttcacac ggaggacacg agactgcttc ctcaagggct cctgcctgcc      60
tggacactgg tgggaggcgc tgtttagttg gctgttttca gaggggtctt tcggagggac     120
ctcctgctgc aggctggagt gtctttattc ctggcgggag accgcacatt ccactgctga     180
ggttgtgggg gcggtttatc aggcagtgat aaacataaga tgtcatttcc ttgactccgg     240
ccttcaattt tctctttggc tgacgacgga gtccgtggtg tcccgatgta actgacccct     300
gctccaaacg tgacatcact gatgctcttc tcgggggtgc tgatggcccg cttggtcacg     360
tgctcaatct cgccattcga ctcttgctcc aaactgtatg aagacacctg actgcacgtt     420
ttttctgggc ttccagaatt taaagtgaaa ggcagcactc ctaagctccg actccgatgc     480
ctg                                                                   483
```

<210> 341
<211> 344
<212> DNA
<213> Homo sapien

<400> 341
ctgctgctga gtcacagatt tcattataaa tagcctccct aaggaaaata cactgaatgc 60
tatttttact aaccattcta tttttataga aatagctgag agtttctaaa ccaactctct 120
gctgccttac aagtattaaa tattttactt ctttccataa agagtagctc aaaatatgca 180
attaatttaa taatttctga tgatggtttt atctgcagta atatgtatat catctattag 240
aatttactta atgaaaaact gaagagaaca aaatttgtaa ccactagcac ttaagtactc 300
ctgattctta acattgtctt taatgaccac aagacaacca acag 344

<210> 342
<211> 592
<212> DNA
<213> Homo sapien

<400> 342
acagcaaaaa agaaactgag aagcccaaty tgctttcttg ttaacatcca cttatccaac 60
caatgtggaa acttcttata cttggttcca ttatgaagtt ggacaattgc tgctatcaca 120
cctggcaggt aaaccaatgc caagagagtg atggaaacca ttggcaagac tttgttgatg 180
accaggattg gaattttata aaaatattgt tgatgggaag ttgctaaagg gtgaattact 240
tccctcagaa gagtgtaaag aaaagtcaga gatgctataa tagcagctat tttaattggc 300
aagtgccact gtggaaagag ttcctgtgtg tgctgaagtt ctgaagggca gtcaaattca 360
tcagcatggg ctgtttggtg caaatgcaaa agcacaggtc tttttagcat gctggtctct 420
cccgtgtcct tatgcaaata atcgtcttct tctaaatttc tcctaggctt cattttccaa 480
agttcttctt ggtttgtgat gtcttttctg ctttccatta attctataaa atagtatggc 540
ttcagccacc cactcttcgc cttagcttga ccgtgagtct cggctgccgc tg 592

<210> 343
<211> 382
<212> DNA
<213> Homo sapien

<400> 343
ttcttgacct cctcctcctt caagctcaaa caccacctcc cttattcagg accggcactt 60
cttaatgttt gtggctttct ctccagcctc tcttaggagg ggtaatggtg gagttggcat 120
cttgtaactc tcctttctcc tttcttcccc tttctctgcc cgcctttccc atcctgctgt 180
agacttcttg attgtcagtc tgtgtcacat ccagtgattg ttttggtttc tgttcccttt 240
ctgactgccc aaggggctca gaaccccagc aatcccttcc tttcactacc ttcttttttg 300
ggggtagttg gaagggactg aaattgtggg gggaaggtag gaggcacatc aataaagagg 360
aaaccaccaa gctgaaaaaa aa 382

<210> 344
<211> 536
<212> DNA
<213> Homo sapien

<400> 344
ctgggcctga agctgtaggg taaatcagag gcaggcttct gagtgatgag agtcctgaga 60
caataggcca cataaacttg gctggatgga acctcacaat aaggtggtca cctcttgttt 120
gtttaggggg atgccaagga taaggccagc tcagttatat gaagagaagc agaacaaaca 180
agtctttcag agaaatggat gcaatcagag tgggatcccg gtcacatcaa ggtcacactc 240
caccttcatg tgcctgaatg gttgccaggt cagaaaaatc cacccccttac gagtgcggct 300
tcgaccctat atccccccgcc cgcgtccctt tctccataaa attcttctta gtagctatta 360
ccttcttatt atttgatcta gaaattgccc tccttttacc cctaccatga gccctacaaa 420

caactaacct gccactaata gttatgtcat ccctcttatt aatcatcatc ctagccctaa 480
gtctggccta tgagtgacta caaaaaggat tagactgagc cgaataacaa aaaaaa 536

<210> 345
<211> 251
<212> DNA
<213> Homo sapien

<400> 345
acctttgag gtctctctca ccacctccac agccaccgtc accgtgggat gtgctggatg 60
tgaatgaagc cccatcttt gtgcctcctg aaaagagagt ggaagtgtcc gaggactttg 120
gcgtgggcca ggaaatcaca tcctacactg cccaggagcc agacacattt atggaacaga 180
aaataacata tcggatttgg agagacactg ccaactggct ggagattaat ccggacactg 240
gtgccatttc c 251

<210> 346
<211> 282
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(282)
<223> n = A,T,C or G

<400> 346
cgcgtctctg acactgtgat catgacaggg gttcaaacag aaagtgcctg ggccctcctt 60
ctaagtcttg ttaccaaaaa aaggaaaaag aaaagatctt ctcagttaca aattctggga 120
agggagacta tacctggctc ttgccctaag tgagaggtct tccctcccgc accaaaaaat 180
agaaaggctt tctatttcac tggcccaggt aggggaaggg agagtaactt tgagtctgtg 240
ggtctcattt cccaaggtgc cttcaatgct catnaaaacc aa 282

<210> 347
<211> 201
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(201)
<223> n = A,T,C or G

<400> 347
acacacataa tattataaaa tgccatctaa ttggaaggag ctttctatca ttgcaagtca 60
taaatataac ttttaaaana ntactancag cttttaccta ngctcctaaa tgcttgtaaa 120
tctgagactg actggaccca cccagaccca gggcaaagat acatgttacc atatcatctt 180
tataaagaat tttttttgt c 201

<210> 348
<211> 251
<212> DNA
<213> Homo sapien

<400> 348
ctgttaatca caacatttgt gcatcacttg tgccaagtga gaaaatgttc taaaatcaca 60
agagagaaca gtgccagaat gaaactgacc ctaagtccca ggtgcccctg ggcaggcaga 120
aggagacact cccagcatgg aggagggttt atcttttcat cctaggtcag gtctacaatg 180
ggggaaggtt ttattataga actcccaaca gcccacctca ctcctgccac ccacccgatg 240

gccctgcctc c 251

<210> 349
<211> 251
<212> DNA
<213> Homo sapien

<400> 349
taaaaatcaa gccatttaat tgtatctttg aaggtaaaca atatatggga gctggatcac 60
aacccctgag gatgccagag ctatgggtcc agaacatggt gtggtattat caacagagtt 120
cagaagggtc tgaactctac gtgttaccag agaacataat gcaattcatg cattccactt 180
agcaattttg taaaatacca gaaacagacc ccaagagtct ttcaagatga ggaaaattca 240
actcctggtt t 251

<210> 350
<211> 908
<212> DNA
<213> Homo sapien

<400> 350
ctggacactt tgcgagggct tttgctggct gctgctgctg cccgtcatgc tactcatcgt 60
agcccgcccg gtgaagctcg ctgctttccc tacctcctta agtgactgcc aaacgcccac 120
cggctggaat tgctctggtt atgatgacag agaaaatgat ctcttcctct gtgacaccaa 180
cacctgtaaa tttgatgggg aatgtttaag aattggagac actgtgactt gcgtctgtca 240
gttcaagtgc aacaatgact atgtgcctgt gtgtggctcc aatggggaga gctaccagaa 300
tgagtgttac ctgcgacagg ctgcatgcaa acagcagagt gagatacttg tggtgtcaga 360
aggatcatgt gccacagtcc atgaaggctc tggagaaact agtcaaaagg agacatccac 420
ctgtgatatt tgccagtttg gtgcagaatg tgacgaagat gccgaggatg tctggtgtgt 480
gtgtaatatt gactgttctc aaaccaactt caatcccctc tgcgcttctg atgggaaatc 540
ttatgataat gcatgccaaa tcaaagaagc atcgtgtcag aaacaggaga aattgaagt 600
catgtctttg ggtcgatgtc aagataacac aactacaact actaagtctg aagatgggca 660
ttatgcaaga acagattatg cagagaatgc taacaaatta gaagaaagtg ccagagaaca 720
ccacatacct tgtccggaac attacaatgg cttctgcatg catgggaagt gtgagcattc 780
tatcaatatg caggagccat cttgcaggtg tgatgctggt tatactggac aacactgtga 840
aaaaaaggac tacagtgttc tatacgttgt tcccggtcct gtacgatttc agtatgtctt 900
aatcgcag 908

<210> 351
<211> 472
<212> DNA
<213> Homo sapien

<400> 351
ccagttattt gcaagtggta agagcctatt taccataaat aatactaaga accaactcaa 60
gtcaaacctt aatgccattg ttattgtgaa ttaggattaa gtagtaattt tcaaaattca 120
cattaacttg attttaaaat cagwtttgyg agtcatttac cacaagctaa atgtgtacac 180
tatgataaaa acaaccattg tattcctgtt tttctaaaca gtcctaattt ctaacactgt 240
atatatcctt cgacatcaat gaactttgtt ttcttttact ccagtaataa agtaggcaca 300
gatctgtcca caacaaactt gccctctcat gccttgcctc tcaccatgct ctgctccagg 360
tcagcccccct tttggcctgt ttgttttgtc aaaaacctaa tctgcttctt gcttttcttg 420
gtaatatata tttagggaag atgttgcttt gcccacacac gaagcaaagt aa 472

<210> 352
<211> 251
<212> DNA
<213> Homo sapien

<400> 352

```
ctcaaagcta atctctcggg aatcaaacca gaaaagggca aggatcttag gcatggtgga      60
tgtggataag gccaggtcaa tggctgcaag catgcagaga aagaggtaca tcggagcgtg     120
caggctgcgt tccgtcctta cgatgaagac cacgatgcag tttccaaaca ttgccactac     180
atacatggaa aggaggggga agccaaccca gaaatgggct ttctctaatc ctgggatacc     240
aataagcaca a                                                          251

      <210> 353
      <211> 436
      <212> DNA
      <213> Homo sapien

      <400> 353
tttttttttt tttttttttt ttttttacaa caatgcagtc atttatttat tgagtatgtg      60
cacattatgg tattattact atactgatta tatttatcat gtgacttcta attaraaaat     120
gtatccaaaa gcaaaacagc agatatacaa aattaaagag acagaagata gacattaaca     180
gataaggcaa cttatacatt gacaatccaa atccaataca tttaaacatt tgggaaatga     240
gggggacaaa tggaagccar atcaaatttg tgtaaaacta ttcagtatgt ttcccttgct     300
tcatgtctga raaggctctc ccttcaatgg ggatgacaaa ctccaaatgc cacacaaatg     360
ttaacagaat actagattca cactggaacg ggggtaaaga agaaattatt ttctataaaa     420
gggctcctaa tgtagt                                                     436

      <210> 354
      <211> 854
      <212> DNA
      <213> Homo sapien

      <400> 354
cctttttctag ttcaccagtt ttctgcaagg atgctggtta gggagtgtct gcaggaggag     60
caagtctgaa accaaatcta ggaaacatag gaaacgagcc aggcacaggg ctggtgggcc     120
atcagggacc accctttggg ttgatatttt gcttaatctg catcttttga gtaagatcat     180
ctggcagtag aagctgttct ccaggtacat ttctctagct catgtacaaa aacatcctga     240
aggactttgt caggtgcctt gctaaaagcc agatgcgttc ggcacttcct tggtctgagg     300
ttaattgcac acctacaggc actgggctca tgctttcaag tattttgtcc tcactttagg     360
gtgagtgaaa gatccccatt ataggagcac ttgggagaga tcatataaaa gctgactctt     420
gagtacatgc agtaatgggg tagatgtgtg tggtgtgtct tcattcctgc aagggtgctt     480
gttagggagt gtttccagga ggaacaagtc tgaaaccaat catgaaataa atggtaggtg     540
tgaactggaa aactaattca aaagagagat cgtgatatca gtgtggttga tacaccttgg     600
caatatggaa ggctctaatt tgcccatatt tgaaataata attcagcttt ttgtaataca     660
aaataacaaa ggattgagaa tcatggtgtc taatgtataa aagacccagg aaacataaat     720
atatcaactg cataaatgta aaatgcatgt gacccaagaa ggccccaaag tggcagacaa     780
cattgtaccc attttccctt ccaaaatgtg agcggcgggc ctgctgcttt caaggctgtc     840
acacgggatg tcag                                                       854

      <210> 355
      <211> 676
      <212> DNA
      <213> Homo sapien

      <400> 355
gaaattaagt atgagctaaa ttccctgtta aaacctctag gggtgacaga tctcttcaac      60
caggtcaaag ctgatctttc tggaatgtca ccaaccaagg gcctatattt atcaaaagcc     120
atccacaagt catacctgga tgtcagcgaa gagggcacgg aggcagcagc agccactggg     180
gacagcatcg ctgtaaaaag cctaccaatg agagctcagt tcaaggcgaa ccaccccttc     240
ctgttcttta taaggcacac tcataccaac acgatcctat tctgtggcaa gcttgcctct     300
ccctaatcag atggggttga gtaaggctca gagttgcaga tgaggtgcag agacaatcct     360
gtgactttcc cacggccaaa aagctgttca cacctcacgc acctctgtgc ctcagtttgc     420
tcatctgcaa aataggtcta ggatttcttc caaccatttc atgagttgtg aagctaaggc     480
tttgttaatc atggaaaaag gtagacttat gcagaaagcc tttctggctt tcttatctgt     540
```

```
ggtgtctcat ttgagtgctg tccagtgaca tgatcaagtc aatgagtaaa attttaaggg      600
attagatttt cttgacttgt atgtatctgt gagatcttga ataagtgacc tgacatctct      660
gcttaaagaa aaccag                                                      676
```

<210> 356
<211> 574
<212> DNA
<213> Homo sapien

<400> 356

```
ttttttttt tttttcagga aaacattctc ttactttatt tgcatctcag caaaggttct        60
catgtggcac ctgactggca tcaaaccaaa gttcgtaggc caacaaagat gggccactca      120
caagcttccc atttgtagat ctcagtgcct atgagtatct gacacctgtt cctctcttca      180
gtctcttagg gaggcttaaa tctgtctcag gtgtgctaag agtgccagcc caaggkggtc      240
aaaagtccac aaaactgcag tctttgctgg gatagtaagc caagcagtgc ctggacagca      300
gagttctttt cttgggcaac agataaccag acaggactct aatcgtgctc ttattcaaca      360
ttcttctgtc tctgcctaga ctggaataaa aagccaatct ctctcgtggc acagggaagg      420
agatacaagc tcgtttacat gtgatagatc taacaaaggc atctaccgaa gtctggtctg      480
gatagacggc acagggagct cttaggtcag cgctgctggt tggaggacat tcctgagtcc      540
agctttgcag cctttgtgca acagtacttt ccca                                  574
```

<210> 357
<211> 393
<212> DNA
<213> Homo sapien

<400> 357

```
tttttttttt tttttttttt tttttttttt tacagaatat aratgcttta tcactgkact       60
taatatggkg kcttgttcac tatacttaaa aatgcaccac tcataaatat ttaattcagc      120
aagccacaac caaracttga ttttatcaac aaaaacccct aaatataaac ggsaaaaaag      180
atagatataa ttattccagt ttttttaaaa cttaaaarat attccattgc cgaattaara      240
araarataag tgttatatgg aaagaagggc attcaagcac actaaaraaa cctgaggkaa      300
gcataatctg tacaaaatta aactgtcctt tttggcattt taacaaattt gcaacgktct      360
tttttttctt tttctgtttt tttttttttt tac                                   393
```

<210> 358
<211> 630
<212> DNA
<213> Homo sapien

<400> 358

```
acagggtaaa caggaggatc cttgctctca cggagcttac attctagcag gaggacaata       60
ttaatgttta taggaaaatg atgagtttat gacaaaggaa gtagatagtg ttttacaaga      120
gcatagagta gggaagctaa tccagcacag ggaggtcaca gagacatccc taaggaagtg      180
gagtttaaac tgagagaagc aagtgcttaa actgaaggat gtgttgaaga agaagggaga      240
gtagaacaat ttgggcagag ggaaccttat agaccctaag gtgggaaggt tcaaagaact      300
gaaagagagc tagaacagct ggagccgttc tccggtgtaa agaggagtca aagagataag      360
attaaagatg tgaagattaa gatcttggtg gcattcaggg attggcactt ctacaagaaa      420
tcactgaagg gagtaatgtg acattacttt tcacttcagg atggccattc taactccagg      480
gggtagactg gactaggtaa gactggaggc aggtagacct cttctaaggc ctgcgatagt      540
gaaagacaaa aataagtggg gaaattcagg ggatagtgaa aatcagtagg acttaatgag      600
caagccagag gttcctccac aacaaccagt                                       630
```

<210> 359
<211> 620
<212> DNA
<213> Homo sapien

```
     <400> 359
acagcattcc aaaatataca tctagagact aarrgtaaat gctctatagt gaagaagtaa      60
taattaaaaa atgctactaa tatagaaaat ttataatcag aaaaataaat attcagggag     120
ctcaccagaa gaataaagtg ctctgccagt tattaaagga ttactgctgg tgaattaaat     180
atggcattcc ccaagggaaa tagagagatt cttctggatt atgttcaata tttatttcac     240
aggattaact gttttaggaa cagatataaa gcttcgccac ggaagagatg gacaaagcac     300
aaagacaaca tgataccttа ggaagcaaca ctaccctttc aggcataaaa tttggagaaa     360
tgcaacatta tgcttcatga ataatatgta gaaagaaggt ctgatgaaaa tgacatcctt     420
aatgtaagat aactttataa gaattctggg tcaaataaaa ttctttgaag aaaacatcca     480
aatgtcattg acttatcaaa tactatcttg gcatataacc tatgaaggca aaactaaaca     540
aacaaaaagc tcacaccaaa caaaaccatc aacttatttt gtattctata acatacgaga     600
ctgtaaagat gtgacagtgt                                                 620

     <210> 360
     <211> 431
     <212> DNA
     <213> Homo sapien

     <400> 360
aaaaaaaaaa agccagaaca acatgtgata gataatatga ttggctgcac acttccagac      60
tgatgaatga tgaacgtgat ggactattgt atggagcaca tcttcagcaa gaggggggaaa     120
tactcatcat ttttggccag cagttgtttg atcaccaaac atcatgccag aatactcagc     180
aaaccttctt agctcttgag aagtcaaagt ccgggggaat ttattcctgg caattttaat     240
tggactcctt atgtgagagc agcggctacc cagctggggt ggtggagcga acccgtcact     300
agtggacatg cagtggcaga gctcctggta accacctaga ggaatacaca ggcacatgtg     360
tgatgccaag cgtgacacct gtagcactca aatttgtctt gtttttgtct ttcggtgtgt     420
agattcttag t                                                          431

     <210> 361
     <211> 351
     <212> DNA
     <213> Homo sapien

     <400> 361
acactgattt ccgatcaaaa gaatcatcat ctttaccttg acttttcagg gaattactga      60
actttcttct cagaagatag ggcacagcca ttgccttggc ctcacttgaa gggtctgcat     120
ttgggtcctc tggtctcttg ccaagtttcc cagccactcg agggagaaat atcgggaggt     180
ttgacttcct ccggggcttt cccgagggct tcaccgtgag ccctgcggcc ctcagggctg     240
caatcctgga ttcaatgtct gaaacctcgc tctctgcctg ctggacttct gaggccgtca     300
ctgccactct gtcctccagc tctgacagct cctcatctgt ggtcctgttg t              351

     <210> 362
     <211> 463
     <212> DNA
     <213> Homo sapien

     <400> 362
acttcatcag gccataatgg gtgcctcccg tgagaatcca agcacctttg gactgcgcga      60
tgtagatgag ccggctgaag atcttgcgca tgcgcggctt cagggcgaag ttcttggcgc     120
ccccggtcac agaaatgacc aggttgggtg ttttcaggtg ccagtgctgg gtcagcagct     180
cgtaaaggat ttccgcgtcc gtgtcgcagg acagacgtat atacttccct ttcttcccca     240
gtgtctcaaa ctgaatatcc ccaaaggcgt cggtaggaaa ttccttggtg tgtttcttgt     300
agttccattt ctcactttgg ttgatctggg tgccttccat gtgctggctc tgggcatagc     360
cacacttgca cacattctcc ctgataagca cgatggtgtg gacaggaagg aaggatttca     420
ttgagcctgc ttatggaaac tggtattgtt agcttaaata gac                       463

     <210> 363
     <211> 653
```

<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(653)
<223> n = A,T,C or G

<400> 363
acccccgagt ncctgnctgg catactgnga acgaccaacg acacacccaa gctcggcctc 60
ctcttggnga ttctgggtga catcttcatg aatggcaacc gtgccagwga ggctgtcctc 120
tgggaggcac tacgcaagat gggactgcgt cctggggtga gacatcctct ccttggagat 180
ctaacgaaac ttctcaccta tgagttgtaa agcagaaata cctgnactac agacgagtgc 240
ccaacagcaa ccccccggaa gtatgagttc ctctrgggcc tccgttccta ccatgagasc 300
tagcaagatg naagtgttga gantcattgc agaggttcag aaaagagacc cntcgtgact 360
ggtctgcaca gttcatggag gctgcagatg aggccttgga tgctctggat gctgctgcag 420
ctgaggccga agcccgggct gaagcaagaa cccgcatggg aattggagat gaggctgtgt 480
ntgggccctg gagctgggat gacattgagt ttgagctgct gacctgggat gaggaaggag 540
attttggaga tccntggtcc agaattccat ttaccttctg ggccagatac caccagaatg 600
cccgctccag attccctcag acctttgccg gtcccattat tggtcstggt ggt 653

<210> 364
<211> 401
<212> DNA
<213> Homo sapien

<400> 364
actagaggaa agacgttaaa ccactctact accacttgtg gaactctcaa agggtaaatg 60
acaaagccaa tgaatgactc taaaaacaat atttacattt aatggtttgt agacaataaa 120
aaaacaaggt ggatagatct agaattgtaa cattttaaga aaaccatagc atttgacaga 180
tgagaaagct caattataga tgcaaagtta taactaaact actatagtag taaagaaata 240
catttcacac ccttcatata aattcactat cttggcttga ggcactccat aaaatgtatc 300
acgtgcatag taaatcttta tatttgctat ggcgttgcac tagaggactt ggactgcaac 360
aagtggatgc gcggaaaatg aaatcttctt caatagccca g 401

<210> 365
<211> 356
<212> DNA
<213> Homo sapien

<400> 365
ccagtgtcat atttgggctt aaaatttcaa gaagggcact tcaaatggct ttgcatttgc 60
atgtttcagt gctagagcgt aggaatagac cctggcgtcc actgtgagat gttcttcagc 120
taccagagca tcaagtctct gcagcaggtc attcttgggt aaagaaatga cttccacaaa 180
ctctccatcc cctggctttg gcttcggcct tgcgttttcg gcatcatctc cgttaatggt 240
gactgtcacg atgtgtatag tacagtttga caagcctggg tccatacaga ccgctggaga 300
acattcggca atgtcccctt tgtagccagt ttcttcttcg agctcccgga gagcag 356

<210> 366
<211> 1851
<212> DNA
<213> Homo sapien

<400> 366
tcatcaccat tgccagcagc ggcaccgtta gtcaggtttt ctgggaatcc cacatgagta 60
cttccgtgtt cttcattctt cttcaatagc cataaatctt ctagctctgg ctggctgttt 120
tcacttcctt taagcctttg tgactcttcc tctgatgtca gctttaagtc ttgttctgga 180
ttgctgtttt cagaagagat ttttaacatc tgtttttctt tgtagtcaga aagtaactgg 240

```
caaattacat gatgatgact agaaacagca tactctctgg ccgtctttcc agatcttgag     300
aagatacatc aacattttgc tcaagtagag ggctgactat acttgctgat ccacaacata     360
cagcaagtat gagagcagtt cttccatatc tatccagcgc atttaaattc gctttttttct     420
tgattaaaaa tttcaccact tgctgttttt gctcatgtat accaagtagc agtggtgtga     480
ggccatgctt gtttttttgat tcgatatcag caccgtataa gagcagtgct ttggccatta     540
atttatcttc attgtagaca gcatagtgta gagtggtatt tccatactca tctggaatat     600
ttggatcagt gccatgttcc agcaacatta acgcacattc atcttcctgg cattgtacgg     660
cctttgtcag agctgtcctc tttttgttgt caaggacatt aagttgacat cgtctgtcca     720
gcacgagttt tactacttct gaattcccat tggcagaggc cagatgtaga gcagtcctct     780
tttgcttgtc cctcttgttc acatccgtgt ccctgagcat gacgatgaga tcctttctgg     840
ggactttacc ccaccaggca gctctgtgga gcttgtccag atcttctcca tggacgtggt     900
acctgggatc catgaaggcg ctgtcatcgt agtctcccca agcgaccacg ttgctcttgc     960
cgctcccctg cagcagggga agcagtggca gcaccacttg cacctcttgc tcccaagcgt    1020
cttcacagag gagtcgttgt ggtctccaga agtgcccacg ttgctcttgc cgctccccct    1080
gtccatccag ggaggaagaa atgcaggaaa tgaaagatgc atgcacgatg gtatactcct    1140
cagccatcaa acttctggac agcaggtcac ttccagcaag gtggagaaag ctgtccaccc    1200
acagaggatg agatccagaa accacaatat ccattcacaa acaaacactt ttcagccaga    1260
cacaggtact gaaatcatgt catctgcggc aacatggtgg aacctaccca atcacacatc    1320
aagagatgaa gacactgcag tatatctgca caacgtaata ctcttcatcc ataacaaaat    1380
aatataattt tcctctggag ccatatggat gaactatgaa ggaagaactc cccgaagaag    1440
ccagtcgcag agaagccaca ctgaagctct gtcctcagcc atcagcgcca cggacaggar    1500
tgtgtttctt ccccagtgat gcagcctcaa gttatcccga agctgccgca gcacacggtg    1560
gctcctgaga aacaccccag ctcttccggt ctaacacagg caagtcaata aatgtgataa    1620
tcacataaac agaattaaaa gcaaagtcac ataagcatct caacagacac agaaaaggca    1680
tttgacaaaa tccagcatcc ttgtatttat tgttgcagtt ctcagaggaa atgcttctaa    1740
cttttcccca tttagtatta tgttggctgt gggcttgtca taggtggttt ttattacttt    1800
aaggtatgtc ccttctatgc ctgttttgct gagggtttta attctcgtgc c             1851
```

<210> 367
<211> 668
<212> DNA
<213> Homo sapien

<400> 367

```
cttgagcttc caaataygga agactggccc ttacacasgt caatgttaaa atgaatgcat      60
ttcagtattt tgaagataaa attrgtagat ctataccttg ttttttgatt cgatatcagc     120
accrtataag agcagtgctt tggccattaa tttatctttc attrtagaca gcrtagtgya     180
gagtggtatt tccatactca tctggaatat ttggatcagt gccatgttcc agcaacatta     240
acgcacattc atcttcctgg cattgtacgg cctgtcagta ttagacccaa aaacaaatta     300
catatcttag gaattcaaaa taacattcca cagctttcac caactagtta tatttaaagg     360
agaaaactca tttttatgcc atgtattgaa atcaaaccca cctcatgctg atatagttgg     420
ctactgcata cctttatcag agctgtcctc tttttgttgt caaggacatt aagttgacat     480
cgtctgtcca gcaggagttt tactacttct gaattcccat tggcagaggc cagatgtaga     540
gcagtcctat gagagtgaga agacttttta ggaaattgta gtgcactagc tacagccata     600
gcaatgattc atgtaactgc aaacactgaa tagcctgcta ttactctgcc ttcaaaaaaa     660
aaaaaaaa                                                              668
```

<210> 368
<211> 1512
<212> DNA
<213> Homo sapien

<400> 368

```
gggtcgccca gggggsgcgt gggctttcct cgggtgggtg tgggttttcc ctgggtgggg      60
tgggctgggc trgaatcccc tgctggggtt ggcaggtttt ggctgggatt gacttttytc     120
ttcaaacaga ttggaaaccc ggagttacct gctagttggt gaaactggtt ggtagacgcg     180
atctgttggc tactactggc ttctcctggc tgttaaaagc agatggtggt tgaggttgat     240
tccatgccgg ctgcttcttc tgtgaagaag ccatttggtc tcaggagcaa gatgggcaag     300
```

```
tggtgctgcc gttgcttccc ctgctgcagg gagagcggca agagcaacgt gggcacttct     360
ggagaccacg acgactctgc tatgaagaca ctcaggagca agatgggcaa gtggtgccgc     420
cactgcttcc cctgctgcag gggagtggc aagagcaacg tgggcgcttc tggagaccac      480
gacgaytctg ctatgaagac actcaggaac aagatgggca agtggtgctg ccactgcttc     540
ccctgctgca gggggagcrg caagagcaag gtgggcgctt ggggagacta cgatgacagt     600
gccttcatgg agcccaggta ccacgtccgt ggagaagatc tggacaagct ccacagagct     660
gcctggtggg gtaaagtccc cagaaaggat ctcatcgtca tgctcaggga cactgacgtg     720
aacaagaagg acaagcaaaa gaggactgct ctacatctgg cctctgccaa tgggaattca     780
gaagtagtaa aactcstgct ggacagacga tgtcaactta atgtccttga caacaaaaag     840
aggacagctc tgayaaaggc cgtacaatgc caggaagatg aatgtgcgtt aatgttgctg     900
gaacatggca ctgatccaaa tattccagat gagtatggaa ataccactct rcactaygct     960
rtctayaatg aagataaatt aatggccaaa gcactgctct tatayggtgc tgatatcgaa    1020
tcaaaaaaca aggtatagat ctactaattt tatcttcaaa atactgaaat gcattcattt    1080
taacattgac gtgtgtaagg gccagtcttc cgtatttgga agctcaagca taacttgaat    1140
gaaaatattt tgaaatgacc taattatctm agactttatt ttaaatattg ttattttcaa    1200
agaagcatta gagggtacag tttttttttt ttaaatgcac ttctggtaaa tacttttgtt    1260
gaaaacactg aatttgtaaa aggtaatact tactattttt caatttttcc ctcctaggat    1320
tttttcccc taatgaatgt aagatggcaa aatttgccct gaaataggtt ttacatgaaa     1380
actccaagaa aagttaaaca tgtttcagtg aatagagatc ctgctccttt ggcaagttcc    1440
taaaaaacag taatagatac gaggtgatgc gcctgtcagt ggcaaggttt aagatatttc    1500
tgatctcgtg cc                                                         1512
```

<210> 369
<211> 1853
<212> DNA
<213> Homo sapien

<400> 369

```
gggtcgccca gggggsgcgt gggctttcct cgggtgggtg tgggttttcc ctgggtgggg      60
tgggctgggc trgaatcccc tgctggggtt ggcaggtttt ggctgggatt gacttttytc     120
ttcaaacaga ttggaaaccc ggagttacct gctagttggt gaaactggtt ggtagacgcg     180
atctgttggc tactactggc ttctcctggc tgttaaaagc agatggtggt tgaggttgat     240
tccatgccgg ctgcttcttc tgtgaagaag ccatttggtc tcaggagcaa gatgggcaag     300
tggtgctgcc gttgcttccc ctgctgcagg gagagcggca agagcaacgt gggcacttct     360
ggagaccacg acgactctgc tatgaagaca ctcaggagca agatgggcaa gtggtgccgc     420
cactgcttcc cctgctgcag gggagtggc aagagcaacg tgggcgcttc tggagaccac      480
gacgaytctg ctatgaagac actcaggaac aagatgggca agtggtgctg ccactgcttc     540
ccctgctgca gggggagcrg caagagcaag gtgggcgctt ggggagacta cgatgacagy     600
gccttcatgg akcccaggta ccacgtccrt ggagaagatc tggacaagct ccacagagct     660
gcctggtggg gtaaagtccc cagaaaggat ctcatcgtca tgctcaggga cackgaygtg     720
aacaagargg acaagcaaaa gaggactgct ctacatctgg cctctgccaa tgggaattca     780
gaagtagtaa aactcstgct ggacagacga tgtcaactta atgtccttga caacaaaaag     840
aggacagctc tgayaaaggc cgtacaatgc caggaagatg aatgtgcgtt aatgttgctg     900
gaacatggca ctgatccaaa tattccagat gagtatggaa ataccactct rcactaygct     960
rtctayaatg aagataaatt aatggccaaa gcactgctct tatayggtgc tgatatcgaa    1020
tcaaaaaaca agcatggcct cacaccactg ytacttggtr tacatgagca aaaacagcaa    1080
gtsgtgaaat ttttaatyaa gaaaaaagcg aatttaaaat gcrctggata gatatggaag    1140
ractgctctc atacttgctg tatgttgtgg atcagcaagt atagtcagcc ytctacttga    1200
gcaaaatrtt gatgtatctt ctcaagatct ggaaagacgg ccagagagta tgctgtttct    1260
agtcatcatc atgtaatttg ccagttactt tctgactaca aagaaaaaca gatgttaaaa    1320
atctcttctg aaaacagcaa tccagaacaa gacttaaagc tgacatcaga ggaagagtca    1380
caaaggctta aaggaagtga aaacagccag ccagaggcat ggaaactttt aaatttaaac    1440
ttttggttta atgttttttt tttttgcctt aataatatta gatagtccca aatgaaatwa    1500
cctatgagac taggctttga gaatcaatag attctttttt taagaatctt ttggctagga    1560
gcggtgtctc acgcctgtaa ttccagcacc ttgagaggct gaggtgggca gatcacgaga    1620
tcaggagatc gagaccatcc tggctaacac ggtgaaaccc catctctact aaaaatacaa    1680
aaacttagct gggtgtggtg gcgggtgcct gtagtcccag ctactcagga rgctgaggca    1740
ggagaatggc atgaacccgg gaggtggagg ttgcagtgag ccgagatccg ccactacact    1800
```

ccagcctggg tgacagagca agactctgtc tcaaaaaaaa aaaaaaaaaa aaa 1853

<210> 370
<211> 2184
<212> DNA
<213> Homo sapien

<400> 370
ggcacgagaa ttaaaaccct cagcaaaaca ggcatagaag ggacatacct taaagtaata 60
aaaaccacct atgacaagcc cacagccaac ataatactaa atggggaaaa gttagaagca 120
tttcctctga gaactgcaac aataaataca aggatgctgg attttgtcaa atgccttttc 180
tgtgtctgtt gagatgctta tgtgactttg cttttaattc tgtttatgtg attatcacat 240
ttattgactt gcctgtgtta gaccggaaga gctggggtgt ttctcaggag ccaccgtgtg 300
ctgcggcagc ttcgggataa cttgaggctg catcactggg gaagaaacac aytcctgtcc 360
gtggcgctga tggctgagga cagagcttca gtgtggcttc tctgcgactg gcttcttcgg 420
ggagttcttc cttcatagtt catccatatg gctccagagg aaaattatat tattttgtta 480
tggatgaaga gtattacgtt gtgcagatat actgcagtgt cttcatctct tgatgtgtga 540
ttgggtaggt tccaccatgt tgccgcagat gacatgattt cagtacctgt gtctggctga 600
aaagtgtttg tttgtgaatg gatattgtgg tttctggatc tcatcctctg tgggtggaca 660
gctttctcca ccttgctgga agtgacctgc tgtccagaag tttgatggct gaggagtata 720
ccatcgtgca tgcatctttc atttcctgca tttcttcctc cctggatgga caggggggagc 780
ggcaagagca acgtgggcac ttctggagac cacaacgact cctctgtgaa gacgcttggg 840
agcaagaggt gcaagtggtg ctgccactgc ttcccctgct gcaggggagc ggcaagagca 900
acgtggtcgc ttggggagac tacgatgaca gcgccttcat ggatcccagg taccacgtcc 960
atggagaaga tctggacaag ctccacagag ctgcctggtg gggtaaagtc cccagaaagg 1020
atctcatcgt catgctcagg gacacggatg tgaacaagag ggacaagcaa aagaggactg 1080
ctctacatct ggcctctgcc aatgggaatt cagaagtagt aaaactcgtg ctggacagac 1140
gatgtcaact taatgtcctt gacaacaaaa agaggacagc tctgacaaag gccgtacaat 1200
gccaggaaga tgaatgtgcg ttaatgttgc tggaacatgg cactgatcca aatattccag 1260
atgagtatgg aaataccact ctacactatg ctgtctacaa tgaagataaa ttaatggcca 1320
aagcactgct cttatacggt gctgatatcg aatcaaaaaa caagcatggc ctcacaccac 1380
tgctacttgg tatacatgag caaaaacagc aagtggtgaa atttttaatc aagaaaaaag 1440
cgaatttaaa tgcgctggat agatatggaa gaactgctct catacttgct gtatgttgtg 1500
gatcagcaag tatagtcagc cctctacttg agcaaaatgt tgatgtatct tctcaagatc 1560
tggaaagacg gccagagagt atgctgtttc tagtcatcat catgtaattt gccagttact 1620
ttctgactac aaagaaaaac agatgttaaa aatctcttct gaaaacagca atccagaaca 1680
agacttaaag ctgacatcag aggaagagtc acaaaggctt aaaggaagtg aaaacagcca 1740
gccagaggca tggaaacttt taaatttaaa cttttggttt aatgtttttt ttttttgcct 1800
taataatatt agatagtccc aaatgaaatw acctatgaga ctaggctttg agaatcaata 1860
gattcttttt ttaagaatct tttggctagg agcggtgtct cacgcctgta attccagcac 1920
cttgagaggc tgaggtgggc agatcacgag atcaggagat cgagaccatc ctggctaaca 1980
cggtgaaacc ccatctctac taaaaataca aaaacttagc tgggtgtggt ggcgggtgcc 2040
tgtagtccca gctactcagg argctgaggc aggagaatgg catgaacccg ggaggtggag 2100
gttgcagtga gccgagatcc gccactacac tccagcctgg gtgacagagc aagactctgt 2160
ctcaaaaaaa aaaaaaaaaa aaaa 2184

<210> 371
<211> 1855
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(1855)
<223> n = A,T,C or G

<400> 371
tgcacgcatc ggccagtgtc tgtgccacgt acactgacgc cccctgagat gtgcacgccg 60

```
cacgcgcacg ttgcacgcgc ggcagcggct tggctggctt gtaacggctt gcacgcgcac     120
gccgcccccg cataaccgtc agactggcct gtaacggctt gcaggcgcac gccgcacgcg     180
cgtaacggct tggctgccct gtaacggctt gcacgtgcat gctgcacgcg cgttaacggc     240
ttggctggca tgtagccgct tggcttggct ttgcattytt tgctkggctk ggcgttgkty     300
tcttggattg acgcttcctc cttggatkga cgtttcctcc ttggatkgac gtttcytyty     360
tcgcgttcct ttgctggact tgaccttttty tctgctgggt ttggcattcc tttggggtgg    420
gctgggtgtt ttctccgggg gggktkgccc ttcctggggt gggcgtgggk cgcccccagg     480
gggcgtgggc tttccccggg tgggtgtggg ttttcctggg gtggggtggg ctgtgctggg     540
atccccctgc tggggttggc agggattgac ttttttcttc aaacagattg gaaacccgga     600
gtaacntgct agttggtgaa actggttggt agacgcgatc tgctggtact actgtttctc     660
ctggctgtta aaagcagatg gtggctgagg ttgattcaat gccggctgct tcttctgtga     720
agaagccatt tggtctcagg agcaagatgg gcaagtggtg cgccactgct tcccctgctg     780
caggggggagc ggcaagagca acgtgggcac ttctggagac cacaacgact cctctgtgaa    840
gacgcttggg agcaagaggt gcaagtggtg ctgcccactg cttcccctgc tgcaggggag     900
cggcaagagc aacgtggkcg cttggggaga ctacgatgac agcgccttca tggakcccag     960
gtaccacgtc crtggagaag atctggacaa gctccacaga gctgcctggt ggggtaaagt    1020
ccccagaaag gatctcatcg tcatgctcag ggacactgay gtgaacaaga rggacaagca    1080
aaagaggact gctctacatc tggcctctgc caatgggaat tcagaagtag taaaactcgt    1140
gctggacaga cgatgtcaac ttaatgtcct tgacaacaaa aagaggacag ctctgacaaa    1200
ggccgtacaa tgccaggaag atgaatgtgc gttaatgttg ctggaacatg gcactgatcc    1260
aaatattcca gatgagtatg gaaataccac tctacactat gctgtctaca atgaagataa    1320
attaatggcc aaagcactgc tcttatacgg tgctgatatc gaatcaaaaa acaaggtata    1380
gatctactaa ttttatcttc aaaatactga aatgcattca ttttaacatt gacgtgtgta    1440
agggccagtc ttccgtattt ggaagctcaa gcataacttg aatgaaaata ttttgaaatg    1500
acctaattat ctaagacttt attttaaata ttgttatttt caaagaagca ttagagggta    1560
cagttttttt tttttaaatg cacttctggt aaatactttt gttgaaaaca ctgaatttgt    1620
aaaaggtaat acttactatt tttcaatttt tccctcctag gatttttttc ccctaatgaa    1680
tgtaagatgg caaaatttgc cctgaaatag gttttacatg aaaactccaa gaaaagttaa    1740
acatgtttca gtgaatagag atcctgctcc tttggcaagt tcctaaaaaa cagtaataga    1800
tacgaggtga tgcgcctgtc agtggcaagg tttaagatat ttctgatctc gtgcc         1855
```

<210> 372
<211> 1059
<212> DNA
<213> Homo sapien

<400> 372

```
gcaacgtggg cacttctgga gaccacaacg actcctctgt gaagacgctt gggagcaaga      60
ggtgcaagtg gtgctgccca ctgcttcccc tgctgcaggg gagcggcaag agcaacgtgg     120
gcgcttgrgg agactmcgat gacagygcct tcatggagcc caggtaccac gtccgtggag     180
aagatctgga caagctccac agagctgccc tggtggggta aagtccccag aaaggatctc     240
atcgtcatgc tcagggacac tgaygtgaac aagarggaca agcaaaagag gactgctcta     300
catctggcct ctgccaatgg gaattcagaa gtagtaaaac tcstgctgga cagacgatgt     360
caacttaatg tccttgacaa caaaaagagg acagctctga yaaaggccgt acaatgccag     420
gaagatgaat gtgcgttaat gttgctggaa catggcactg atccaaatat tccagatgag     480
tatggaaata ccactctrca ctaygctrtc tayaatgaag ataaattaat ggccaaagca     540
ctgctcttat ayggtgctga tatcgaatca aaaaacaagg tatagatcta ctaattttat     600
cttcaaaata ctgaaatgca ttcattttaa cattgacgtg tgtaagggcc agtcttccgt     660
atttggaagc tcaagcataa cttgaatgaa aatattttga aatgacctaa ttatctaaga     720
ctttatttta aatattgtta ttttcaaaga agcattagag ggtacagttt tttttttttta    780
aatgcacttc tggtaaatac ttttgttgaa aacactgaat ttgtaaaagg taatacttac     840
tatttttcaa tttttccctc ctaggatttt tttcccctaa tgaatgtaag atggcaaaat     900
ttgccctgaa ataggtttta catgaaaact ccaagaaaag ttaaacatgt ttcagtgaat     960
agagatcctg ctcctttggc aagttcctaa aaaacagtaa tagatacgag gtgatgcgcc    1020
tgtcagtggc aaggtttaag atatttctga tctcgtgcc                           1059
```

<210> 373
<211> 1155

<212> DNA
<213> Homo sapien

<400> 373
```
atggtggttg aggttgattc catgccggct gcctcttctg tgaagaagcc atttggtctc      60
aggagcaaga tgggcaagtg gtgctgccgt tgcttcccct gctgcaggga gagcggcaag     120
agcaacgtgg gcacttctgg agaccacgac gactctgcta tgaagacact caggagcaag     180
atgggcaagt ggtgccgcca ctgcttcccc tgctgcaggg ggagtggcaa gagcaacgtg     240
ggcgcttctg gagaccacga cgactctgct atgaagacac tcaggaacaa gatgggcaag     300
tggtgctgcc actgcttccc ctgctgcagg gggagcggca agagcaaggt gggcgcttgg     360
ggagactacg atgacagtgc cttcatggag cccaggtacc acgtccgtgg agaagatctg     420
gacaagctcc acagagctgc ctggtggggt aaagtcccca gaaaggatct catcgtcatg     480
ctcagggaca ctgacgtgaa caagaaggac aagcaaaaga ggactgctct acatctggcc     540
tctgccaatg ggaattcaga agtagtaaaa ctcctgctgg acagacgatg tcaacttaat     600
gtccttgaca acaaaaagag gacagctctg ataaaggccg tacaatgcca ggaagatgaa     660
tgtgcgttaa tgttgctgga acatggcact gatccaaata ttccagatga gtatggaaat     720
accactctgc actacgctat ctataatgaa gataaattaa tggccaaagc actgctctta     780
tatggtgctg atatcgaatc aaaaaacaag catggcctca caccactgtt acttggtgta     840
catgagcaaa aacagcaagt cgtgaaattt ttaatcaaga aaaaagcgaa tttaaatgca     900
ctggatagat atggaaggac tgctctcata cttgctgtat gttgtggatc agcaagtata     960
gtcagccttc tacttgagca aaatattgat gtatcttctc aagatctatc tggacagacg    1020
gccagagagt atgctgtttc tagtcatcat catgtaattt gccagttact ttctgactac    1080
aaagaaaaac agatgctaaa aatctcttct gaaaacagca atccagaaaa tgtctcaaga    1140
accagaaata aataa                                                     1155
```

<210> 374
<211> 2000
<212> DNA
<213> Homo sapien

<400> 374
```
atggtggttg aggttgattc catgccggct gcctcttctg tgaagaagcc atttggtctc      60
aggagcaaga tgggcaagtg gtgctgccgt tgcttcccct gctgcaggga gagcggcaag     120
agcaacgtgg gcacttctgg agaccacgac gactctgcta tgaagacact caggagcaag     180
atgggcaagt ggtgccgcca ctgcttcccc tgctgcaggg ggagtggcaa gagcaacgtg     240
ggcgcttctg gagaccacga cgactctgct atgaagacac tcaggaacaa gatgggcaag     300
tggtgctgcc actgcttccc ctgctgcagg gggagcggca agagcaaggt gggcgcttgg     360
ggagactacg atgacagtgc cttcatggag cccaggtacc acgtccgtgg agaagatctg     420
gacaagctcc acagagctgc ctggtggggt aaagtcccca gaaaggatct catcgtcatg     480
ctcagggaca ctgacgtgaa caagaaggac aagcaaaaga ggactgctct acatctggcc     540
tctgccaatg ggaattcaga agtagtaaaa ctcctgctgg acagacgatg tcaacttaat     600
gtccttgaca acaaaaagag gacagctctg ataaaggccg tacaatgcca ggaagatgaa     660
tgtgcgttaa tgttgctgga acatggcact gatccaaata ttccagatga gtatggaaat     720
accactctgc actacgctat ctataatgaa gataaattaa tggccaaagc actgctctta     780
tatggtgctg atatcgaatc aaaaaacaag catggcctca caccactgtt acttggtgta     840
catgagcaaa aacagcaagt cgtgaaattt ttaatcaaga aaaaagcgaa tttaaatgca     900
ctggatagat atggaaggac tgctctcata cttgctgtat gttgtggatc agcaagtata     960
gtcagccttc tacttgagca aaatattgat gtatcttctc aagatctatc tggacagacg    1020
gccagagagt atgctgtttc tagtcatcat catgtaattt gccagttact ttctgactac    1080
aaagaaaaac agatgctaaa aatctcttct gaaaacagca atccagaaca agacttaaag    1140
ctgacatcag aggaagagtc acaaaggttc aaaggcagtg aaaatagcca gccagagaaa    1200
atgtctcaag aaccagaaat aaataaggat ggtgatagag aggttgaaga agaaatgaag    1260
aagcatgaaa gtaataatgt gggattacta gaaaacctga ctaatggtgt cactgctggc    1320
aatggtgata atggattaat tcctcaaagg aagagcagaa cacctgaaaa tcagcaattt    1380
cctgacaacg aaagtgaaga gtatcacaga atttgcgaat tagtttctga ctacaaagaa    1440
aaacagatgc caaaatactc ttctgaaaac agcaacccag aacaagactt aaagctgaca    1500
tcagaggaag agtcacaaag gcttgagggc agtgaaaatg gccagccaga gctagaaaat    1560
tttatggcta tcgaagaaat gaagaagcac ggaagtactc atgtcggatt cccagaaaac    1620
```

ctgactaatg gtgccactgc tggcaatggt gatgatggat taattcctcc aaggaagagc 1680
agaacacctg aaagccagca atttcctgac actgagaatg aagagtatca cagtgacgaa 1740
caaaatgata ctcagaagca attttgtgaa gaacagaaca ctggaatatt acacgatgag 1800
attctgattc atgaagaaaa gcagatagaa gtggttgaaa aaatgaattc tgagctttct 1860
cttagttgta agaaagaaaa agacatcttg catgaaaata gtacgttgcg ggaagaaatt 1920
gccatgctaa gactggagct agacacaatg aaacatcaga gccagctaaa aaaaaaaaaa 1980
aaaaaaaaaa aaaaaaaaaa 2000

<210> 375
<211> 2040
<212> DNA
<213> Homo sapien

<400> 375
atggtggttg aggttgattc catgccggct gcctcttctg tgaagaagcc atttggtctc 60
aggagcaaga tgggcaagtg gtgctgccgt tgcttcccct gctgcaggga gagcggcaag 120
agcaacgtgg gcacttctgg agaccacgac gactctgcta tgaagacact caggagcaag 180
atgggcaagt ggtgccgcca ctgcttcccc tgctgcaggg ggagtggcaa gagcaacgtg 240
ggcgcttctg gagaccacga cgactctgct atgaagacac tcaggaacaa gatgggcaag 300
tggtgctgcc actgcttccc ctgctgcagg gggagcggca agagcaaggt gggcgcttgg 360
ggagactacg atgacagtgc cttcatggag cccaggtacc acgtccgtgg agaagatctg 420
gacaagctcc acagagctgc ctggtggggt aaagtcccca gaaaggatct catcgtcatg 480
ctcagggaca ctgacgtgaa caagaaggac aagcaaaaga ggactgctct acatctggcc 540
tctgccaatg ggaattcaga agtagtaaaa ctcctgctgg acagacgatg tcaacttaat 600
gtccttgaca acaaaaagag gacagctctg ataaaggccg tacaatgcca ggaagatgaa 660
tgtgcgttaa tgttgctgga acatggcact gatccaaata ttccagatga gtatggaaat 720
accactctgc actacgctat ctataatgaa gataaattaa tggccaaagc actgctctta 780
tatggtgctg atatcgaatc aaaaaacaag catggcctca caccactgtt acttggtgta 840
catgagcaaa aacagcaagt cgtgaaattt ttaatcaaga aaaaagcgaa tttaaatgca 900
ctggatagat atggaaggac tgctctcata cttgctgtat gttgtggatc agcaagtata 960
gtcagccttc tacttgagca aaatattgat gtatcttctc aagatctatc tggacagacg 1020
gccagagagt atgctgtttc tagtcatcat catgtaattt gccagttact ttctgactac 1080
aaagaaaaac agatgctaaa aatctcttct gaaaacagca atccagaaca agacttaaag 1140
ctgacatcag aggaagagtc acaaaggttc aaaggcagtg aaaatagcca gccagagaaa 1200
atgtctcaag aaccagaaat aaataaggat ggtgatagag aggttgaaga agaaatgaag 1260
aagcatgaaa gtaataatgt gggattacta gaaaacctga ctaatggtgt cactgctggc 1320
aatggtgata atggattaat tcctcaaagg aagagcagaa cacctgaaaa tcagcaattt 1380
cctgacaacg aaagtgaaga gtatcacaga atttgcgaat tagtttctga ctacaaagaa 1440
aaacagatgc caaaatactc ttctgaaaac agcaacccag aacaagactt aaagctgaca 1500
tcagaggaag agtcacaaag gcttgagggc agtgaaaatg gccagccaga gaaaagatct 1560
caagaaccag aaataaataa ggatggtgat agagagctag aaaattttat ggctatcgaa 1620
gaaatgaaga agcacggaag tactcatgtc ggattcccag aaaacctgac taatggtgcc 1680
actgctggca atggtgatga tggattaatt cctccaagga agagcagaac acctgaaagc 1740
cagcaatttc ctgacactga gaatgaagag tatcacagtg acgaacaaaa tgatactcag 1800
aagcaatttt gtgaagaaca gaacactgga atattacacg atgagattct gattcatgaa 1860
gaaaagcaga tagaagtggt tgaaaaaatg aattctgagc tttctcttag ttgtaagaaa 1920
gaaaaagaca tcttgcatga aaatagtacg ttgcgggaag aaattgccat gctaagactg 1980
gagctagaca caatgaaaca tcagagccag ctaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2040

<210> 376
<211> 329
<212> PRT
<213> Homo sapien

<400> 376
Met Asp Ile Val Val Ser Gly Ser His Pro Leu Trp Val Asp Ser Phe
1 5 10 15
Leu His Leu Ala Gly Ser Asp Leu Leu Ser Arg Ser Leu Met Ala Glu

```
            20                  25                  30
Glu Tyr Thr Ile Val His Ala Ser Phe Ile Ser Cys Ile Ser Ser Ser
        35                  40                  45
Leu Asp Gly Gln Gly Glu Arg Gln Glu Gln Arg Gly His Phe Trp Arg
    50                  55                  60
Pro Gln Arg Leu Leu Cys Glu Asp Ala Trp Glu Gln Glu Val Gln Val
65                  70                  75                  80
Val Leu Pro Leu Leu Pro Leu Leu Gln Gly Ser Gly Lys Ser Asn Val
                85                  90                  95
Val Ala Trp Gly Asp Tyr Asp Asp Ser Ala Phe Met Asp Pro Arg Tyr
            100                 105                 110
His Val His Gly Glu Asp Leu Asp Lys Leu His Arg Ala Ala Trp Trp
        115                 120                 125
Gly Lys Val Pro Arg Lys Asp Leu Ile Val Met Leu Arg Asp Thr Asp
    130                 135                 140
Val Asn Lys Arg Asp Lys Gln Lys Arg Thr Ala Leu His Leu Ala Ser
145                 150                 155                 160
Ala Asn Gly Asn Ser Glu Val Val Lys Leu Val Leu Asp Arg Arg Cys
                165                 170                 175
Gln Leu Asn Val Leu Asp Asn Lys Lys Arg Thr Ala Leu Thr Lys Ala
            180                 185                 190
Val Gln Cys Gln Glu Asp Glu Cys Ala Leu Met Leu Leu Glu His Gly
        195                 200                 205
Thr Asp Pro Asn Ile Pro Asp Glu Tyr Gly Asn Thr Thr Leu His Tyr
    210                 215                 220
Ala Val Tyr Asn Glu Asp Lys Leu Met Ala Lys Ala Leu Leu Leu Tyr
225                 230                 235                 240
Gly Ala Asp Ile Glu Ser Lys Asn Lys His Gly Leu Thr Pro Leu Leu
                245                 250                 255
Leu Gly Ile His Glu Gln Lys Gln Gln Val Val Lys Phe Leu Ile Lys
            260                 265                 270
Lys Lys Ala Asn Leu Asn Ala Leu Asp Arg Tyr Gly Arg Thr Ala Leu
        275                 280                 285
Ile Leu Ala Val Cys Cys Gly Ser Ala Ser Ile Val Ser Pro Leu Leu
    290                 295                 300
Glu Gln Asn Val Asp Val Ser Ser Gln Asp Leu Glu Arg Arg Pro Glu
305                 310                 315                 320
Ser Met Leu Phe Leu Val Ile Ile Met
                325

      <210> 377
      <211> 148
      <212> PRT
      <213> Homo sapien

      <220>
      <221> VARIANT
      <222> (1)...(148)
      <223> Xaa = Any Amino Acid

      <400> 377
Met Thr Xaa Pro Ser Trp Ser Pro Gly Thr Thr Ser Val Glu Lys Ile
 1               5                  10                  15
Trp Thr Ser Ser Thr Glu Leu Pro Trp Trp Gly Lys Val Pro Arg Lys
            20                  25                  30
Asp Leu Ile Val Met Leu Arg Asp Thr Asp Val Asn Lys Xaa Asp Lys
        35                  40                  45
Gln Lys Arg Thr Ala Leu His Leu Ala Ser Ala Asn Gly Asn Ser Glu
```

```
    50                  55                  60
Val Val Lys Leu Xaa Leu Asp Arg Arg Cys Gln Leu Asn Val Leu Asp
65                  70                  75                  80
Asn Lys Lys Arg Thr Ala Leu Xaa Lys Ala Val Gln Cys Gln Glu Asp
                85                  90                  95
Glu Cys Ala Leu Met Leu Leu Glu His Gly Thr Asp Pro Asn Ile Pro
            100                 105                 110
Asp Glu Tyr Gly Asn Thr Thr Leu His Tyr Ala Xaa Tyr Asn Glu Asp
        115                 120                 125
Lys Leu Met Ala Lys Ala Leu Leu Leu Tyr Gly Ala Asp Ile Glu Ser
    130                 135                 140
Lys Asn Lys Val
145

      <210> 378
      <211> 1719
      <212> PRT
      <213> Homo sapien

      <400> 378
Met Val Val Glu Val Asp Ser Met Pro Ala Ala Ser Ser Val Lys Lys
 1               5                  10                  15
Pro Phe Gly Leu Arg Ser Lys Met Gly Lys Trp Cys Cys Arg Cys Phe
            20                  25                  30
Pro Cys Cys Arg Glu Ser Gly Lys Ser Asn Val Gly Thr Ser Gly Asp
        35                  40                  45
His Asp Asp Ser Ala Met Lys Thr Leu Arg Ser Lys Met Gly Lys Trp
    50                  55                  60
Cys Arg His Cys Phe Pro Cys Cys Arg Gly Ser Gly Lys Ser Asn Val
65                  70                  75                  80
Gly Ala Ser Gly Asp His Asp Asp Ser Ala Met Lys Thr Leu Arg Asn
                85                  90                  95
Lys Met Gly Lys Trp Cys Cys His Cys Phe Pro Cys Cys Arg Gly Ser
            100                 105                 110
Gly Lys Ser Lys Val Gly Ala Trp Gly Asp Tyr Asp Asp Ser Ala Phe
        115                 120                 125
Met Glu Pro Arg Tyr His Val Arg Gly Glu Asp Leu Asp Lys Leu His
    130                 135                 140
Arg Ala Ala Trp Trp Gly Lys Val Pro Arg Lys Asp Leu Ile Val Met
145                 150                 155                 160
Leu Arg Asp Thr Asp Val Asn Lys Lys Asp Lys Gln Lys Arg Thr Ala
                165                 170                 175
Leu His Leu Ala Ser Ala Asn Gly Asn Ser Glu Val Val Lys Leu Leu
            180                 185                 190
Leu Asp Arg Arg Cys Gln Leu Asn Val Leu Asp Asn Lys Lys Arg Thr
        195                 200                 205
Ala Leu Ile Lys Ala Val Gln Cys Gln Glu Asp Glu Cys Ala Leu Met
    210                 215                 220
Leu Leu Glu His Gly Thr Asp Pro Asn Ile Pro Asp Glu Tyr Gly Asn
225                 230                 235                 240
Thr Thr Leu His Tyr Ala Ile Tyr Asn Glu Asp Lys Leu Met Ala Lys
                245                 250                 255
Ala Leu Leu Leu Tyr Gly Ala Asp Ile Glu Ser Lys Asn Lys His Gly
            260                 265                 270
Leu Thr Pro Leu Leu Leu Gly Val His Glu Gln Lys Gln Gln Val Val
        275                 280                 285
Lys Phe Leu Ile Lys Lys Lys Ala Asn Leu Asn Ala Leu Asp Arg Tyr
    290                 295                 300
```

```
Gly Arg Thr Ala Leu Ile Leu Ala Val Cys Cys Gly Ser Ala Ser Ile
305                 310                 315                 320
Val Ser Leu Leu Leu Glu Gln Asn Ile Asp Val Ser Ser Gln Asp Leu
                325                 330                 335
Ser Gly Gln Thr Ala Arg Glu Tyr Ala Val Ser Ser His His His Val
            340                 345                 350
Ile Cys Gln Leu Leu Ser Asp Tyr Lys Glu Lys Gln Met Leu Lys Ile
        355                 360                 365
Ser Ser Glu Asn Ser Asn Pro Glu Asn Val Ser Arg Thr Arg Asn Lys
    370                 375                 380
Pro Arg Thr His Met Val Val Glu Val Asp Ser Met Pro Ala Ala Ser
385                 390                 395                 400
Ser Val Lys Lys Pro Phe Gly Leu Arg Ser Lys Met Gly Lys Trp Cys
                405                 410                 415
Cys Arg Cys Phe Pro Cys Cys Arg Glu Ser Gly Lys Ser Asn Val Gly
            420                 425                 430
Thr Ser Gly Asp His Asp Asp Ser Ala Met Lys Thr Leu Arg Ser Lys
        435                 440                 445
Met Gly Lys Trp Cys Arg His Cys Phe Pro Cys Cys Arg Gly Ser Gly
    450                 455                 460
Lys Ser Asn Val Gly Ala Ser Gly Asp His Asp Asp Ser Ala Met Lys
465                 470                 475                 480
Thr Leu Arg Asn Lys Met Gly Lys Trp Cys Cys His Cys Phe Pro Cys
                485                 490                 495
Cys Arg Gly Ser Gly Lys Ser Lys Val Gly Ala Trp Gly Asp Tyr Asp
            500                 505                 510
Asp Ser Ala Phe Met Glu Pro Arg Tyr His Val Arg Gly Glu Asp Leu
        515                 520                 525
Asp Lys Leu His Arg Ala Ala Trp Trp Gly Lys Val Pro Arg Lys Asp
    530                 535                 540
Leu Ile Val Met Leu Arg Asp Thr Asp Val Asn Lys Lys Asp Lys Gln
545                 550                 555                 560
Lys Arg Thr Ala Leu His Leu Ala Ser Ala Asn Gly Asn Ser Glu Val
                565                 570                 575
Val Lys Leu Leu Leu Asp Arg Arg Cys Gln Leu Asn Val Leu Asp Asn
            580                 585                 590
Lys Lys Arg Thr Ala Leu Ile Lys Ala Val Gln Cys Gln Glu Asp Glu
        595                 600                 605
Cys Ala Leu Met Leu Leu Glu His Gly Thr Asp Pro Asn Ile Pro Asp
    610                 615                 620
Glu Tyr Gly Asn Thr Thr Leu His Tyr Ala Ile Tyr Asn Glu Asp Lys
625                 630                 635                 640
Leu Met Ala Lys Ala Leu Leu Leu Tyr Gly Ala Asp Ile Glu Ser Lys
                645                 650                 655
Asn Lys His Gly Leu Thr Pro Leu Leu Leu Gly Val His Glu Gln Lys
            660                 665                 670
Gln Gln Val Val Lys Phe Leu Ile Lys Lys Lys Ala Asn Leu Asn Ala
        675                 680                 685
Leu Asp Arg Tyr Gly Arg Thr Ala Leu Ile Leu Ala Val Cys Cys Gly
    690                 695                 700
Ser Ala Ser Ile Val Ser Leu Leu Leu Glu Gln Asn Ile Asp Val Ser
705                 710                 715                 720
Ser Gln Asp Leu Ser Gly Gln Thr Ala Arg Glu Tyr Ala Val Ser Ser
                725                 730                 735
His His His Val Ile Cys Gln Leu Leu Ser Asp Tyr Lys Glu Lys Gln
            740                 745                 750
Met Leu Lys Ile Ser Ser Glu Asn Ser Asn Pro Glu Gln Asp Leu Lys
        755                 760                 765
```

```
Leu Thr Ser Glu Glu Glu Ser Gln Arg Phe Lys Gly Ser Glu Asn Ser
    770                 775                 780
Gln Pro Glu Lys Met Ser Gln Glu Pro Glu Ile Asn Lys Asp Gly Asp
785                 790                 795                 800
Arg Glu Val Glu Glu Glu Met Lys Lys His Glu Ser Asn Asn Val Gly
                805                 810                 815
Leu Leu Glu Asn Leu Thr Asn Gly Val Thr Ala Gly Asn Gly Asp Asn
            820                 825                 830
Gly Leu Ile Pro Gln Arg Lys Ser Arg Thr Pro Glu Asn Gln Gln Phe
        835                 840                 845
Pro Asp Asn Glu Ser Glu Glu Tyr His Arg Ile Cys Glu Leu Val Ser
    850                 855                 860
Asp Tyr Lys Glu Lys Gln Met Pro Lys Tyr Ser Ser Glu Asn Ser Asn
865                 870                 875                 880
Pro Glu Gln Asp Leu Lys Leu Thr Ser Glu Glu Glu Ser Gln Arg Leu
                885                 890                 895
Glu Gly Ser Glu Asn Gly Gln Pro Glu Leu Glu Asn Phe Met Ala Ile
            900                 905                 910
Glu Glu Met Lys Lys His Gly Ser Thr His Val Gly Phe Pro Glu Asn
        915                 920                 925
Leu Thr Asn Gly Ala Thr Ala Gly Asn Gly Asp Asp Gly Leu Ile Pro
    930                 935                 940
Pro Arg Lys Ser Arg Thr Pro Glu Ser Gln Gln Phe Pro Asp Thr Glu
945                 950                 955                 960
Asn Glu Glu Tyr His Ser Asp Glu Gln Asn Asp Thr Gln Lys Gln Phe
                965                 970                 975
Cys Glu Glu Gln Asn Thr Gly Ile Leu His Asp Glu Ile Leu Ile His
            980                 985                 990
Glu Glu Lys Gln Ile Glu Val Val Glu Lys Met Asn Ser Glu Leu Ser
        995                 1000                1005
Leu Ser Cys Lys Lys Glu Lys Asp Ile Leu His Glu Asn Ser Thr Leu
    1010                1015                1020
Arg Glu Glu Ile Ala Met Leu Arg Leu Glu Leu Asp Thr Met Lys His
1025                1030                1035                1040
Gln Ser Gln Leu Pro Arg Thr His Met Val Val Glu Val Asp Ser Met
                1045                1050                1055
Pro Ala Ala Ser Ser Val Lys Lys Pro Phe Gly Leu Arg Ser Lys Met
            1060                1065                1070
Gly Lys Trp Cys Cys Arg Cys Phe Pro Cys Cys Arg Glu Ser Gly Lys
        1075                1080                1085
Ser Asn Val Gly Thr Ser Gly Asp His Asp Asp Ser Ala Met Lys Thr
    1090                1095                1100
Leu Arg Ser Lys Met Gly Lys Trp Cys Arg His Cys Phe Pro Cys Cys
1105                1110                1115                1120
Arg Gly Ser Gly Lys Ser Asn Val Gly Ala Ser Gly Asp His Asp Asp
                1125                1130                1135
Ser Ala Met Lys Thr Leu Arg Asn Lys Met Gly Lys Trp Cys Cys His
            1140                1145                1150
Cys Phe Pro Cys Cys Arg Gly Ser Gly Lys Ser Lys Val Gly Ala Trp
        1155                1160                1165
Gly Asp Tyr Asp Asp Ser Ala Phe Met Glu Pro Arg Tyr His Val Arg
    1170                1175                1180
Gly Glu Asp Leu Asp Lys Leu His Arg Ala Ala Trp Trp Gly Lys Val
1185                1190                1195                1200
Pro Arg Lys Asp Leu Ile Val Met Leu Arg Asp Thr Asp Val Asn Lys
                1205                1210                1215
Lys Asp Lys Gln Lys Arg Thr Ala Leu His Leu Ala Ser Ala Asn Gly
            1220                1225                1230
```

```
Asn Ser Glu Val Val Lys Leu Leu Leu Asp Arg Arg Cys Gln Leu Asn
        1235                1240                1245
Val Leu Asp Asn Lys Lys Arg Thr Ala Leu Ile Lys Ala Val Gln Cys
    1250                1255                1260
Gln Glu Asp Glu Cys Ala Leu Met Leu Leu Glu His Gly Thr Asp Pro
1265                1270                1275                1280
Asn Ile Pro Asp Glu Tyr Gly Asn Thr Thr Leu His Tyr Ala Ile Tyr
                1285                1290                1295
Asn Glu Asp Lys Leu Met Ala Lys Ala Leu Leu Leu Tyr Gly Ala Asp
            1300                1305                1310
Ile Glu Ser Lys Asn Lys His Gly Leu Thr Pro Leu Leu Leu Gly Val
        1315                1320                1325
His Glu Gln Lys Gln Gln Val Val Lys Phe Leu Ile Lys Lys Lys Ala
    1330                1335                1340
Asn Leu Asn Ala Leu Asp Arg Tyr Gly Arg Thr Ala Leu Ile Leu Ala
1345                1350                1355                1360
Val Cys Cys Gly Ser Ala Ser Ile Val Ser Leu Leu Leu Glu Gln Asn
                1365                1370                1375
Ile Asp Val Ser Ser Gln Asp Leu Ser Gly Gln Thr Ala Arg Glu Tyr
            1380                1385                1390
Ala Val Ser Ser His His His Val Ile Cys Gln Leu Leu Ser Asp Tyr
        1395                1400                1405
Lys Glu Lys Gln Met Leu Lys Ile Ser Ser Glu Asn Ser Asn Pro Glu
    1410                1415                1420
Gln Asp Leu Lys Leu Thr Ser Glu Glu Glu Ser Gln Arg Phe Lys Gly
1425                1430                1435                1440
Ser Glu Asn Ser Gln Pro Glu Lys Met Ser Gln Glu Pro Glu Ile Asn
                1445                1450                1455
Lys Asp Gly Asp Arg Glu Val Glu Glu Glu Met Lys Lys His Glu Ser
            1460                1465                1470
Asn Asn Val Gly Leu Leu Glu Asn Leu Thr Asn Gly Val Thr Ala Gly
        1475                1480                1485
Asn Gly Asp Asn Gly Leu Ile Pro Gln Arg Lys Ser Arg Thr Pro Glu
    1490                1495                1500
Asn Gln Gln Phe Pro Asp Asn Glu Ser Glu Glu Tyr His Arg Ile Cys
1505                1510                1515                1520
Glu Leu Val Ser Asp Tyr Lys Glu Lys Gln Met Pro Lys Tyr Ser Ser
                1525                1530                1535
Glu Asn Ser Asn Pro Glu Gln Asp Leu Lys Leu Thr Ser Glu Glu Glu
            1540                1545                1550
Ser Gln Arg Leu Glu Gly Ser Glu Asn Gly Gln Pro Glu Lys Arg Ser
        1555                1560                1565
Gln Glu Pro Glu Ile Asn Lys Asp Gly Asp Arg Glu Leu Glu Asn Phe
    1570                1575                1580
Met Ala Ile Glu Glu Met Lys Lys His Gly Ser Thr His Val Gly Phe
1585                1590                1595                1600
Pro Glu Asn Leu Thr Asn Gly Ala Thr Ala Gly Asn Gly Asp Asp Gly
                1605                1610                1615
Leu Ile Pro Pro Arg Lys Ser Arg Thr Pro Glu Ser Gln Gln Phe Pro
            1620                1625                1630
Asp Thr Glu Asn Glu Glu Tyr His Ser Asp Glu Gln Asn Asp Thr Gln
        1635                1640                1645
Lys Gln Phe Cys Glu Glu Gln Asn Thr Gly Ile Leu His Asp Glu Ile
    1650                1655                1660
Leu Ile His Glu Glu Lys Gln Ile Glu Val Val Glu Lys Met Asn Ser
1665                1670                1675                1680
Glu Leu Ser Leu Ser Cys Lys Lys Glu Lys Asp Ile Leu His Glu Asn
                1685                1690                1695
```

```
Ser Thr Leu Arg Glu Glu Ile Ala Met Leu Arg Leu Glu Leu Asp Thr
            1700                1705                1710
Met Lys His Gln Ser Gln Leu
        1715

      <210> 379
      <211> 656
      <212> PRT
      <213> Homo sapien

      <400> 379
Met Val Val Glu Val Asp Ser Met Pro Ala Ala Ser Ser Val Lys Lys
 1               5                  10                  15
Pro Phe Gly Leu Arg Ser Lys Met Gly Lys Trp Cys Cys Arg Cys Phe
            20                  25                  30
Pro Cys Cys Arg Glu Ser Gly Lys Ser Asn Val Gly Thr Ser Gly Asp
        35                  40                  45
His Asp Asp Ser Ala Met Lys Thr Leu Arg Ser Lys Met Gly Lys Trp
    50                  55                  60
Cys Arg His Cys Phe Pro Cys Cys Arg Gly Ser Gly Lys Ser Asn Val
65                  70                  75                  80
Gly Ala Ser Gly Asp His Asp Asp Ser Ala Met Lys Thr Leu Arg Asn
                85                  90                  95
Lys Met Gly Lys Trp Cys Cys His Cys Phe Pro Cys Cys Arg Gly Ser
            100                 105                 110
Gly Lys Ser Lys Val Gly Ala Trp Gly Asp Tyr Asp Asp Ser Ala Phe
        115                 120                 125
Met Glu Pro Arg Tyr His Val Arg Gly Glu Asp Leu Asp Lys Leu His
    130                 135                 140
Arg Ala Ala Trp Trp Gly Lys Val Pro Arg Lys Asp Leu Ile Val Met
145                 150                 155                 160
Leu Arg Asp Thr Asp Val Asn Lys Lys Asp Lys Gln Lys Arg Thr Ala
                165                 170                 175
Leu His Leu Ala Ser Ala Asn Gly Asn Ser Glu Val Val Lys Leu Leu
            180                 185                 190
Leu Asp Arg Arg Cys Gln Leu Asn Val Leu Asp Asn Lys Lys Arg Thr
        195                 200                 205
Ala Leu Ile Lys Ala Val Gln Cys Gln Glu Asp Glu Cys Ala Leu Met
    210                 215                 220
Leu Leu Glu His Gly Thr Asp Pro Asn Ile Pro Asp Glu Tyr Gly Asn
225                 230                 235                 240
Thr Thr Leu His Tyr Ala Ile Tyr Asn Glu Asp Lys Leu Met Ala Lys
                245                 250                 255
Ala Leu Leu Leu Tyr Gly Ala Asp Ile Glu Ser Lys Asn Lys His Gly
            260                 265                 270
Leu Thr Pro Leu Leu Leu Gly Val His Glu Gln Lys Gln Gln Val Val
        275                 280                 285
Lys Phe Leu Ile Lys Lys Lys Ala Asn Leu Asn Ala Leu Asp Arg Tyr
    290                 295                 300
Gly Arg Thr Ala Leu Ile Leu Ala Val Cys Cys Gly Ser Ala Ser Ile
305                 310                 315                 320
Val Ser Leu Leu Leu Glu Gln Asn Ile Asp Val Ser Ser Gln Asp Leu
                325                 330                 335
Ser Gly Gln Thr Ala Arg Glu Tyr Ala Val Ser Ser His His His Val
            340                 345                 350
Ile Cys Gln Leu Leu Ser Asp Tyr Lys Glu Lys Gln Met Leu Lys Ile
        355                 360                 365
Ser Ser Glu Asn Ser Asn Pro Glu Gln Asp Leu Lys Leu Thr Ser Glu
```

```
    370                 375                 380
Glu Glu Ser Gln Arg Phe Lys Gly Ser Glu Asn Ser Gln Pro Glu Lys
385                 390                 395                 400
Met Ser Gln Glu Pro Glu Ile Asn Lys Asp Gly Asp Arg Glu Val Glu
                405                 410                 415
Glu Glu Met Lys Lys His Glu Ser Asn Asn Val Gly Leu Leu Glu Asn
            420                 425                 430
Leu Thr Asn Gly Val Thr Ala Gly Asn Gly Asp Asn Gly Leu Ile Pro
        435                 440                 445
Gln Arg Lys Ser Arg Thr Pro Glu Asn Gln Gln Phe Pro Asp Asn Glu
    450                 455                 460
Ser Glu Glu Tyr His Arg Ile Cys Glu Leu Val Ser Asp Tyr Lys Glu
465                 470                 475                 480
Lys Gln Met Pro Lys Tyr Ser Ser Glu Asn Ser Asn Pro Glu Gln Asp
                485                 490                 495
Leu Lys Leu Thr Ser Glu Glu Glu Ser Gln Arg Leu Glu Gly Ser Glu
            500                 505                 510
Asn Gly Gln Pro Glu Leu Glu Asn Phe Met Ala Ile Glu Glu Met Lys
        515                 520                 525
Lys His Gly Ser Thr His Val Gly Phe Pro Glu Asn Leu Thr Asn Gly
    530                 535                 540
Ala Thr Ala Gly Asn Gly Asp Asp Gly Leu Ile Pro Pro Arg Lys Ser
545                 550                 555                 560
Arg Thr Pro Glu Ser Gln Gln Phe Pro Asp Thr Glu Asn Glu Glu Tyr
                565                 570                 575
His Ser Asp Glu Gln Asn Asp Thr Gln Lys Gln Phe Cys Glu Glu Gln
            580                 585                 590
Asn Thr Gly Ile Leu His Asp Glu Ile Leu Ile His Glu Glu Lys Gln
        595                 600                 605
Ile Glu Val Val Glu Lys Met Asn Ser Glu Leu Ser Leu Ser Cys Lys
    610                 615                 620
Lys Glu Lys Asp Ile Leu His Glu Asn Ser Thr Leu Arg Glu Glu Ile
625                 630                 635                 640
Ala Met Leu Arg Leu Glu Leu Asp Thr Met Lys His Gln Ser Gln Leu
                645                 650                 655

      &lt;210&gt; 380
      &lt;211&gt; 671
      &lt;212&gt; PRT
      &lt;213&gt; Homo sapien

      &lt;400&gt; 380
Met Val Val Glu Val Asp Ser Met Pro Ala Ala Ser Ser Val Lys Lys
 1               5                  10                  15
Pro Phe Gly Leu Arg Ser Lys Met Gly Lys Trp Cys Cys Arg Cys Phe
            20                  25                  30
Pro Cys Cys Arg Glu Ser Gly Lys Ser Asn Val Gly Thr Ser Gly Asp
        35                  40                  45
His Asp Asp Ser Ala Met Lys Thr Leu Arg Ser Lys Met Gly Lys Trp
    50                  55                  60
Cys Arg His Cys Phe Pro Cys Cys Arg Gly Ser Gly Lys Ser Asn Val
65                  70                  75                  80
Gly Ala Ser Gly Asp His Asp Asp Ser Ala Met Lys Thr Leu Arg Asn
                85                  90                  95
Lys Met Gly Lys Trp Cys Cys His Cys Phe Pro Cys Cys Arg Gly Ser
            100                 105                 110
Gly Lys Ser Lys Val Gly Ala Trp Gly Asp Tyr Asp Asp Ser Ala Phe
        115                 120                 125
```

```
Met Glu Pro Arg Tyr His Val Arg Gly Glu Asp Leu Asp Lys Leu His
    130                 135                 140
Arg Ala Ala Trp Trp Gly Lys Val Pro Arg Lys Asp Leu Ile Val Met
145                 150                 155                 160
Leu Arg Asp Thr Asp Val Asn Lys Lys Asp Lys Gln Lys Arg Thr Ala
                165                 170                 175
Leu His Leu Ala Ser Ala Asn Gly Asn Ser Glu Val Val Lys Leu Leu
            180                 185                 190
Leu Asp Arg Arg Cys Gln Leu Asn Val Leu Asp Asn Lys Lys Arg Thr
        195                 200                 205
Ala Leu Ile Lys Ala Val Gln Cys Gln Glu Asp Glu Cys Ala Leu Met
    210                 215                 220
Leu Leu Glu His Gly Thr Asp Pro Asn Ile Pro Asp Glu Tyr Gly Asn
225                 230                 235                 240
Thr Thr Leu His Tyr Ala Ile Tyr Asn Glu Asp Lys Leu Met Ala Lys
                245                 250                 255
Ala Leu Leu Leu Tyr Gly Ala Asp Ile Glu Ser Lys Asn Lys His Gly
            260                 265                 270
Leu Thr Pro Leu Leu Leu Gly Val His Glu Gln Lys Gln Gln Val Val
        275                 280                 285
Lys Phe Leu Ile Lys Lys Lys Ala Asn Leu Asn Ala Leu Asp Arg Tyr
    290                 295                 300
Gly Arg Thr Ala Leu Ile Leu Ala Val Cys Cys Gly Ser Ala Ser Ile
305                 310                 315                 320
Val Ser Leu Leu Leu Glu Gln Asn Ile Asp Val Ser Ser Gln Asp Leu
                325                 330                 335
Ser Gly Gln Thr Ala Arg Glu Tyr Ala Val Ser Ser His His His Val
            340                 345                 350
Ile Cys Gln Leu Leu Ser Asp Tyr Lys Glu Lys Gln Met Leu Lys Ile
        355                 360                 365
Ser Ser Glu Asn Ser Asn Pro Glu Gln Asp Leu Lys Leu Thr Ser Glu
    370                 375                 380
Glu Glu Ser Gln Arg Phe Lys Gly Ser Glu Asn Ser Gln Pro Glu Lys
385                 390                 395                 400
Met Ser Gln Glu Pro Glu Ile Asn Lys Asp Gly Asp Arg Glu Val Glu
                405                 410                 415
Glu Glu Met Lys Lys His Glu Ser Asn Asn Val Gly Leu Leu Glu Asn
            420                 425                 430
Leu Thr Asn Gly Val Thr Ala Gly Asn Gly Asp Asn Gly Leu Ile Pro
        435                 440                 445
Gln Arg Lys Ser Arg Thr Pro Glu Asn Gln Gln Phe Pro Asp Asn Glu
    450                 455                 460
Ser Glu Glu Tyr His Arg Ile Cys Glu Leu Val Ser Asp Tyr Lys Glu
465                 470                 475                 480
Lys Gln Met Pro Lys Tyr Ser Ser Glu Asn Ser Asn Pro Glu Gln Asp
                485                 490                 495
Leu Lys Leu Thr Ser Glu Glu Glu Ser Gln Arg Leu Glu Gly Ser Glu
            500                 505                 510
Asn Gly Gln Pro Glu Lys Arg Ser Gln Glu Pro Glu Ile Asn Lys Asp
        515                 520                 525
Gly Asp Arg Glu Leu Glu Asn Phe Met Ala Ile Glu Glu Met Lys Lys
    530                 535                 540
His Gly Ser Thr His Val Gly Phe Pro Glu Asn Leu Thr Asn Gly Ala
545                 550                 555                 560
Thr Ala Gly Asn Gly Asp Asp Gly Leu Ile Pro Pro Arg Lys Ser Arg
                565                 570                 575
Thr Pro Glu Ser Gln Gln Phe Pro Asp Thr Glu Asn Glu Glu Tyr His
            580                 585                 590
```

Ser Asp Glu Gln Asn Asp Thr Gln Lys Gln Phe Cys Glu Glu Gln Asn
595 600 605
Thr Gly Ile Leu His Asp Glu Ile Leu Ile His Glu Glu Lys Gln Ile
610 615 620
Glu Val Val Glu Lys Met Asn Ser Glu Leu Ser Leu Ser Cys Lys Lys
625 630 635 640
Glu Lys Asp Ile Leu His Glu Asn Ser Thr Leu Arg Glu Glu Ile Ala
645 650 655
Met Leu Arg Leu Glu Leu Asp Thr Met Lys His Gln Ser Gln Leu
660 665 670

<210> 381
<211> 251
<212> DNA
<213> Homo sapien

<400> 381
ggagaagcgt ctgctggggc aggaaggggt ttccctgccc tctcacctgt ccctcaccaa 60
ggtaacatgc ttcccctaag ggtatcccaa cccaggggcc tcaccatgac ctctgagggg 120
ccaatatccc aggagaagca ttggggagtt gggggcaggt gaaggaccca ggactcacac 180
atcctgggcc tccaaggcag aggagagggt cctcaagaag gtcaggagga aaatccgtaa 240
caagcagtca g 251

<210> 382
<211> 3279
<212> DNA
<213> Homo sapiens

<400> 382
cttcctgcag cccccatgct ggtgaggggc acgggcagga acagtggacc caacatggaa 60
atgctggagg gtgtcaggaa gtgatcgggc tctggggcag ggaggagggg tggggagtgt 120
cactgggagg ggacatcctg cagaaggtag gagtgagcaa acacccgctg caggggaggg 180
gagagccctg cggcacctgg gggagcagag ggagcagcac ctgcccaggc ctgggaggag 240
gggcctggag ggcgtgagga ggagcgaggg ggctgcatgg ctggagtgag ggatcagggg 300
cagggcgcga gatggcctca cacagggaag agagggcccc tcctgcaggg cctcacctgg 360
gccacaggag gacactgctt ttcctctgag gagtcaggag ctgtggatgg tgctggacag 420
aagaaggaca gggcctggct caggtgtcca gaggctgtcg ctggcttccc tttgggatca 480
gactgcaggg agggagggcg gcagggttgt gggggagtg acgatgagga tgacctgggg 540
gtggctccag gccttgcccc tgcctgggcc ctcacccagc ctccctcaca gtctcctggc 600
cctcagtctc tcccctccac tccatcctcc atctggcctc agtgggtcat tctgatcact 660
gaactgacca tacccagccc tgcccacggc cctccatggc tccccaatgc cctggagagg 720
ggacatctag tcagagagta gtcctgaaga ggtggcctct gcgatgtgcc tgtgggggca 780
gcatcctgca gatggtcccg gccctcatcc tgctgacctg tctgcaggga ctgtcctcct 840
ggaccttgcc ccttgtgcag gagctggacc ctgaagtccc ctccccatag gccaagactg 900
gagccttgtt ccctctgttg gactccctgc ccatattctt gtgggagtgg gttctggaga 960
catttctgtc tgttcctgag agctgggaat tgctctcagt catctgcctg cgcggttctg 1020
agagatggag ttgcctaggc agttattggg gccaatcttt ctcactgtgt ctctcctcct 1080
ttacccttag ggtgattctg gggtccact tgtctgtaat ggtgtgcttc aaggtatcac 1140
atcatggggc cctgagccat gtgccctgcc tgaaaagcct gctgtgtaca ccaaggtggt 1200
gcattaccgg aagtggatca aggacaccat cgcagccaac ccctgagtgc ccctgtccca 1260
cccctacctc tagtaaattt aagtccacct cacgttctgg catcacttgg cctttctgga 1320
tgctggacac ctgaagcttg gaactcacct ggccgaagct cgagcctcct gagtcctact 1380
gacctgtgct ttctggtgtg gagtccaggg ctgctaggaa aaggaatggg cagacacagg 1440
tgtatgccaa tgtttctgaa atgggtataa tttcgtcctc tccttcggaa cactggctgt 1500
ctctgaagac ttctcgctca gtttcagtga ggacacacac aaagacgtgg gtgaccatgt 1560
tgtttgtggg gtgcagagat gggaggggtg gggcccaccc tggaagagtg gacagtgaca 1620
caaggtggac actctctaca gatcactgag gataagctgg agccacaatg catgaggcac 1680
acacacagca aggttgacgc tgtaaacata gcccacgctg tcctgggggc actgggaagc 1740

```
ctagataagg ccgtgagcag aaagaagggg aggatcctcc tatgttgttg aaggagggac 1800
tagggggaga aactgaaagc tgattaatta caggaggttt gttcaggtcc cccaaaccac 1860
cgtcagattt gatgatttcc tagcaggact tacagaaata aagagctatc atgctgtggt 1920
ttattatggt ttgttacatt gataggatac atactgaaat cagcaaacaa aacagatgta 1980
tagattagag tgtggagaaa acagaggaaa acttgcagtt acgaagactg gcaacttggc 2040
tttactaagt tttcagactg gcaggaagtc aaacctatta ggctgaggac cttgtggagt 2100
gtagctgatc cagctgatag aggaactagc caggtggggg cctttccctt tggatggggg 2160
gcatatccga cagttattct ctccaagtgg agacttacgg acagcatata attctccctg 2220
caaggatgta tgataatatg tacaaagtaa ttccaactga ggaagctcac ctgatcctta 2280
gtgtccaggg tttttactgg gggtctgtag gacgagtatg gagtacttga ataattgacc 2340
tgaagtcctc agacctgagg ttccctagag ttcaaacaga tacagcatgg tccagagtcc 2400
cagatgtaca aaaacaggga ttcatcacaa atcccatctt tagcatgaag ggtctggcat 2460
ggcccaaggc cccaagtata tcaaggcact tgggcagaac atgccaagga atcaaatgtc 2520
atctcccagg agttattcaa gggtgagccc tttacttggg atgtacaggc tttgagcagt 2580
gcagggctgc tgagtcaacc ttttattgta caggggatga gggaaaggga gaggatgagg 2640
aagcccccct ggggatttgg tttggtcttg tgatcaggtg gtctatgggg ctatccctac 2700
aaagaagaat ccagaaatag gggcacattg aggaatgata ctgagcccaa agagcattca 2760
atcattgttt tatttgcctt cttttcacac cattggtgag ggagggatta ccaccctggg 2820
gttatgaaga tggttgaaca ccccacacat agcaccggag atatgagatc aacagtttct 2880
tagccataga gattcacagc ccagagcagg aggacgctgc acaccatgca ggatgacatg 2940
ggggatgcgc tcgggattgg tgtgaagaag caaggactgt tagaggcagg ctttatagta 3000
acaagacggt ggggcaaact ctgatttccg tgggggaatg tcatggtctt gctttactaa 3060
gttttgagac tggcaggtag tgaaactcat taggctgaga accttgtgga atgcagctga 3120
cccagctgat agaggaagta gccaggtggg agcctttccc agtgggtgtg ggacatatct 3180
ggcaagattt tgtggcactc ctggttacag atactggggc agcaaataaa actgaatctt 3240
gttttcagac cttaaaaaaa aaaaaaaaaa aaaagtttt                        3279
```

<210> 383
<211> 154
<212> PRT
<213> Homo sapiens

<400> 383

```
Met Ala Gly Val Arg Asp Gln Gly Gln Gly Ala Arg Trp Pro His Thr
                5                   10                  15
Gly Lys Arg Gly Pro Leu Leu Gln Gly Leu Thr Trp Ala Thr Gly Gly
            20                  25                  30
His Cys Phe Ser Ser Glu Glu Ser Gly Ala Val Asp Gly Ala Gly Gln
        35                  40                  45
Lys Lys Asp Arg Ala Trp Leu Arg Cys Pro Glu Ala Val Ala Gly Phe
    50                  55                  60
Pro Leu Gly Ser Asp Cys Arg Glu Gly Gly Arg Gln Gly Cys Gly Gly
65                  70                  75                  80
Ser Asp Asp Glu Asp Asp Leu Gly Val Ala Pro Gly Leu Ala Pro Ala
                85                  90                  95
Trp Ala Leu Thr Gln Pro Pro Ser Gln Ser Pro Gly Pro Gln Ser Leu
            100                 105                 110
Pro Ser Thr Pro Ser Ser Ile Trp Pro Gln Trp Val Ile Leu Ile Thr
        115                 120                 125
Glu Leu Thr Ile Pro Ser Pro Ala His Gly Pro Pro Trp Leu Pro Asn
    130                 135                 140
Ala Leu Glu Arg Gly His Leu Val Arg Glu
145                 150
```

<210> 384
<211> 557
<212> DNA
<213> Homo sapiens

<400> 384
ggatcctcta gagcggccgc ctactactac taaattcgcg gccgcgtcga cgaagaagag 60
aaagatgtgt tttgttttgg actctctgtg gtcccttcca atgctgtggg tttccaacca 120
ggggaagggt cccttttgca ttgccaagtg ccataaccat gagcactact ctaccatggt 180
tctgcctcct ggccaagcag gctggtttgc aagaatgaaa tgaatgattc tacagctagg 240
acttaacctt gaaatggaaa gtcttgcaat cccatttgca ggatccgtct gtgcacatgc 300
ctctgtagag agcagcattc ccagggacct tggaaacagt tggcactgta aggtgcttgc 360
tccccaagac acatcctaaa aggtgttgta atggtgaaaa cgtcttcctt ctttattgcc 420
ccttcttatt tatgtgaaca actgtttgtc ttttttgta tctttttaa actgtaaagt 480
tcaattgtga aaatgaatat catgcaaata aattatgcga tttttttttc aaagtaaaaa 540
aaaaaaaaaa aaaaaaa 557

<210> 385
<211> 337
<212> DNA
<213> Homo sapiens

<400> 385
ttcccaggtg atgtgcgagg gaagacacat ttactatcct tgatggggct gattccttta 60
gtttctctag cagcagatgg gttaggagga agtgacccaa gtggttgact cctatgtgca 120
tctcaaagcc atctgctgtc ttcgagtacg gacacatcat cactcctgca ttgttgatca 180
aaacgtggag gtgcttttcc tcagctaaga agcccttagc aaaagctcga atagacttag 240
tatcagacag gtccagtttc cgcaccaaca cctgctggtt ccctgtcgtg gtctggatct 300
ctttggccac caattccccc ttttccacat cccggca 337

<210> 386
<211> 300
<212> DNA
<213> Homo sapiens

<400> 386
gggcccgcta ccggcccagg ccccgcctcg cgagtcctcc tccccgggtg cctgcccgca 60
gcccgctcgg cccagagggt gggcgcgggg ctgcctctac cggctggcgg ctgtaactca 120
gcgaccttgg cccgaaggct ctagcaagga cccaccgacc ccagccgcgg cggcggcggc 180
gcggactttg cccggtgtgt ggggcggagc ggactgcgtg tccgcggacg ggcagcgaag 240
atgttagcct tcgctgccag gaccgtggac cgatcccagg gctgtggtgt aacctcagcc 300

<210> 387
<211> 537
<212> DNA
<213> Homo sapiens

<400> 387
gggccgagtc gggcaccaag ggactctttg caggcttcct tcctcggatc atcaaggctg 60
ccccctcctg tgccatcatg atcagcacct atgagttcgg caaaagcttc ttccagaggc 120
tgaaccagga ccggcttctg ggcggctgaa aggggcaagg aggcaaggac cccgtctctc 180
ccacggatgg ggagagggca ggaggagacc cagccaagtg ccttttcctc agcactgagg 240
gaggggcctt gtttcccttc cctcccggcg acaagctcca gggcagggct gtccctctgg 300
gcggcccagc acttcctcag acacaacttc ttcctgctgc tccagtcgtg gggatcatca 360
cttacccacc ccccaagttc aagaccaaat cttccagctg ccccttcgt gtttccctgt 420
gtttgctgta gctgggcatg tctccaggaa ccaagaagcc ctcagcctgg tgtagtctcc 480
ctgacccttg ttaattcctt aagtctaaag atgatgaact tcaaaaaaaa aaaaaaa 537

<210> 388
<211> 520
<212> DNA
<213> Homo sapiens

<400> 388
aggataattt ttaaaccaat caaatgaaaa aaacaaacaa acaaaaaagg aaatgtcatg 60
tgaggttaaa ccagtttgca ttcccctaat gtggaaaaag taagaggact actcagcact 120
gtttgaagat tgcctcttct acagcttctg agaattgtgt tatttcactt gccaagtgaa 180
ggacccccctc cccaacatgc cccagcccac ccctaagcat ggtcccttgt caccaggcaa 240
ccaggaaact gctacttgtg gacctcacca gagaccagga gggtttggtt agctcacagg 300
acttcccccca ccccagaaga ttagcatccc atactagact catactcaac tcaactaggc 360
tcatactcaa ttgatggtta ttagacaatt ccatttcttt ctggttatta taaacagaaa 420
atctttcctc ttctcattac cagtaaaggc tcttggtatc tttctgttgg aatgatttct 480
atgaacttgt cttattttaa tggtgggttt tttttctggt 520

<210> 389
<211> 365
<212> DNA
<213> Homo sapiens

<400> 389
cgttgcccca gtttgacaga aggaaaggcg gagcttattc aaagtctaga gggagtggag 60
gagttaaggc tggatttcag atctgcctgg ttccagccgc agtgtgccct ctgctccccc 120
aacgactttc caaataatct caccagcgcc ttccagctca ggcgtcctag aagcgtcttg 180
aagcctatgg ccagctgtct ttgtgttccc tctcacccgc ctgtcctcac agctgagact 240
cccaggaaac cttcagacta ccttcctctg ccttcagcaa ggggcgttgc ccacattctc 300
tgagggtcag tggaagaacc tagactccca ttgctagagg tagaaagggg aagggtgctg 360
gggag 365

<210> 390
<211> 221
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(221)
<223> n = A,T,C or G

<400> 390
tgcctctcca tcctggcccc gacttctctg tcaggaaagt ggggatggac cccatctgca 60
tacacggntt ctcatgggtg tggaacatct ctgcttgcgg tttcaggaag gcctctggct 120
gctctangag tctgancnga ntcgttgccc cantntgaca naaggaaagg cggagcttat 180
tcaaagtcta gagggagtgg aggagttaag gctggatttc a 221

<210> 391
<211> 325
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(325)
<223> n = A,T,C or G

<400> 391
tggagcaggt cccgaggcct ccctagagcc tggggccgac tctgtgncga tgcangcttt 60
ctctcgcgcc cagcctggag ctgctcctgg catctaccaa caatcagncg aggcgagcag 120
tagccagggc actgctgcca acagccagtc cnnataccat catgtnaccc ggtgngctct 180
naanttngat ntccanagcc ctacccatcn tagttctgct ctcccaccgg ntaccagccc 240
cactgcccag gaatcctaca gccagtaccc tgtcccgacg tctctaccta ccagtacgat 300

gagacctccg gctactacta tgacc 325

<210> 392
<211> 277
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(277)
<223> n = A,T,C or G

<400> 392
atattgttta actccttcct ttatatcttt taacattttc atggngaaag gttcacatct 60
agtctcactt nggcnagngn ctcctacttg agtctcttcc ccggcctgnn ccagtngnaa 120
antaccanga accgncatgn cttaanaacn ncctggtttn tgggttnntc aatgactgca 180
tgcagtgcac caccctgtcc actacgtgat gctgtaggat taaagtctca cagtgggcgg 240
ctgaggatac agcgccgcgt cctgtgttgc tggggaa 277

<210> 393
<211> 566
<212> DNA
<213> Homo sapiens

<400> 393
actagtccag tgtggtggaa ttcgcggccg cgtcgacgga caggtcagct gtctggctca 60
gtgatctaca ttctgaagtt gtctgaaaat gtcttcatga ttaaattcag cctaaacgtt 120
ttgccgggaa cactgcagag acaatgctgt gagtttccaa ccttagccca tctgcgggca 180
gagaaggtct agtttgtcca tcagcattat catgatatca ggactggtta cttggttaag 240
gaggggtcta ggagatctgt ccctttttaga gacaccttac ttataatgaa gtatttggga 300
gggtggtttt caaaagtaga aatgtcctgt attccgatga tcatcctgta aacattttat 360
catttattaa tcatccctgc ctgtgtctat tattatattc atatctctac gctggaaact 420
ttctgcctca atgtttactg tgcctttgtt tttgctagtt tgtgttgttg aaaaaaaaaa 480
cattctctgc ctgagtttta atttttgtcc aaagttattt taatctatac aattaaaagc 540
ttttgcctat caaaaaaaaa aaaaaa 566

<210> 394
<211> 384
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(384)
<223> n = A,T,C or G

<400> 394
gaacatacat gtcccggcac ctgagctgca gtctgacatc atcgccatca cgggcctcgc 60
tgcaaattng gaccgggcca aggctggact gctggagcgt gtgaaggagc tacaggccna 120
gcaggaggac cgggctttaa ggagttttaa gctgagtgtc actgtagacc ccaaatacca 180
tcccaagatt atcgggagaa agggggcagt aattacccaa atccggttgg agcatgacgt 240
gaacatccag tttcctgata aggacgatgg gaaccagccc caggaccaaa ttaccatcac 300
agggtacgaa aagaacacag aagctgccag ggatgctata ctgagaattg tgggtgaact 360
tgagcagatg gtttctgagg acgt 384

<210> 395
<211> 399
<212> DNA

<213> Homo sapiens

<400> 395
ggcaaaactg tgtgacctca ataagacctc gcagatccaa ggtcaagtat cagaagtgac 60
tctgaccttg gactccaaga cctacatcaa cagcctggct atattagatg atgagccagt 120
tatcagaggt ttcatcattg cggaaattgt ggagtctaag gaaatcatgg cctctgaagt 180
attcacgtct ttccagtacc ctgagttctc tatagagttg cctaacacag gcagaattgg 240
ccagctactt gtctgcaatt gtatcttcaa gaataccctg gccatccctt tgactgacgt 300
caagttctct ttggaaagcc tgggcatctc ctcactacag acctctgacc atgggacggt 360
gcagcctggt gagaccatcc aatcccaaat aaaatgcac 399

<210> 396
<211> 403
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(403)
<223> n = A,T,C or G

<400> 396
tggagttntc agtgcaaaca agccataaag cttcagtagc aaattactgt ctcacagaaa 60
gacattttca acttctgctc cagctgctga taaaacaaat catgtgttta gcttgactcc 120
agacaaggac aacctgttcc ttcataactc tctagagaaa aaaaggagtt gttagtagat 180
actaaaaaaa gtggatgaat aatctggata tttttcctaa aaagattcct tgaaacacat 240
taggaaaatg gagggcctta tgatcagaat gctagaatta gtccattgtg ctgaagcagg 300
gtttagggga gggagtgagg gataaaagaa ggaaaaaaag aagagtgaga aaacctattt 360
atcaaagcag gtgctatcac tcaatgttag gccctgctct ttt 403

<210> 397
<211> 100
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(100)
<223> n = A,T,C or G

<400> 397
actagtncag tgtggtggaa ttcgcggccg cgtcgaccta naanccatct ctatagcaaa 60
tccatccccg ctcctggttg gtnacagaat gactgacaaa 100

<210> 398
<211> 278
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(278)
<223> n = A,T,C or G

<400> 398
gcggccgcgt cgacagcagt tccgccagcg ctcgcccctg ggtggggatg tgctgcacgc 60
ccacctggac atctggaagt cagcggcctg gatgaaagag cggacttcac ctggggcgat 120
tcactactgt gcctcgacca gtgaggagag ctggaccgac agcgaggtgg actcatcatg 180

ctccgggcag cccatccacc tgtggcagtt cctcaaggag ttgctactca agccccacag 240
ctatggccgc ttcattangt ggctcaacaa ggagaagg 278

<210> 399
<211> 298
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(298)
<223> n = A,T,C or G

<400> 399
acggaggtgg aggaagcgnc cctgggatcg anaggatggg tcctgncatt gaccncctcn 60
ggggtgccng catggagcgc atgggcgcgg gcctgggcca cggcatggat cgcgtgggct 120
ccgagatcga gcgcatgggc ctggtcatgg accgcatggg ctccgtggag cgcatgggct 180
ccggcattga gcgcatgggc ccgctgggcc tcgaccacat ggcctccanc attgancgca 240
tgggccagac catggagcgc attggctctg gcgtggagcn catgggtgcc ggcatggg 298

<210> 400
<211> 548
<212> DNA
<213> Homo sapiens

<400> 400
acatcaacta cttcctcatt ttaaggtatg gcagttccct tcatcccctt ttcctgcctt 60
gtacatgtac atgtatgaaa tttccttctc ttaccgaact ctctccacac atcacaaggt 120
caaagaacca cacgcttaga agggtaagag ggcaccctat gaaatgaaat ggtgatttct 180
tgagtctctt ttttccacgt ttaagggggcc atggcaggac ttagagttgc gagttaagac 240
tgcagagggc tagagaatta tttcatacag gctttgaggc cacccatgtc acttatcccg 300
tataccctct caccatcccc ttgtctactc tgatgccccc aagatgcaac tgggcagcta 360
gttggcccca taattctggg cctttgttgt ttgttttaat tacttgggca tcccaggaag 420
ctttccagtg atctcctacc atgggccccc ctcctgggat caagcccctc ccaggccctg 480
tccccagccc ctcctgcccc agcccacccg cttgccttgg tgctcagccc tcccattggg 540
agcaggtt 548

<210> 401
<211> 355
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(355)
<223> n = A,T,C or G

<400> 401
actgtttcca tgttatgttt ctacacattg ctacctcagt gctcctggaa acttagcttt 60
tgatgtctcc aagtagtcca ccttcattta actctttgaa actgtatcat ctttgccaag 120
taagagtggt ggcctatttc agctgctttg acaaaatgac tggctcctga cttaacgttc 180
tataaatgaa tgtgctgaag caaagtgccc atggtggcgg cgaagaagan aaagatgtgt 240
tttgttttgg actctctgtg gtcccttcca atgctgnggg tttccaacca ggggaagggt 300
ccttttgca ttgccaagtg ccataaccat gagcactact ctaccatggn tctgc 355

<210> 402
<211> 407
<212> DNA

<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(407)
<223> n = A,T,C or G

<400> 402
atggggcaag ctggataaag aaccaagacc cactggagta tgctgtcttc aagaaaccca 60
tctcacatgc ggtggcatac ataggctcaa aataaaggaa tggagaaaaa tatttcaagc 120
aaatggaaaa cagaaaaaag caggtgttgc actcctactt tctgacaaaa cagactatgc 180
gaataaagat aaaaaagaga aggacattac aaaggtggtc ctgacctttg ataaatctca 240
ttgcttgata ccaacctggg ctgttttaat tgcccaaacc aaaaggataa tttgctgagg 300
ttgtggagct tctcccctgc agagagtccc tgatctccca aaatttggtt gagatgtaag 360
gntgattttg ctgacaactc cttttctgaa gttttactca tttccaa 407

<210> 403
<211> 303
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(303)
<223> n = A,T,C or G

<400> 403
cagtatttat agccnaactg aaaagctagt agcaggcaag tctcaaatcc aggcaccaaa 60
tcctaagcaa gagccatggc atggtgaaaa tgcaaaagga gagtctggcc aatctacaaa 120
tagagaacaa gacctactca gtcatgaaca aaaaggcaga caccaacatg gatctcatgg 180
gggattggat attgtaatta tagagcagga agatgacagt gatcgtcatt tggcacaaca 240
tcttaacaac gaccgaaacc cattatttac ataaacctcc attcggtaac catgttgaaa 300
gga 303

<210> 404
<211> 225
<212> DNA
<213> Homo sapiens

<400> 404
aagtgtaact tttaaaaatt tagtggattt tgaaaattct tagaggaaag taaaggaaaa 60
attgttaatg cactcattta cctttacatg gtgaaagttc tctcttgatc ctacaaacag 120
acattttcca ctcgtgtttc catagttgtt aagtgtatca gatgtgttgg gcatgtgaat 180
ctccaagtgc ctgtgtaata aataaagtat ctttatttca ttcat 225

<210> 405
<211> 334
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(334)
<223> n = A,T,C or G

<400> 405
gagctgttat actgtgagtt ctactaggaa atcatcaaat ctgagggttg tctggaggac 60
ttcaatacac ctccccccat agtgaatcag cttccagggg gtccagtccc tctccttact 120

tcatccccat cccatgccaa aggaagaccc tccctccttg gctcacagcc ttctctaggc 180
ttcccagtgc ctccaggaca gagtgggtta tgttttcagc tccatccttg ctgtgagtgt 240
ctggtgcggt tgtgcctcca gcttctgctc agtgcttcat ggacagtgtc cagcccatgt 300
cactctccac tctctcanng tggatcccac ccct 334

<210> 406
<211> 216
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(216)
<223> n = A,T,C or G

<400> 406
tttcatacct aatgagggag ttganatnac atnnaaccag gaaatgcatg gatctcaang 60
gaaacaaaca cccaataaac tcggagtggc agactgacaa ctgtgagaca tgcacttgct 120
acnaaacaca aatttnatgt tgcacccttg tttctacacc tgtgggttat gacaaagaca 180
actgccaaag aatnttcaag aaggaggact gccant 216

<210> 407
<211> 413
<212> DNA
<213> Homo sapiens

<400> 407
gctgacttgc tagtatcatc tgcattcatt gaagcacaag aacttcatgc cttgactcat 60
gtaaatgcaa taggattaaa aaataaattt gatatcacat ggaaacagac aaaaaatatt 120
gtacaacatt gcacccagtg tcagattcta cacctggcca ctcaggaagc aagagttaat 180
cccagaggtc tatgtcctaa tgtgttatgg caaatggatg tcatgcacgt accttcattt 240
ggaaaattgt catttgtcca tgtgacagtt gatacttatt cacatttcat atgggcaacc 300
tgccagacag gagaaagtct tcccatgtta aaagacattt attatcttgt tttcctgtca 360
tgggagttcc agaaaaagtt aaaacagaca atgggccagg ttctgtagta aag 413

<210> 408
<211> 183
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(183)
<223> n = A,T,C or G

<400> 408
ggagctngcc ctcaattcct ccatntctat gttancatat ttaatgtctt ttgnnattaa 60
tncttaacta gttaatcctt aaagggctan ntaatcctta actagtccct ccattgtgag 120
cattatcctt ccagtattcn ccttctnttt tatttactcc ttcctggcta cccatgtact 180
ntt 183

<210> 409
<211> 250
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature

<222> (1)...(250)
<223> n = A,T,C or G

<400> 409
cccacgcatg ataagctctt tatttctgta agtcctgcta ggaaatcatc aaatctgacg 60
gtggtttggg ggacctgaac aaacctcctg taattaatca gctttcagtt tctcccccta 120
gtccctcctt caacaacata ggaggatcct cccccttcttt ctgctcacgg ccttatctag 180
gcttcccagt gcccccagga cagcgtgggc tatgtttaca gcgcntcctt gctgggggg 240
ggccntatgc 250

<210> 410
<211> 306
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(306)
<223> n = A,T,C or G

<400> 410
ggctggtttg caagaatgaa atgaatgatt ctacagctag gacttaacct tgaaatggaa 60
agtcttgcaa tcccatttgc aggatccgtc tgtgcacatg cctctgtaga gagcagcatt 120
cccagggacc ttggaaacag ttggcactgt aaggtgcttg ctccccaaga cacatcctaa 180
aaggtgttgt aatggtgaaa accgcttcct tctttattgc cccttcttat ttatgtgaac 240
nactggttgg cttttttgn atctttttta aactggaaag ttcaattgng aaaatgaata 300
tcntgc 306

<210> 411
<211> 261
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(261)
<223> n = A,T,C or G

<400> 411
agagatattn cttaggtnaa agttcataga gttcccatga actatatgac tggccacaca 60
ggatcttttg tatttaagga ttctgagatt ttgcttgagc aggattagat aaggctgttc 120
tttaaatgtc tgaaatggaa cagatttcaa aaaaaaaccc cacaatctag ggtgggaaca 180
aggaaggaaa gatgtgaata ggctgatggg caaaaaacca atttacccat cagttccagc 240
cttctctcaa ggngaggcaa a 261

<210> 412
<211> 241
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(241)
<223> n = A,T,C or G

<400> 412
gttcaatgtt acctgacatt tctacaacac cccactcacc gatgtattcg ttgcccagtg 60
ggaacatacc agcctgaatt tggaaaaaat aattgtgttt cttgcccagg aaatactacg 120

actgactttg atggctccac aaacataacc cagtgtaaaa acagaagatg tggaggggag 180
ctgggagatt tcactgggta cattgaattc ccaaactacc cangcaatta cccagccaac 240
a 241

<210> 413
<211> 231
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(231)
<223> n = A,T,C or G

<400> 413
aactcttaca atccaagtga ctcatctgtg tgcttgaatc ctttccactg tctcatctcc 60
ctcatccaag tttctagtac cttctctttg ttgtgaagga taatcaaact gaacaacaaa 120
aagtttactc tcctcatttg gaacctaaaa actctcttct tcctgggtct gagggctcca 180
agaatccttg aatcanttct cagatcattg gggacaccan atcaggaacc t 231

<210> 414
<211> 234
<212> DNA
<213> Homo sapiens

<400> 414
actgtccatg aagcactgag cagaagctgg aggcacaacg caccagacac tcacagcaag 60
gatggagctg aaaacataac ccactctgtc ctggaggcac tgggaagcct agagaaggct 120
gtgagccaag gagggagggt cttcctttgg catgggatgg ggatgaagta aggagaggga 180
ctggaccccc tggaagctga ttcactatgg ggggaggtgt attgaagtcc tcca 234

<210> 415
<211> 217
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(217)
<223> n = A,T,C or G

<400> 415
gcataggatt aagactgagt atcttttcta cattctttta actttctaag ggcacttct 60
caaaacacag accaggtagc aaatctccac tgctctaagg ntctcaccac cactttctca 120
cacctagcaa tagtagaatt cagtcctact tctgaggcca gaagaatggt tcagaaaaat 180
antggattat aaaaaataac aattaagaaa aataatc 217

<210> 416
<211> 213
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(213)
<223> n = A,T,C or G

<400> 416

atgcatatnt aaagganact gcctcgcttt tagaagacat ctggnctgct ctctgcatga 60
ggcacagcag taaagctctt tgattcccag aatcaagaac tctccccttc agactattac 120
cgaatgcaag gtggttaatt gaaggccact aattgatgct caaatagaag gatattgact 180
atattggaac agatggagtc tctactacaa aag 213

<210> 417
<211> 303
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(303)
<223> n = A,T,C or G

<400> 417
nagtcttcag gcccatcagg gaagttcaca ctggagagaa gtcatacata tgtactgtat 60
gtgggaaagg ctttactctg agttcaaatc ttcaagccca tcagagagtc cacactggag 120
agaagccata caaatgcaat gagtgtggga agagcttcag gagggattcc cattatcaag 180
ttcatctagt ggtccacaca ggagagaaac cctataaatg tgagatatgt gggaagggct 240
tcantcaaag ttcgtatctt caaatccatc ngaaggncca cagtatanan aaacctttta 300
agt 303

<210> 418
<211> 328
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(328)
<223> n = A,T,C or G

<400> 418
tttttggcgg tggtggggca gggacgggac angagtctca ctctgttgcc caggctggag 60
tgcacaggca tgatctcggc tcactacaac ccctgcctcc catgtccaag cgattcttgt 120
gcctcagcct tccctgtagc tagaattaca ggcacatgcc accacaccca gctagttttt 180
gtatttttag tagagacagg gtttcaccat gttggccagg ctggtctcaa actcctnacc 240
tcagnggtca ggctggtctc aaactcctga cctcaagtga tctgcccacc tcagcctccc 300
aaagtgctan gattacaggc cgtgagcc 328

<210> 419
<211> 389
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(389)
<223> n = A,T,C or G

<400> 419
cctcctcaag acggcctgtg gtccgcctcc cggcaaccaa gaagcctgca gtgccatatg 60
acccctgagc catggactgg agcctgaaag gcagcgtaca ccctgctcct gatcttgctg 120
cttgtttcct ctctgtggct ccattcatag cacagttgtt gcactgaggc ttgtgcaggc 180
cgagcaaggc caagctggct caaagagcaa ccagtcaact ctgccacggt gtgccaggca 240
ccggttctcc agccaccaac ctcactcgct cccgcaaatg gcacatcagt tcttctaccc 300
taaaggtagg accaaagggc atctgctttt ctgaagtcct ctgctctatc agccatcacg 360

tggcagccac tcnggctgtg tcgacgcgg 389

<210> 420
<211> 408
<212> DNA
<213> Homo sapiens

<400> 420
gttcctccta actcctgcca gaaacagctc tcctcaacat gagagctgca cccctcctcc 60
tggccagggc agcaagcctt agccttggct tcttgtttct gctttttttc tggctagacc 120
gaagtgtact agccaaggag ttgaagtttg tgactttggt gtttcggcat ggagaccgaa 180
gtcccattga cacctttccc actgacccca taaaggaatc ctcatggcca caaggatttg 240
gccaactcac ccagctgggc atggagcagc attatgaact tggagagtat ataagaaaga 300
gatatagaaa attcttgaat gagtcctata aacatgaaca ggtttatatt cgaagcacag 360
acgttgaccg gactttgatg aagtgctatg acaaacctgg caagcccg 408

<210> 421
<211> 352
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(352)
<223> n = A,T,C or G

<400> 421
gctcaaaaat ctttttactg atnggcatgg ctacacaatc attgactatt acggaggcca 60
gaggagaatg aggcctggcc tgggagccct gtgcctacta naagcacatt agattatcca 120
ttcactgaca gaacaggtct tttttgggtc cttcttctcc accacnatat acttgcagtc 180
ctccttcttg aagattcttt ggcagttgtc tttgtcataa cccacaggtg tagaaacaag 240
ggtgcaacat gaaatttctg tttcgtagca agtgcatgtc tcacaagttg gcangtctgc 300
cactccgagt ttattgggtg tttgtttcct ttgagatcca tgcatttcct gg 352

<210> 422
<211> 337
<212> DNA
<213> Homo sapiens

<400> 422
atgccaccat gctggcaatg cagcgggcgg tcgaaggcct gcatatccag cccaagctgg 60
cgatgatcga cggcaaccgt tgcccgaagt tgccgatgcc agccgaagcg gtggtcaagg 120
gcgatagcaa ggtgccggcg atcgcggcgg cgtcaatcct ggccaaggtc agccgtgatc 180
gtgaaatggc agctgtcgaa ttgatctacc cgggttatgg catcggcggg cataagggct 240
atccgacacc ggtgcacctg gaagccttgc agcggctggg gccgacgccg attcaccgac 300
gcttcttccg ccggtacggc tggcctatga aaattat 337

<210> 423
<211> 310
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(310)
<223> n = A,T,C or G

<400> 423

gctcaaaaat ctttttactg atatggcatg gctacacaat cattgactat tagaggccag 60
aggagaatga ggcctggcct gggagccctg tgcctactan aagcncatta gattatccat 120
tcactgacag aacaggtctt ttttgggtcc ttcttctcca ccacgatata cttgcagtcc 180
tccttcttga agattctttg gcagttgtct ttgtcataac ccacaggtgt anaaacaagg 240
gtgcaacatg aaatttctgt ttcgtagcaa gtgcatgtct cacagttgtc aagtctgccc 300
tccgagttta 310

<210> 424
<211> 370
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(370)
<223> n = A,T,C or G

<400> 424
gctcaaaaat ctttttactg ataggcatgg ctacacaatc attgactatt agaggccaga 60
ggagaatgag gcctggcctg ggagccctgt gcctactaga agcacattag attatccatt 120
cactgacaga acaggtcttt tttgggtcct tcttctccac cacgatatac ttgcagtcct 180
ccttcttgaa gattctttgg cagttgtctt tgtcataacc cacaggtgta gaaacatcct 240
ggttgaatct cctggaactc cctcattagg tatgaaatag catgatgcat tgcataaagt 300
cacgaaggtg gcaaagatca caacgctgcc cagganaaca ttcattgtga taagcaggac 360
tccgtcgacg 370

<210> 425
<211> 216
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(216)
<223> n = A,T,C or G

<400> 425
aattgctatn ntttattttg ccactcaaaa taattaccaa aaaaaaaaaa tnttaaatga 60
taacaacnca acatcaaggn aaananaaca ggaatggntg actntgcata aatnggccga 120
anattatcca ttatnttaag ggttgacttc aggntacagc acacagacaa acatgcccag 180
gaggntntca ggaccgctcg atgtnttntg aggagg 216

<210> 426
<211> 596
<212> DNA
<213> Homo sapiens

<400> 426
cttccagtga ggataaccct gttgccccgg gccgaggttc tccattaggc tctgattgat 60
tggcagtcag tgatggaagg gtgttctgat cattccgact gccccaaggg tcgctggcca 120
gctctctgtt ttgctgagtt ggcagtagga cctaatttgt taattaagag tagatggtga 180
gctgtccttg tattttgatt aacctaatgg ccttcccagc acgactcgga ttcagctgga 240
gacatcacgg caacttttaa tgaaatgatt tgaagggcca ttaagaggca cttcccgtta 300
ttaggcagtt catctgcact gataacttct tggcagctga gctggtcgga gctgtggccc 360
aaacgcacac ttggcttttg gttttgagat acaactctta atcttttagt catgcttgag 420
ggtggatggc cttttcagct ttaacccaat ttgcactgcc ttggaagtgt agccaggaga 480
atacactcat atactcgtgg gcttagaggc cacagcagat gtcattggtc tactgcctga 540
gtcccgctgg tcccatccca ggaccttcca tcggcgagta cctgggagcc cgtgct 596

<210> 427
<211> 107
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(107)
<223> n = A,T,C or G

<400> 427
gaagaattca agttaggttt attcaaaggg cttacngaga atcctanacc caggncccag 60
cccgggagca gccttanaga gctcctgttt gactgcccgg ctcagng 107

<210> 428
<211> 38
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(38)
<223> n = A,T,C or G

<400> 428
gaacttccna anaangactt tattcactat tttacatt 38

<210> 429
<211> 544
<212> DNA
<213> Homo sapiens

<400> 429
ctttgctgga cggaataaaa gtggacgcaa gcatgacctc ctgatgaggg cgctgcattt 60
attgaagagc ggctgcagcc ctgcggttca gattaaaatc cgagaattgt atagacgccg 120
atatccacga actcttgaag gactttctga tttatccaca atcaaatcat cggttttcag 180
tttggatggt ggctcatcac ctgtagaacc tgacttggcc gtggctggaa tccactcgtt 240
gccttccact tcagttacac ctcactcacc atcctctcct gttggttctg tgctgcttca 300
agatactaag cccacatttg agatgcagca gccatctccc ccaattcctc ctgtccatcc 360
tgatgtgcag ttaaaaaatc tgccctttta tgatgtcctt gatgttctca tcaagcccac 420
gagtttagtt caaagcagta ttcagcgatt tcaagagaag ttttttattt ttgctttgac 480
acctcaacaa gttagagaga tatgcatatc cagggatttt ttgccaggtg gtaggagaga 540
ttat 544

<210> 430
<211> 507
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(507)
<223> n = A,T,C or G

<400> 430
cttatcncaa tggggctccc aaacttggct gtgcagtgga aactccgggg gaattttgaa 60
gaacactgac acccatcttc caccccgaca ctctgattta attgggctgc agtgagaaca 120

gagcatcaat ttaaaaagct gcccagaatg ttntcctggg cagcgttgtg atctttgccn 180
ccttcgtgac tttatgcaat gcatcatgct atttcatacc taatgaggga gttccaggag 240
attcaaccag gatgtttcta cncctgtggg ttatgacaaa gacaactgcc aaagaatntt 300
caagaaggag gactgcaagt atatcgtggt ggagaagaag gacccaaaaa agacctgttc 360
tgtcagtgaa tggataatct aatgtgcttc tagtaggcac agggctccca ggccaggcct 420
cattctcctc tggcctctaa tagtcaatga ttgtgtagcc atgcctatca gtaaaaagat 480
ttttgagcaa aaaaaaaaaa aaaaaaa 507

<210> 431
<211> 392
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(392)
<223> n = A,T,C or G

<400> 431
gaaaattcag aatggataaa aacaaatgaa gtacaaaata tttcagattt acatagcgat 60
aaacaagaaa gcacttatca ggaggactta caaatggaag tacactctan aaccatcatc 120
tatcatggct aaatgtgaga ttagcacagc tgtattattt gtacattgca aacacctaga 180
aagagatggg aaacaaaatc ccaggagttt tgtgtgtgga gtcctgggtt ttccaacaga 240
catcattcca gcattctgag attagggnga ttggggatca ttctggagtt ggaatgttca 300
acaaaagtga tgttgttagg taaaatgtac aacttctgga tctatgcaga cattgaaggt 360
gcaatgagtc tggcttttac tctgctgttt ct 392

<210> 432
<211> 387
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(387)
<223> n = A,T,C or G

<400> 432
ggtatccnta cataatcaaa tatagctgta gtacatgttt tcattggngt agattaccac 60
aaatgcaagg caacatgtgt agatctcttg tcttattctt ttgtctataa tactgtattg 120
ngtagtccaa gctctcggna gtccagccac tgngaaacat gctcccttta gattaacctc 180
gtggacnctn ttgttgnatt gtctgaactg tagngccctg tattttgctt ctgtctgnga 240
attctgttgc ttctggggca tttccttgng atgcagagga ccaccacaca gatgacagca 300
atctgaattg ntccaatcac agctgcgatt aagacatact gaaatcgtac aggaccggga 360
acaacgtata gaacactgga gtccttt 387

<210> 433
<211> 281
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(281)
<223> n = A,T,C or G

<400> 433
ttcaactagc anagaanact gcttcagggn gtgtaaaatg aaaggcttcc acgcagttat 60

ctgattaaag aacactaaga gagggacaag gctagaagcc gcaggatgtc tacactatag 120
caggcnctat ttgggttggc tggaggagct gtggaaaaca tggagagatt ggcgctggag 180
atcgccgtgg ctattcctcn ttgntattac accagngagg ntctctgtnt gcccactggt 240
tnnaaaaccg ntatacaata atgatagaat aggacacaca t 281

<210> 434
<211> 484
<212> DNA
<213> Homo sapiens

<400> 434
ttttaaaata agcatttagt gctcagtccc tactgagtac tctttctctc ccctcctctg 60
aatttaattc tttcaacttg caatttgcaa ggattacaca tttcactgtg atgtatattg 120
tgttgcaaaa aaaaaaaagt gtctttgttt aaaattactt ggtttgtgaa tccatcttgc 180
tttttcccca ttggaactag tcattaaccc atctctgaac tggtagaaaa acatctgaag 240
agctagtcta tcagcatctg acaggtgaat tggatggttc tcagaaccat ttcacccaga 300
cagcctgttt ctatcctgtt taataaatta gtttgggttc tctacatgca taacaaaccc 360
tgctccaatc tgtcacataa aagtctgtga cttgaagttt agtcagcacc cccaccaaac 420
tttatttttc tatgtgtttt ttgcaacata tgagtgtttt gaaaataaag tacccatgtc 480
ttta 484

<210> 435
<211> 424
<212> DNA
<213> Homo sapiens

<400> 435
gcgccgctca gagcaggtca ctttctgcct tccacgtcct ccttcaagga agccccatgt 60
gggtagcttt caatatcgca ggttcttact cctctgcctc tataagctca aacccaccaa 120
cgatcgggca agtaaacccc ctccctcgcc gacttcggaa ctggcgagag ttcagcgcag 180
atgggcctgt ggggaggggg caagatagat gagggggagc ggcatggtgc ggggtgaccc 240
cttggagaga ggaaaaaggc cacaagaggg gctgccaccg ccactaacgg agatggccct 300
ggtagagacc tttgggggtc tggaacctct ggactcccca tgctctaact cccacactct 360
gctatcagaa acttaaactt gaggattttc tctgtttttc actcgcaata aattcagagc 420
aaac 424

<210> 436
<211> 667
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(667)
<223> n = A,T,C or G

<400> 436
accttgggaa nactctcaca atataaaggg tcgtagactt tactccaaat tccaaaaagg 60
tcctggccat gtaatcctga aagttttccc aaggtagcta taaaatcctt ataagggtgc 120
agcctcttct ggaattcctc tgatttcaaa gtctcactct caagttcttg aaaacgaggg 180
cagttcctga aaggcaggta tagcaactga tcttcagaaa gaggaactgt gtgcaccggg 240
atgggctgcc agagtaggat aggattccag atgctgacac cttctggggg aaacagggct 300
gccaggtttg tcatagcact catcaaagtc cggtcaacgt ctgtgcttcg aatataaacc 360
tgttcatgtt tataggactc attcaagaat tttctatatc tctttcttat atactctcca 420
agttcataat gctgctccat gcccagctgg gtgagttggc caaatccttg tggccatgag 480
gattccttta tggggtcagt gggaaaggtg tcaatgggac ttcggtctcc atgccgaaac 540
accaaagtca caaacttcaa ctccttggct agtacacttc ggtctagcca gaaaaaaagc 600
agaaacaaga agccaaggct aaggcttgct gccctgccag gaggaggggt gcagctctca 660

tgttgag 667

<210> 437
<211> 693
<212> DNA
<213> Homo sapiens

<400> 437
ctacgtctca accctcattt ttaggtaagg aatcttaagt ccaaagatat taagtgactc 60
acacagccag gtaaggaaag ctggattggc acactaggac tctaccatac cgggttttgt 120
taaagctcag gttaggaggc tgataagctt ggaaggaact tcagacagct ttttcagatc 180
ataaaagata attcttagcc catgttcttc tccagagcag acctgaaatg acagcacagc 240
aggtactcct ctattttcac ccctcttgct tctactctct ggcagtcaga cctgtgggag 300
gccatgggag aaagcagctc tctggatgtt tgtacagatc atggactatt ctctgtggac 360
catttctcca ggttacccta ggtgtcacta ttggggggac agccagcatc tttagctttc 420
atttgagttt ctgtctgtct tcagtagagg aaactttgc tcttcacact tcacatctga 480
acacctaact gctgttgctc ctgaggtggt gaaagacaga tatagagctt acagtattta 540
tcctatttct aggcactgag ggctgtgggg taccttgtgg tgccaaaaca gatcctgttt 600
taaggacatg ttgcttcaga gatgtctgta actatctggg ggctctgttg gctctttacc 660
ctgcatcatg tgctctcttg gctgaaaatg acc 693

<210> 438
<211> 360
<212> DNA
<213> Homo sapiens

<400> 438
ctgcttatca caatgaatgt tctcctgggc agcgttgtga tctttgccac cttcgtgact 60
ttatgcaatg catcatgcta tttcatacct aatgagggag ttccaggaga ttcaaccagg 120
atgtttctac acctgtgggt tatgacaaag acaactgcca aagaatcttc aagaaggagg 180
actgcaagta tatctggtgg agaagaagga cccaaaaaag acctgttctg tcagtgaatg 240
gataatctaa tgtgcttcta gtaggcacag ggctcccagg ccaggcctca ttctcctctg 300
gcctctaata gtcaataatt gtgtagccat gcctatcagt aaaaagattt ttgagcaaac 360

<210> 439
<211> 431
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(431)
<223> n = A,T,C or G

<400> 439
gttcctnnta actcctgcca gaaacagctc tcctcaacat gagagctgca cccctcctcc 60
tggccagggc agcaagcctt agccttggct tcttgtttct gctttttttc tggctagacc 120
gaagtgtact agccaaggag ttgaagtttg tgactttggt gtttcggcat ggagaccgaa 180
gtcccattga cacctttccc actgacccca taaaggaatc ctcatggcca caaggatttg 240
gccaactcac ccagctgggc atggagcagc attatgaact tggagagtat ataagaaaga 300
gatatagaaa attcttgaat gagtcctata aacatgaaca ggtttatatt cgaagcacag 360
acgttgaccg gactttgatg agtgctatga caaacctggc agcccgtcga cgcggccgcg 420
aatttagtag t 431

<210> 440
<211> 523
<212> DNA
<213> Homo sapiens

<400> 440
agagataaag cttaggtcaa agttcataga gttcccatga actatatgac tggccacaca 60
ggatcttttg tatttaagga ttctgagatt ttgcttgagc aggattagat aaggctgttc 120
tttaaatgtc tgaaatggaa cagatttcaa aaaaaaaccc cacaatctag ggtgggaaca 180
aggaaggaaa gatgtgaata ggctgatggg caaaaaacca atttacccat cagttccagc 240
cttctctcaa ggagaggcaa agaaaggaga tacagtggag acatctggaa agttttctcc 300
actggaaaac tgctactatc tgtttttata tttctgttaa aatatatgag gctacagaac 360
taaaaattaa aacctctttg tgtcccttgg tcctggaaca tttatgttcc ttttaaagaa 420
acaaaaatca aactttacag aaagatttga tgtatgtaat acatatagca gctcttgaag 480
tatatatatc atagcaaata agtcatctga tgagaacaag cta 523

<210> 441
<211> 430
<212> DNA
<213> Homo sapiens

<400> 441
gttcctccta actcctgcca gaaacagctc tcctcaacat gagagctgca cccctcctcc 60
tggccagggc agcaagcctt agccttggct tcttgtttct gctttttttc tggctagacc 120
gaagtgtact agccaaggag ttgaagtttg tgactttggt gtttcggcat ggagaccgaa 180
gtcccattga cacctttccc actgacccca taaaggaatc ctcatggcca caaggatttg 240
gccaactcac ccagctgggc atggagcagc attatgaact tggagagtat ataagaaaga 300
gatatagaaa attcttgaat gagtcctata aacatgaaca ggtttatatt cgaagcacag 360
acgttgaccg gactttgatg agtgctatga caaacctggc agcccgtcga cgcggccgcg 420
aatttagtag 430

<210> 442
<211> 362
<212> DNA
<213> Homo sapiens

<400> 442
ctaaggaatt agtagtgttc ccatcacttg tttggagtgt gctattctaa aagattttga 60
tttcctggaa tgacaattat attttaactt tggtgggggа aagagttata ggaccacagt 120
cttcacttct gatacttgta aattaatctt ttattgcact tgttttgacc attaagctat 180
atgtttagaa atggtcattt tacggaaaaa ttagaaaaat tctgataata gtgcagaata 240
aatgaattaa tgttttactt aatttatatt gaactgtcaa tgacaaataa aaattctttt 300
tgattatttt ttgttttcat ttaccagaat aaaaactaag aattaaaagt ttgattacag 360
tc 362

<210> 443
<211> 624
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(624)
<223> n = A,T,C or G

<400> 443
tttttttttt gcaacacaat atacatcaca gtgaaatgtg taatccttgc aaattgcaag 60
ttgaaagaat taaattcaga ggaggggaga gaaagagtac tcagtaggga ctgagcacta 120
aatgcttatt ttaaaagaaa tgtaaagagc agaaagcaat tcaggctacc ctgccttttg 180
tgctggctag tactccggtc ggtgtcagca gcacgtggca ttgaacattg caatgtggag 240
cccaaaccac agaaaatggg gtgaaattgg ccaactttct attaacttgg cttcctgttt 300
tataaaatat tgtgaataat atcacctact tcaaagggca gttatgaggc ttaaatgaac 360

taacgcctac aaaacactta aacatagata acataggtgc aagtactatg tatctggtac 420
atggtaaaca tccttattat taaagtcaac gctaaaatga atgtgtgtgc atatgctaat 480
agtacagaga gagggcactt aaaccaacta agggcctgga gggaaggttt cctggaaaga 540
ngatgcttgt gctgggtcca aatcttggtc tactatgacc ttggccaaat tatttaaact 600
ttgtccctat ctgctaaaca gatc 624

<210> 444
<211> 425
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(425)
<223> n = A,T,C or G

<400> 444
gcacatcatt nntcttgcat tctttgagaa taagaagatc agtaaatagt tcagaagtgg 60
gaagctttgt ccaggcctgt gtgtgaaccc aatgttttgc ttagaaatag aacaagtaag 120
ttcattgcta tagcataaca caaaatttgc ataagtggtg gtcagcaaat ccttgaatgc 180
tgcttaatgt gagaggttgg taaaatcctt tgtgcaacac tctaactccc tgaatgtttt 240
gctgtgctgg gacctgtgca tgccagacaa ggccaagctg gctgaaagag caaccagcca 300
cctctgcaat ctgccacctc ctgctggcag gatttgtttt tgcatcctgt gaagagccaa 360
ggaggcacca gggcataagt gagtagactt atggtcgacg cggccgcgaa tttagtagta 420
gtaga 425

<210> 445
<211> 414
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(414)
<223> n = A,T,C or G

<400> 445
catgtttatg nttttggatt actttgggca cctagtgttt ctaaatcgtc tatcattctt 60
ttctgttttt caaaagcaga gatggccaga gtctcaacaa actgtatctt caagtctttg 120
tgaaattctt tgcatgtggc agattattgg atgtagtttc ctttaactag catataaatc 180
tggtgtgttt cagataaatg aacagcaaaa tgtggtggaa ttaccatttg gaacattgtg 240
aatgaaaaat tgtgtctcta gattatgtaa caaataacta tttcctaacc attgatcttt 300
ggatttttat aatcctactc acaaatgact aggcttctcc tcttgtattt tgaagcagtg 360
tgggtgctgg attgataaaa aaaaaaaaag tcgacgcggc cgcgaattta gtag 414

<210> 446
<211> 631
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(631)
<223> n = A,T,C or G

<400> 446
acaaattaga anaaagtgcc agagaacacc acataccttg tccggaacat tacaatggct 60
tctgcatgca tgggaagtgt gagcattcta tcaatatgca ggagccatct tgcaggtgtg 120

atgctggtta tactggacaa cactgtgaaa aaaaggacta cagtgttcta tacgttgttc 180
ccggtcctgt acgatttcag tatgtcttaa tcgcagctgt gattggaaca attcagattg 240
ctgtcatctg tgtggtggtc ctctgcatca caagggccaa actttaggta atagcattgg 300
actgagattt gtaaactttc caaccttcca ggaaatgccc cagaagcaac agaattcaca 360
gacagaagca aaatacaggg cactacagtt cagacaatac aacaagagcg tccacgaggt 420
taatctaaag ggagcatgtt tcacagtggc tggactaccg agagcttgga ctacacaata 480
cagtattata gacaaaagaa taagacaaga gatctacaca tgttgccttg catttgtggt 540
aatctacacc aatgaaaaca tgtactacag ctatatttga ttatgtatgg atatatttga 600
aatagtatac attgtcttga tgttttttct g 631

<210> 447
<211> 585
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(585)
<223> n = A,T,C or G

<400> 447
ccttgggaaa antntcacaa tataaagggt cgtagacttt actccaaatt ccaaaaaggt 60
cctggccatg taatcctgaa agttttccca aggtagctat aaaatcctta taagggtgca 120
gcctcttctg gaattcctct gatttcaaag tctcactctc aagttcttga aaacgagggc 180
agttcctgaa aggcaggtat agcaactgat cttcagaaag aggaactgtg tgcaccggga 240
tgggctgcca gagtaggata ggattccaga tgctgacacc ttctgggggga aacagggctg 300
ccaggtttgt catagcactc atcaaagtcc ggtcaacgtc tgtgcttcga atataaacct 360
gttcatgttt ataggactca ttcaagaatt ttctatatct ctttcttata tactctccaa 420
gttcataatg ctgctccatg cccagctggg tgagttggcc aaatccttgt ggccatgagg 480
attcctttat ggggtcagtg ggaaaggtgt caatgggact tcggtctcca tgccgaaaca 540
ccaaagtcac aaacttcaac tccttggcta gtacacttcg gtcta 585

<210> 448
<211> 93
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(93)
<223> n = A,T,C or G

<400> 448
tgctcgtggg tcattctgan nnccgaactg accntgccag ccctgccgan gggccnccat 60
ggctccctag tgccctggag agganggggc tag 93

<210> 449
<211> 706
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(706)
<223> n = A,T,C or G

<400> 449
ccaagttcat gctntgtgct ggacgctgga cagggggcaa aagcnnttgc tcgtgggtca 60

ttctgancac cgaactgacc atgccagccc tgccgatggt cctccatggc tccctagtgc 120
cctggagagg aggtgtctag tcagagagta gtcctggaag gtggcctctg ngaggagcca 180
cggggacagc atcctgcaga tggtcgggcg cgtcccattc gccattcagg ctgcgcaact 240
gttgggaagg gcgatcggtg cgggcctctt cgctattacg ccagctggcg aaagggggat 300
gtgctgcaag gcgattaagt tgggtaacgc cagggttttc ccagtcncga cgttgtaaaa 360
cgacggccag tgaattgaat ttaggtgacn ctatagaaga gctatgacgt cgcatgcacg 420
cgtacgtaag cttggatcct ctagagcggc cgcctactac tactaaattc gcggccgcgt 480
cgacgtggga tccncactga gagagtggag agtgacatgt gctggacnct gtccatgaag 540
cactgagcag aagctggagg cacaacgcnc cagacactca cagctactca ggaggctgag 600
aacaggttga acctgggagg tggaggttgc aatgagctga gatcaggccn ctgcncccca 660
gcatggatga cagagtgaaa ctccatctta aaaaaaaaaa aaaaaa 706

<210> 450
<211> 493
<212> DNA
<213> Homo sapiens

<400> 450
gagacggagt gtcactctgt tgcccaggct ggagtgcagc aagacactgt ctaagaaaaa 60
acagttttaa aaggtaaaac aacataaaaa gaaatatcct atagtggaaa taagagagtc 120
aaatgaggct gagaacttta caaagggatc ttacagacat gtcgccaata tcactgcatg 180
agcctaagta taagaacaac ctttggggag aaaccatcat ttgacagtga ggtacaattc 240
caagtcaggt agtgaaatgg gtggaattaa actcaaatta atcctgccag ctgaaacgca 300
agagacactg tcagagagtt aaaaagtgag ttctatccat gaggtgattc cacagtcttc 360
tcaagtcaac acatctgtga actcacagac caagttctta aaccactgtt caaactctgc 420
tacacatcag aatcacctgg agagctttac aaactcccat tgccgagggt cgacgcggcc 480
gcgaatttag tag 493

<210> 451
<211> 501
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(501)
<223> n = A,T,C or G

<400> 451
gggcgcgtcc cattcgccat tcaggctgcg caactgttgg gaagggcgat cggtgcgggc 60
ctcttcgcta ttacgccagc tggcgaaagg gggatgtgct gcaaggcgat taagttgggt 120
aacgccaggg ttttcccagt cncgacgttg taaaacgacg gccagtgaat tgaatttagg 180
tgacnctata gaagagctat gacgtcgcat gcacgcgtac gtaagcttgg atcctctaga 240
gcggccgcct actactacta aattcgcggc cgcgtcgacg tgggatccnc actgagagag 300
tggagagtga catgtgctgg acnctgtcca tgaagcactg agcagaagct ggaggcacaa 360
cgcnccagac actcacagct actcaggagg ctgagaacag gttgaacctg ggaggtggag 420
gttgcaatga gctgagatca ggccnctgcn ccccagcatg gatgacagag tgaaactcca 480
tcttaaaaaa aaaaaaaaaa a 501

<210> 452
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(51)
<223> n = A,T,C or G

<400> 452
agacggtttc accnttacaa cnccttttag gatgggnntt ggggagcaag c 51

<210> 453
<211> 317
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(317)
<223> n = A,T,C or G

<400> 453
tacatcttgc tttttcccca ttggaactag tcattaaccc atctctgaac tggtagaaaa 60
acatctgaag agctagtcta tcagcatctg gcaagtgaat tggatggttc tcagaaccat 120
ttcacccana cagcctgttt ctatcctgtt taataaatta gtttgggttc tctacatgca 180
taacaaaccc tgctccaatc tgtcacataa aagtctgtga cttgaagttt antcagcacc 240
cccaccaaac tttatttttc tatgtgtttt ttgcaacata tgagtgtttt gaaaataagg 300
tacccatgtc tttatta 317

<210> 454
<211> 231
<212> DNA
<213> Homo sapiens

<400> 454
ttcgaggtac aatcaactct cagagtgtag tttccttcta tagatgagtc agcattaata 60
taagccacgc cacgctcttg aaggagtctt gaattctcct ctgctcactc agtagaacca 120
agaagaccaa attcttctgc atcccagctt gcaaacaaaa ttgttcttct aggtctccac 180
ccttcctttt tcagtgttcc aaagctcctc acaatttcat gaacaacagc t 231

<210> 455
<211> 231
<212> DNA
<213> Homo sapiens

<400> 455
taccaaagag ggcataataa tcagtctcac agtagggttc accatcctcc aagtgaaaaa 60
cattgttccg aatgggcttt ccacaggcta cacacacaaa acaggaaaca tgccaagttt 120
gtttcaacgc attgatgact tctccaagga tcttcctttg gcatcgacca cattcagggg 180
caaagaattt ctcatagcac agctcacaat acagggctcc tttctcctct a 231

<210> 456
<211> 231
<212> DNA
<213> Homo sapiens

<400> 456
ttggcaggta cccttacaaa gaagacacca taccttatgc gttattaggt ggaataatca 60
ttccattcag tattatcgtt attattcttg gagaaaccct gtctgtttac tgtaaccttt 120
tgcactcaaa ttcctttatc aggaataact acatagccac tatttacaaa gccattggaa 180
cctttttatt tggtgcagct gctagtcagt ccctgactga cattgccaag t 231

<210> 457
<211> 231
<212> DNA

<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(231)
<223> n = A,T,C or G

<400> 457
cgaggtaccc aggggtctga aaatctctnn tttantagtc gatagcaaaa ttgttcatca 60
gcattcctta atatgatctt gctataatta gatttttctc cattagagtt catacagttt 120
tatttgattt tattagcaat ctctttcaga agacccttga gatcattaag ctttgtatcc 180
agttgtctaa atcgatgcct catttcctct gaggtgtcgc tggcttttgt g 231

<210> 458
<211> 231
<212> DNA
<213> Homo sapiens

<400> 458
aggtctggtt ccccccactt ccactcccct ctactctctc taggactggg ctgggccaag 60
agaagagggg tggttaggga agccgttgag acctgaagcc ccaccctcta ccttccttca 120
acaccctaac cttgggtaac agcatttgga attatcattt gggatgagta gaatttccaa 180
ggtcctgggt taggcatttt ggggggccag accccaggag aagaagattc t 231

<210> 459
<211> 231
<212> DNA
<213> Homo sapiens

<400> 459
ggtaccgagg ctcgctgaca cagagaaacc ccaacgcgag gaaaggaatg gccagccaca 60
ccttcgcgaa acctgtggtg gcccaccagt cctaacggga caggacagag agacagagca 120
gccctgcact gttttccctc caccacagcc atcctgtccc tcattggctc tgtgctttcc 180
actatacaca gtcaccgtcc caatgagaaa caagaaggag caccctccac a 231

<210> 460
<211> 231
<212> DNA
<213> Homo sapiens

<400> 460
gcaggtataa catgctgcaa caacagatgt gactaggaac ggccggtgac atggggaggg 60
cctatcaccc tattcttggg ggctgcttct tcacagtgat catgaagcct agcagcaaat 120
cccacctccc cacacgcaca cggccagcct ggagcccaca gaagggtcct cctgcagcca 180
gtggagcttg gtccagcctc cagtccaccc ctaccaggct taaggataga a 231

<210> 461
<211> 231
<212> DNA
<213> Homo sapiens

<400> 461
cgaggtttga gaagctctaa tgtgcagggg agccgagaag caggcggcct agggagggtc 60
gcgtgtgctc cagaagagtg tgtgcatgcc agaggggaaa caggcgcctg tgtgtcctgg 120
gtggggttca gtgaggagtg ggaaattggt tcagcagaac caagccgttg ggtgaataag 180
agggggattc catggcactg atagagccct atagtttcag agctgggaat t 231

<210> 462

<211> 231
<212> DNA
<213> Homo sapiens

<400> 462
aggtaccctc attgtagcca tgggaaaatt gatgttcagt ggggatcagt gaattaaatg 60
gggtcatgca agtataaaaa ttaaaaaaaa aagacttcat gcccaatctc atatgatgtg 120
gaagaactgt tagagagacc aacagggtag tgggttagag atttccagag tcttacattt 180
tctagaggag gtatttaatt tcttctcact catccagtgt tgtatttagg a 231

<210> 463
<211> 231
<212> DNA
<213> Homo sapiens

<400> 463
tactccagcc tggtgacaga gcgagaccct atcaccgccc cccaccccac caaaaaaaaa 60
actgagtaga caggtgtcct cttggcatgg taagtcttaa gtcccctccc agatctgtga 120
catttgacag gtgtcttttc ctctggacct cggtgtcccc atctgagtga gaaaaggcag 180
tggggaggtg gatcttccag tcgaagcggt atagaagccc gtgtgaaaag c 231

<210> 464
<211> 231
<212> DNA
<213> Homo sapiens

<400> 464
gtactctaag atttatctta agttgccttt tctgggtggg aaagtttaac cttagtgact 60
aaggacatca catatgaaga atgtttaagt tggaggtggc aacgtgaatt gcaaacaggg 120
cctgcttcag tgactgtgtg cctgtagtcc cagctactcg ggagtctgtg tgaggccagg 180
ggtgccagcg caccagctag atgctctgta acttctaggc cccattttcc c 231

<210> 465
<211> 231
<212> DNA
<213> Homo sapiens

<400> 465
catgttgttg tagctgtggt aatgctggct gcatctcaga cagggttaac ttcagctcct 60
gtggcaaatt agcaacaaat tctgacatca tatttatggt ttctgtatct ttgttgatga 120
aggatggcac aatttttgct tgtgttcata atatactcag attagttcag ctccatcaga 180
taaactggag acatgcagga cattagggta gtgttgtagc tctggtaatg a 231

<210> 466
<211> 231
<212> DNA
<213> Homo sapiens

<400> 466
caggtacctc tttccattgg atactgtgct agcaagcatg ctctccgggg tttttttaat 60
ggccttcgaa cagaacttgc cacataccca ggtataatag tttctaacat ttgcccagga 120
cctgtgcaat caaatattgt ggagaattcc ctagctggag aagtcacaaa gactataggc 180
aataatggag accagtccca caagatgaca accagtcgtt gtgtgcggct g 231

<210> 467
<211> 311
<212> DNA
<213> Homo sapiens

<400> 467
gtacaccctg gcacagtcca atctgaactg gttcggcact catctttcat gagatggatg 60
tggtggcttt tctccttttt catcaagact cctcagcagg gagcccagac cagcctgcac 120
tgtgccttaa cagaaggtct tgagattcta agtgggaatc atttcagtga ctgtcatgtg 180
gcatgggtct ctgcccaagc tcgtaatgag actatagcaa ggcggctgtg ggacgtcagt 240
tgtgacctgc tgggcctccc aatagactaa caggcagtgc cagttggacc caagagaaga 300
ctgcagcaga c 311

<210> 468
<211> 3112
<212> DNA
<213> Homo sapiens

<400> 468
cattgtgttg ggagaaaaac agaggggaga tttgtgtggc tgcagccgag ggagaccagg 60
aagatctgca tggtgggaag gacctgatga tacagagttt gataggagac aattaaaggc 120
tggaaggcac tggatgcctg atgatgaagt ggactttcaa actggggcac tactgaaacg 180
atgggatggc cagagacaca ggagatgagt tggagcaagc tcaataacaa agtggttcaa 240
cgaggacttg gaattgcatg gagctggagc tgaagtttag cccaattgtt tactagttga 300
gtgaatgtgg atgattggat gatcatttct catctctgag cctcaggttc cccatccata 360
aaatgggata cacagtatga tctataaagt gggatatagt atgatctact tcactgggtt 420
atttgaagga tgaattgaga taatttattt caggtgccta gaacaatgcc cagattagta 480
catttggtgg aactgagaaa tggcataaca ccaaatttaa tatatgtcag atgttactat 540
gattatcatt caatctcata gttttgtcat ggcccaattt atcctcactt gtgcctcaac 600
aaattgaact gttaacaaag gaatctctgg tcctgggtaa tggctgagca ccactgagca 660
tttccattcc agttggcttc ttgggtttgc tagctgcatc actagtcatc ttaaataaat 720
gaagttttaa catttctcca gtgatttttt tatctcacct ttgaagatac tatgttatgt 780
gattaaataa agaacttgag aagaacaggt ttcattaaac ataaaatcaa tgtagacgca 840
aattttctgg atgggcaata cttatgttca caggaaatgc tttaaaatat gcagaagata 900
attaaatggc aatggacaaa gtgaaaaact tagacttttt tttttttttt ggaagtatct 960
ggatgttcct tagtcactta aaggagaact gaaaaatagc agtgagttcc acataatcca 1020
acctgtgaga ttaaggctct ttgtggggaa ggacaaagat ctgtaaattt acagtttcct 1080
tccaaagcca acgtcgaatt ttgaaacata tcaaagctct tcttcaagac aaataatcta 1140
tagtacatct ttcttatggg atgcacttat gaaaaatggt ggctgtcaac atctagtcac 1200
tttagctctc aaaatggttc atttaagagg aaagttttag aatctcatat ttattcctgt 1260
ggaaggacag cattgtggct tggactttat aaggtcttta ttcaactaaa taggtgagaa 1320
ataagaaagg ctgctgactt taccatctga ggccacacat ctgctgaaat ggagataatt 1380
aacatcacta gaaacagcaa gatgacaata taatgtctaa gtagtgacat gtttttgcac 1440
atttccagcc cctttaaata tccacacaca caggaagcac aaaaggaagc acagagatcc 1500
ctgggagaaa tgcccggccg ccatcttggg tcatcgatga gcctcgccct gtgcctggtc 1560
ccgcttgtga gggaaggaca ttagaaaatg aattgatgtg ttccttaaag gatgggcagg 1620
aaaacagatc ctgttgtgga tatttatttg aacgggatta cagatttgaa atgaagtcac 1680
aaagtgagca ttaccaatga gaggaaaaca gacgagaaaa tcttgatggc ttcacaagac 1740
atgcaacaaa caaaatggaa tactgtgatg acatgaggca gccaagctgg ggaggagata 1800
accacggggc agagggtcag gattctggcc ctgctgccta aactgtgcgt tcataaccaa 1860
atcatttcat atttctaacc ctcaaaacaa agctgttgta atatctgatc tctacggttc 1920
cttctgggcc caacattctc catatatcca gccacactca tttttaatat ttagttccca 1980
gatctgtact gtgacctttc tacactgtag aataacatta ctcattttgt tcaaagaccc 2040
ttcgtgttgc tgcctaatat gtagctgact gtttttccta aggagtgttc tggcccaggg 2100
gatctgtgaa caggctggga agcatctcaa gatctttcca gggttatact tactagcaca 2160
cagcatgatc attacggagt gaattatcta atcaacatca tcctcagtgt ctttgcccat 2220
actgaaattc atttcccact tttgtgccca ttctcaagac ctcaaaatgt cattccatta 2280
atatcacagg attaactttt ttttttaacc tggaagaatt caatgttaca tgcagctatg 2340
ggaatttaat tacatatttt gttttccagt gcaaagatga ctaagtcctt tatccctccc 2400
ctttgtttga ttttttttcc agtataaagt taaaatgctt agccttgtac tgaggctgta 2460
tacagccaca gcctctcccc atccctccag ccttatctgt catcaccatc aacccctccc 2520
atgcacctaa acaaaatcta acttgtaatt ccttgaacat gtcaggcata cattattcct 2580

tctgcctgag aagctcttcc ttgtctctta aatctagaat gatgtaaagt tttgaataag 2640
ttgactatct tacttcatgc aaagaaggga cacatatgag attcatcatc acatgagaca 2700
gcaaatacta aaagtgtaat ttgattataa gagtttagat aaatatatga aatgcaagag 2760
ccacagaggg aatgtttatg ggcacgtttt gtaagcctgg gatgtgaagc aaaggcaggg 2820
aacctcatag tatcttatat aatatacttc atttctctat ctctatcaca atatccaaca 2880
agcttttcac agaattcatg cagtgcaaat ccccaaaggt aacctttatc catttcatgg 2940
tgagtgcgct ttagaatttt ggcaaatcat actggtcact tatctcaact ttgagatgtg 3000
tttgtccttg tagttaattg aaagaaatag ggcactcttg tgagccactt tagggttcac 3060
tcctggcaat aaagaattta caaagagcaa aaaaaaaaaa aaaaaaaaaa aa 3112

<210> 469
<211> 2229
<212> DNA
<213> Homo sapiens

<400> 469
agctctttgt aaattcttta ttgccaggag tgaaccctaa agtggctcac aagagtgccc 60
tatttctttc aattaactac aaggacaaac acatctcaaa gttgagataa gtgaccagta 120
tgatttgcca aaattctaaa gcgcactcac catgaaatgg ataaaggtta cctttgggga 180
tttgcactgc atgaattctg tgaaaagctt gttggatatt gtgatagaga tagagaaatg 240
aagtatatta tataagatac tatgaggttc cctgcctttg cttcacatcc caggcttaca 300
aacgtgcccc ataaacattc cctctgtggc tcttgcattt catatattta tctaaactct 360
tataatcaaa tacactttta gtatttgctg tctcatgtga tgatgaatct catatgtgtc 420
ccttctttgc atgaagtaag atagtcaact tattcaaaac tttacatcat tctagattta 480
agagacaagg aagagcttct caggcagaag gaataatgta tgcctgacat gttcaaggaa 540
ttacaagtta gattttgttt aggtgcatgg gaggggttga tggtgatgac agataaggct 600
ggagggatgg ggagaggctg tggctgtata cagcctcagt acaaggctaa gcattttaac 660
tttatactgg aaaaaaaatc aaacaaaggg gagggataaa ggacttagtc atctttgcac 720
tggaaaacaa aatatgtaat taaattccca tagctgcatg taacattgaa ttcttccagg 780
ttaaaaaaaa agttaatcct gtgatattaa tggaatgaca ttttgaggtc ttgagaatgg 840
gcacaaaagt gggaaatgaa tttcagtatg ggcaaagaca ctgaggatga tgttgattag 900
ataattcact ccgtaatgat catgctgtgt gctagtaagt ataaccctgg aaagatcttg 960
agatgcttcc cagcctgttc acagatcccc tgggccagaa cactccttag gaaaaacagt 1020
cagctacata ttaggcagca acacgaaggg tctttgaaca aaatgagtaa tgttattcta 1080
cagtgtagaa aggtcacagt acagatctgg gaactaaata ttaaaaatga gtgtggctgg 1140
atatatggag aatgttgggc ccagaaggaa ccgtagagat cagatattac aacagctttg 1200
ttttgagggt tagaaatatg aaatgatttg gttatgaacg cacagtttag gcagcagggc 1260
cagaatcctg accctctgcc ccgtggttat ctcctcccca gcttggctgc ctcatgtcat 1320
cacagtattc cattttgttt gttgcatgtc ttgtgaagcc atcaagattt tctcgtctgt 1380
tttcctctca ttggtaatgc tcactttgtg acttcatttc aaatctgtaa tcccgttcaa 1440
ataaatatcc acaacaggat ctgttttcct gcccatcctt taaggaacac atcaattcat 1500
tttctaatgt ccttccctca caagcgggac caggcacagg gcgaggctca tcgatgaccc 1560
aagatggcgg ccgggcattt ctcccaggga tctctgtgct tccttttgtg cttcctgtgt 1620
gtgtggatat ttaaaggggc tggaaatgtg caaaaacatg tcactactta gacattatat 1680
tgtcatcttg ctgtttctag tgatgttaat tatctccatt tcagcagatg tgtggcctca 1740
gatggtaaag tcagcagcct ttcttatttc tcacctggaa atacatacga ccatttgagg 1800
agacaaatgg caaggtgtca gcataccctg aacttgagtt gagagctaca cacaatatta 1860
ttggtttccg agcatcacaa acaccctctc tgtttcttca ctgggcacag aattttaata 1920
cttatttcag tgggctgttg gcaggaacaa atgaagcaat ctacataaag tcactagtgc 1980
agtgcctgac acacaccatt ctcttgaggt cccctctaga gatcccacag gtcatatgac 2040
ttcttgggga gcagtggctc acacctgtaa tcccagcact ttgggaggct gaggcaggtg 2100
ggtcacctga ggtcaggagt tcaagaccag cctggccaat atggtgaaac cccatctcta 2160
ctaaaaatac aaaaattagc tgggcgtgct ggtgcatgcc tgtaatccca gccccaacac 2220
aatggaatt 2229

<210> 470
<211> 2426
<212> DNA

<213> Homo sapiens

<400> 470
gtaaattctt tattgccagg agtgaaccct aaagtggctc acaagagtgc cctatttctt 60
tcaattaact acaaggacaa acacatctca aagttgagat aagtgaccag tatgatttgc 120
caaaattcta aagcgcactc accatgaaat ggataaaggt tacctttggg gatttgcact 180
gcatgaattc tgtgaaaagc ttgttggata ttgtgataga gatagagaaa tgaagtatat 240
tatataagat actatgaggt tccctgcctt tgcttcacat cccaggctta caaacgtgcc 300
ccataaacat tccctctgtg gctcttgcat ttcatatatt tatctaaact cttataatca 360
aattacactt ttagtatttg ctgtctcatg tgatgatgaa tctcatatgt gtcccttctt 420
tgcatgaagt aagatagtca acttattcaa aactttacat cattctagat ttaagagaca 480
aggaagagct tctcaggcag aaggaataat gtatgcctga catgttcaag gaattacaag 540
ttagattttg tttaggtgca tgggaggggt tgatggtgat gacagataag gctggaggga 600
tggggagagg ctgtggctgt atacagcctc agtacaaggc taagcatttt aactttatac 660
tggaaaaaaa atcaaacaaa ggggagggat aaaggactta gtcatctttg cactggaaaa 720
caaaatatgt aattaaattc ccatagctgc atgtaacatt gaattcttcc aggttaaaaa 780
aaaaagttaa tcctgtgata ttaatggaat gacattttga ggtcttgaga atgggcacaa 840
aagtgggaaa tgaatttcag tatgggcaaa gacactgagg atgatgttga ttagataatt 900
cactccgtaa tgatcatgct gtgtgctagt aagtataacc ctggaaagat cttgagatgc 960
ttcccagcct gttcacagat cccctgggcc agaacactcc ttaggaaaaa cagtcagcta 1020
catattaggc agcaacacga agggtctttg aacaaaatga gtaatgttat tctacagtgt 1080
agaaaggtca cagtacagat ctgggaacta aatattaaaa atgagtgtgg ctggatatat 1140
ggagaatgtt gggcccagaa ggaaccgtag agatcagata ttacaacagc tttgttttga 1200
gggttagaaa tatgaaatga tttggttatg aacgcacagt ttaggcagca gggccagaat 1260
cctgaccctc tgccccgtgg ttatctcctc cccagcttgg ctgcctcatg tcatcacagt 1320
attccatttt gtttgttgca tgtcttgtga agccatcaag attttctcgt ctgttttcct 1380
ctcattggta atgctcactt tgtgacttca tttcaaatct gtaatcccgt tcaaataaat 1440
atccacaaca ggatctgttt tcctgcccat cctttaagga acacatcaat tcatttcta 1500
atgtccttcc ctcacaagcg ggaccaggca cagggcgagg ctcatcgatg acccaagatg 1560
gcggccgggc atttctccca gggatctctg tgcttccttt tgtgcttcct gtgtgtgtgg 1620
atatttaaag gggctggaaa tgtgcaaaaa catgtcacta cttagacatt atattgtcat 1680
cttgctgttt ctagtgatgt taattatctc catttcagca gatgtgtggc ctcagatggt 1740
aaagtcagca gcctttctta tttctcacct ggaaatacat acgaccattt gaggagacaa 1800
atggcaaggt gtcagcatac cctgaacttg agttgagagc tacacacaat attattggtt 1860
tccgagcatc acaaacaccc tctctgtttc ttcactgggc acagaatttt aatacttatt 1920
tcagtgggct gttggcagga acaaatgaag caatctacat aaagtcacta gtgcagtgcc 1980
tgacacacac cattctcttg aggtcccctc tagagatccc acaggtcata tgacttcttg 2040
gggagcagtg gctcacacct gtaatcccag cactttggga ggctgaggca ggtgggtcac 2100
ctgaggtcag gagttcaaga ccagcctggc caatatggtg aaacccccatc tctactaaaa 2160
atacaaaaat tagctgggcg tgctggtgca tgcctgtaat cccagctact tgggaggctg 2220
aggcaggaga attgctggaa catgggaggc ggaggttgca gtgagctgta attgtgccat 2280
tgcactcgaa cctgggcgac agagtggaac tctgtttcca aaaaacaaac aaacaaaaaa 2340
ggcatagtca gatacaacgt gggtgggatg tgtaaataga agcaggatat aaagggcatg 2400
gggtgacggt tttgcccaac acaatg 2426

<210> 471
<211> 812
<212> DNA
<213> Homo sapiens

<400> 471
gaacaaaatg agtaatgtta ttctacagtg tagaaaggtc acagtacaga tctgggaact 60
aaatattaaa aatgagtgtg gctggatata tggagaatgt tgggcccaga aggaaccgta 120
gagatcagat attacaacag ctttgttttg agggttagaa atatgaaatg atttggttat 180
gaacgcacag tttaggcagc agggccagaa tcctgaccct ctgccccgtg gttatctcct 240
ccccagcttg gctgcctcat gtcatcacag tattccattt tgtttgttgc atgtcttgtg 300
aagccatcaa gatttctcg tctgttttcc tctcattggt aatgctcact ttgtgacttc 360
atttcaaatc tgtaatcccg ttcaaataaa tatccacaac aggatctgtt ttcctgccca 420

tcctttaagg aacacatcaa ttcattttct aatgtccttc cctcacaagc gggaccaggc 480
acagggcgag gctcatcgat gacccaagat ggcggccggg catttctccc agggatctct 540
gtgcttcctt ttgtgcttcc tgtgtgtgtg gatatttaaa ggggctggaa atgtgcaaaa 600
acatgtcact acttagacat tatattgtca tcttgctgtt tctagtgatg ttaattatct 660
ccatttcagc agatgtgtgg cctcagatgg taaagtcagc agcctttctt atttctcacc 720
tctgtatcat caggtccttc ccaccatgca gatcttcctg gtctccctcg gctgcagcca 780
cacaaatctc ccctctgttt ttctgatgcc ag 812

<210> 472
<211> 515
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(515)
<223> n = A,T,C or G

<400> 472
acggagactt attttctgat attgtctgca tatgtatgtt tttaagagtc tggaaatagt 60
cttatgactt tcctatcatg cttattaata aataatacag cccagagaag atgaaaatgg 120
gttccagaat tattggtcct tgcagcccgg tgaatctcag caagaggaac caccaactga 180
caatcaggat attgaacctg gacaagagag agaaggaaca cctccgatcg aagaacgtaa 240
agtagaaggt gattgccagg aaatggatct ggaaaagact cggagtgagc gtggagatgg 300
ctctgatgta aaagagaaga ctccacctaa tcctaagcat gctaagacta aagaagcagg 360
agatgggcag ccataagtta aaaagaagac aagctgaagc tacacacatg gctgatgtca 420
cattgaaaat gtgactgaaa atttgaaaat tctctcaata aagtttgagt tttctctgaa 480
gaaaaaaaaa naaaaaaaaa aaanaaaaan aaaaa 515

<210> 473
<211> 5829
<212> DNA
<213> Homo sapiens

<400> 473
cgcatgccgg ggaagcccaa gctggctcga agagccacca gccacctgtg caagggtggg 60
cctggaccag ttggaccagc caccaagctc acctactcaa ggaagcaggg atggccaggt 120
tgcaacagcc tgagtggctg ccacctgata gctgatggag cagaggcctg aggaaaatca 180
gatggcacat ttagctcttt aatggatctt aagttaattt ttctataaag cacatggcac 240
cagtccatgc ctcagagctc gtatggcact gcggaccaca gcaggccgag ttcccaggat 300
tgccatccag gggggccttc tgtagccctg gccagacctt gcagaggtgg ctgggtgctc 360
tttgagcgag ctcggcctcc ctggcatgca caggccccag gtactgacac gctgctctga 420
gtgagcttgt cctgccttgg ctgccaccta actgctgatg gagcagcggc cttaggaaaa 480
gcaaatggcg ctgtagccca actttagggt agaagaagat gtaccatgtc cggccgctag 540
ttggtgactg gtgcacctgc tcctggcgta cccttgcaga ggtgggtggt tgctctttgg 600
ccagcttggc cttgcctggc atgcacaagc ctcagtgcaa caactgtcct acaaatggag 660
acacagagag gaaacaagca gcgggctcag gagcagggtg tgtgctgcct ttggggctcc 720
agtccatgcc tcgggtcgta tggtactgca ggcttcttgg ttgccaagag gcggaccaca 780
ggccttcttg aggaggactt tacgttcaag tgcagaaagc agccaaaatt accatccatg 840
agactaagcc ttctgtggcc ctggcgagac ttaaaatttg tgccaaggca ggacaagctc 900
actcggagca gcgtgtcagt agctggggcc tatgcatgcc gggcagggcc gggctggctg 960
aaggagcaac cagccacctc tgcaagggtg cgcctagtgc aggcggagca tccaccacct 1020
cacccgctcg aggaagtggg gatggccagg ttcccacagc ctgagtgtct gccaccttat 1080
tgctgatgga gcagaggcct taagaaaagc agatggcact gtggccctac ctttagggtg 1140
gaagaagtga tgtacatgtc cggacgctaa ttggtgactg gtacaccggc tcctgctaca 1200
cctttgcaga ggtggctggt tgctctttga gccagcttgt ccttgcccgg catgcacaag 1260
tttcagtgca acaactttgc cacaaatgga gccatataga ggaaacaaga agcaggttca 1320
ggagaagggt gtaccctgcc tttggggctc cagtccatgc ctcaggtgtc acatggcact 1380

gcgggcttct tggttgccag gaggcggacc acaggccatc ttggggagga ctttgtgttc 1440
aagtgcagaa agcagccagg attgccatcc agggggacct tctatagccc tggccaaacc 1500
ttgcaggggt gtctggttgc tctttgagcc ggcttggcct ccctggcatg cacgggcccc 1560
aggtgctggc acgctgctcc gagtgtgctt gtcctgcctt ggctgccacc tctgcggggg 1620
tgcgtctgga gggggtggac cggccaccaa ccttacccag tcaaggaagt ggatggccat 1680
gttcccacag cctgagtggc tgccacctga tggctgatgg agcaaaggcc ttaggaaaag 1740
cagatggccc ttggccctac ctttttgtta gaagaactga tgttccatgt cctgcagcga 1800
gtgaggttgg tggctgtgcc cccagctcct ggcgcgccct cgcagaggtg actggttgct 1860
ctttgggccc tcttggcctt gcccagcatg cacaagcctc agtgctacta ctgtgctaca 1920
aatggagcca tatagggggaa acgagcagcc atctcaggag caaggtgtat gctgcctttg 1980
ggggctccag tccttgcctc aagggtctta tgtcactgtg ggcttcttgg ttgtcaagag 2040
gcagaccata ggccgtcttg agagggactt tatgttcaag tgcagaaagc agccaggatt 2100
gccaccctcg ggactctgcc ttctgtggcc ctggccaaac ttagaatttg gccgtagaca 2160
ggacaggctc acttggagta gcgtgtccgt agctggggtc tgtgcatgcc gggcaaggcc 2220
gggctggctc ggggagcaac cagccacctc tgcgggggtg cgcctggagc aggtggagca 2280
gccaccagct cacccactcc aggaagccgg ggtagccagg ttcccaaggc ctgagtgggt 2340
gccacctaat ggctgaagaa acagaggcct tgggaaaacc agatggcact gtggccctac 2400
ctttatggta gaagagctga tttagcctga ctggcagcgt gtggggttgg tggctggtct 2460
gcctgctgct ggcgcatccg tgcaaggatg gctggttgcc ctttgagcca gcttgcccctt 2520
gcccggcatg cgcaagcctc agtgcaacaa ctgtgctgca aatggggcca tatagaggaa 2580
aggagcagct ggctctggag catggtgtgc actccctttg ggccttcagt ccatgtctca 2640
tgggtcgtat gacactgcgg gcttgttggt tgccaagagg cagaccacag gtcatcttga 2700
ggaggacttt atgttccagt ccagaaagca gccagtggta ccacccaggg gacttgtgct 2760
tctgtgccca ggccagacgt agaatttgac aaagtcagga cggtctcagt cagagcggcg 2820
tgtcggtccc cggggcctgt gcatgccggg cagggccggg ctggcttggg gagcaagcag 2880
ccacctctgt taagggtgtg cctggagcag gtggagcagc caccaacctc acgcactgaa 2940
agaagcaggg atggccaggt tccaacatcc tgagtggctg ccacctgatg gctgatggag 3000
cagaggcctg aggaaaagca gatggcactg ctttgtagtg ctgttctttg tctctcttga 3060
tctttttcag ttaatgtctg ttttatcaga gactaggatt gcaaaccctg ctcttttttg 3120
ctttccattt gcttggtaaa tattcctcca tccctttatt ttaagcctat gtgtgtcttt 3180
gcacatgaga tgggtctcct gaatacagga caacaatggg tctttactct ttatccaact 3240
tgccagtctg tgtcttttaa ctggggcatt tagcccattt acatttaagt ttagtattgt 3300
tacatgtgaa atttatcctg tcatgatgtt gctagctttt tatttttccc attagtttgc 3360
agtttcttta tagtgtcaat ggtctttaca attcgatatg tttttgtagt ggctggtact 3420
ggtttttcct ttctacgttt agtgtctcct tcaggagctc ttgtaacaca agaatgtgga 3480
tttatttctt gtaaggtaaa tatgtggatt tatttcttgg gactgtattc tatggccttt 3540
accccaagaa tcattacttt ttaaaatgca attcaaatta gcataaaaca tttacagcct 3600
atggaaaggc ttgtggcatt agaatcctta tttataggat tattttgtgt ttttttgaga 3660
tatggtcttt gtcatcgagg cagaagtgcc gtggtttgat cataattcac cacagccctg 3720
aactcttgag tccaagccat ccttttgcct taatctccca accagttgga tctgcaggca 3780
taaggcatca tgcgtggcta atttttttcac gttttttttt ttttttgtc gagattatgg 3840
tgtcactgtg ttgctctggc tgatctcaaa tgtttgacct caagggatct ttctgccacg 3900
gcctcctaaa gtgctaggat tatatgcatg atacaccatg cctattgtag agtattacat 3960
tattttcaaa gtcttattgt aagagccatt tattgccttt ggcctaaata actcaatata 4020
atatctctga aactttttttt tgacaaattt tggggcgtga tgatgagaga agggggtttg 4080
aaactttcta ataagagtta acttagagcc atttaagaaa ggaaaaaaca caaattatca 4140
gaaaaacaac agtaagatca agtgcaaaag ttctgtggca aagatgatga gagtaaagaa 4200
tatatgtttg tgactcatgg tggcttttac tttgttcttg aatttctgag tacgggttaa 4260
catttaaaga atctacatta tagataacat tttattgcaa gtaaatgtat ttcaaaattt 4320
gttattggtt ttgtatgaga ttattctcag cctacttcat tatcaagcta tattatttta 4380
ttaatgtagt tcgatgatct tacagcaaag ctgaaagctg tatcttcaaa atatgtctat 4440
ttgactaaaa agttattcaa caggagttat tatctataaa aaaaatacaa caggaatata 4500
aaaaacttga ggataaaaag atgttggaaa aagtaatatt aaatcttaaa aaacatatgg 4560
aaactacaca atggtgaaga cacattggtg aagtacaaaa atataaattg gatctagaag 4620
aaagggcaat gcaggcaata gaaaaattag tagaaatccc tttaaaggtt agtttgtaaa 4680
atcaggtaag tttatttata atttgctttc atttatttca ctgcaaatta tattttggat 4740
atgtatatat attgtgcttc ctctgcctgt cttacagcaa tttgccttgc agagttctag 4800
gaaaaaggtg gcatgtgttt ttactttcaa aatatttaaa tttccatcat tataacaaaa 4860

```
tcaatttttc agagtaatga ttctcactgt ggagtcattt gattattaag acccgttggc 4920
ataagattac atcctctgac tataaaaatc ctggaagaaa acctaggaaa tattcgtctg 4980
gacattgcac ttggcaatga atttatgggt aaccactgat ccacttccag tcactatcca 5040
tgagttttta tttccagata catgaaatca tatgagttga aactttcttt tgattgagca 5100
gtttggaaac cgtctttttg tagaatctgc aagtggatat ttggaaccct ttgaggccta 5160
tgctgaaaaa agaaatatct tcactacatg atgaccacca gcagcagctg ggaaaccag 5220
cacccctgtgg aattccatac ggtgcataga atacatcctc ccttcagtcg gcttgggtca 5280
acttaggtca tgggccacct ggctgatagc agtttccaca gaaatgcttc aagatgaaag 5340
tggatgaccg ggccaccctc caccactgcc ctgtaagacc atgggacaca caggccacca 5400
gttcttttca tgtggtcatc ccctgttaga tgggagaaaa tacacctgcc tcatttttgt 5460
accttctgtg tgaacattcc acggcagact gtcgctaaat gtggatgaag aattgaatga 5520
atgaatgaat atgagagaaa atgaataaat ggttcagatc ctgggctgga aggctgtgta 5580
tgaggatggt gggtagagga gggtctgttt ttcttgcctt taagtcacta attgtcactt 5640
tggggcagga gcacaggctt tgaatgcaga ccgactggac tttaattctg gctttactag 5700
ttgtgattgt gtgaccttgt gaaagttact taaaccctct gtgcctgttt ctttatctgt 5760
aaaatggaga taataagatg tcaaaggact gtggtaagaa ttaaatgctt taaaaaaaaa 5820
aaaaaaaaa 5829
```

<210> 474
<211> 1594
<212> DNA
<213> Homo sapiens

<400> 474

```
atttatggat cattaatgcc tctttagtag tttagagaaa acgtcaaaag aaatggcccc 60
agaataagct tcttgatttg taaaattcta tgtcattggc tcaaatttgt atagtatctc 120
aaaatataaa tatatagaca tctcagataa tatatttgaa atagcaaatt cctgttagaa 180
aataatagta cttaactaga tgagaataac aggtcgccat tatttgaatt gtctcctatt 240
cgtttttcat ttgttgtgtt actcatgttt tacttatgag ggatatatat aacttccact 300
gttttcagaa ttattgtatg cagtcagtat gagaatgcaa tttaagtttc cttgatgctt 360
tttcacactt ctattactag aaataagaat acagtaatat tggcaaagaa aattgaccag 420
ttcaataaaa ttttttagta aatctgattg aaaataaaca ttgcttatgg ctttcttaca 480
tcaatattgt tatgtcctag acaccttatc tgaaattacg gcttcaaaat tctaattatg 540
tgcaaatgtg taaaatatca atactttatg ttcaagctgg ggcctcttca ggcgtcctgg 600
gctgagagag aaagatgcta gctccgcaag ccggagaggg aacaccgcca cattgttaca 660
cggacacacc gccacgtgga cacatgacca gactcacatg tacagacaca cggagacatt 720
accacatgga gacaccgtca cacagtcaca cggacacact ggcatagtca catggacgga 780
cacacagaca tatggagaaa tcacatggac acaccaccac actatcacag ggacacagac 840
acacggagac atcaccacat ggacacactg tcacactacc acagggacac gagacatcac 900
actgtcacat ggacacacca tcacacacat gaacacaccg acacactgcc atatggacac 960
tggcacacac actgccacac tgtcacatgg acacacctcc acaccatcac accaccacac 1020
acactgcctg tggacacaag gacacacaga cactgtcaca cagatacaca aaacactgtc 1080
acacggagac atcaccatgc agatacacca ccactctggt gccgtctgaa ttaccctgct 1140
gggggggacag cagtggcata ctcatgccta agtgactggc tttcacccca gtagtgattg 1200
ccctccatca acactgccca ccccaggttg ggctaccccc agcccatctt tacaaaacag 1260
ggcaaggtga actaatggag tgggtggagg agttggaaga aatcccagcg tcagtcaccg 1320
ggatagaatt cccaaggaac cctcttttttg gaggatggtt tccatttctg gaggcgatct 1380
gccgacaggg tgaatgcctt cttgcttgtc ttctggggaa tcagagagag tccgttttgt 1440
ggtgggaaga gtgtggctgt gtactttgaa ctcctgtaaa ttctctgact catgtccaca 1500
aaaccaacag ttttgtgaat gtgtctggag gcaagggaag ggccactcag gatctatgtt 1560
gaagggaaga ggcctggggc tggagtattc gctt 1594
```

<210> 475
<211> 2414
<212> DNA
<213> Homo sapiens

<220>

<221> unsure
<222> (33)
<223> n=A,T,C or G

<400> 475
cccaacacaa tggctttata agaatgcttc acntgtgaaa aacaaatatc aaagtcttct 60
tgtagattat ttttaaggac aaatctttat tccatgttta atttatttag ctttccctgt 120
agctaatatt tcatgctgaa cacattttaa atgctgtaaa tgtagataat gtaatttatg 180
tatcattaat gcctctttag tagtttagag aaaacgtcaa aagaaatggc cccagaataa 240
gcttcttgat ttgtaaaatt ctatgtcatt ggctcaaatt tgtatagtat ctcaaaatat 300
aaatatatag acatctcaga taatatattt gaaatagcaa attcctgtta gaaaataata 360
gtacttaact agatgagaat aacaggtcgc cattatttga attgtctcct attcgttttt 420
catttgttgt gttactcatg ttttacttat gggggggatat atataacttc cgctgttttc 480
agaagtattg tatgcagtca gtatgagaat gcaatttaag tttccttgat gctttttcac 540
acttctatta ctagaaataa gaatacagta atattggcaa agaaaattga ccagttcaat 600
aaaatttttt agtaaatctg attgaaaata aacattgctt atggctttct tacatcaata 660
ttgttatgtc ctagacacct tatctgaaat tacggcttca aaattctaat tatgtgcaaa 720
tgtgtaaaat atcaatactt tatgttcaag ctgggggcctc ttcaggcgtc ctgggctgag 780
agagaaagat gctagctccg caagccgggg agggaacacc gccacattgt tacatggaca 840
caccgccacg tggacacatg accagactca catgtacaga cacacggaga cattaccaca 900
tggagacacc gtcacacagt cacacgagca cactggcata gtcacatgga cggacacaca 960
gacatatgga gaaatcacac tgacacacca ccacactatc acagggacac agacacacgg 1020
agacatcacc acatggacac actgtcacac taccacaggg acacgagaca tcacactgtc 1080
acatggacac accatcacac acatgaacac accgacacac tgccatatgg acactgccac 1140
acacactgcc acactgtcac atggacacac ctccatacca tcacaccacc acacacactg 1200
ccatgtggac acaaggacac acagacactg tcacacagat acacaaaaca ctgtcacacg 1260
gagacatcac catgcagata caccaccaca tggacatagc accagacact ctgccacaca 1320
gatacaccac cacacagaaa tgcggacaca ctgccacaca gacaccacca catcgttgcc 1380
acactttcat gtgtcagctg gcggtgtggg ccccacgact ctgggctcta atcgagaaat 1440
tacttggaca tatagtgaag gcaaaatttt tttttatttt ctgggtaacc aagcgcgact 1500
ctgtctcaaa aaaagaaaaa aaaagcaata tactgtgtaa tcgttgacag cataattcac 1560
tattatgtag atcggagagc agaggattct gaatgcatga acatatcatt aacatttcaa 1620
tacattactc ataattactg atgaactaaa gagaaaccaa gaaattatgg tgatagttat 1680
attgacctgg agaaatgtag acacaaaaga accgtaagat gagaaatgtg ttaacacagt 1740
ctataagggc atgcaagaat aaaaataggg gagaaaacag gagagttttt caagagcttt 1800
ctggtcatgt aagtcaactt gtatcggtta atttttaaaa ggtttattta catgcaataa 1860
actgcacata cttcaattgt acattttggt aattcttggc atttgtagct ctataaaacc 1920
agcaacatat taaaatagca aacatatcca ttacctttac caccaaagtt ttcttgtgtt 1980
ttttctactc actttttcct gcctatcccc ccatctcttc cacaggtaac cactgatcca 2040
cttccagtca ctatccatga gtttttattt ccaaatacat gaaatcatat gaatttctgg 2100
tttttcctgt tggagcccaa ggagcaaggg cagaatgagg aacatgatgt ttcttwccga 2160
cagttactca tgacgtctcc atccaggact gaggggggca tccttctcca tctaggactg 2220
ggggcatcct tctccatcca gtattggggg tcatccttct ccatccagta ttgggggtca 2280
tcctcctcca tccaggacct gaggggtgtc cttttctgcg cttccttgga tggcagtctt 2340
tcccttcatg tttatagtra cttaccatta aatcactgtg ccgtttttttc ctaaaataaa 2400
aaaaaaaaaa aaaa 2414

<210> 476
<211> 3434
<212> DNA
<213> Homo sapiens

<400> 476
ctgtgctgca aatggggcca tatagaggaa aggagcagct ggctctggag catggtgtgc 60
actccctttg ggccttcagt ccatgtctca tgggtcgtat gacactgcgg gcttgttggt 120
tgccaagagg cagaccacag gtcatcttga ggaggacttt atgttccagt ccagaaagca 180
gccagtggta ccacccaggg gacttgtgct tctgtggccc aggccagacg tagaatttga 240
caaagtcagg acggtctcag tcagagcagc atgtcggtcc ccggggcctg tgcatgccgg 300

```
gcagggccag gctggcttaa ggagcaagca gccacctctg ttaggggtgt gcctggagca 360
ggtggagcag ccaccaacct cacgcactga aagaagcagg gatggccagg ttccaacatc 420
ctgagtggct gccacctgat ggctgatgga gcagaggcct gaggaaaagc agatggcact 480
gctttgtagt gctgttcttt gtctctcttg atctttttca gttaatgtct gttttatcag 540
agactaggat tgcaaaccct gctctttttt gctttccatt tgcttggtaa atattcctcc 600
atccctttat tttaagccta tgtgtgtctt tgcacatgag atgggtctcc tgaatacagg 660
acaacaatgg gtctttactc tttatccaac ttgccagtct gtgtctttta actggggcat 720
ttagcccatt tacatttaag tttagtattt gttacatgtg aaatttatcc tgtcatgatg 780
ttgctagctt tttattttc ccattagttt gcagtttctt tatagtgtca atggtcttta 840
caattcgata tgtttttgta gtggctggta ctggtttttc ctttctacgt ttagtgtctc 900
cttcaggagc tcttgtaaca caagaatgtg gatttatttc ttgtaaggta aatatgtgga 960
tttattctgg gactgtattc tatggccttt accccaagaa tcattacttt ttaaaatgca 1020
attcaaatta gcataaaaca tttacagcct atggaaaggc ttgtggcatt agaatcctta 1080
tttataggat tattttgtgt ttttttgaga tatggtcttt gtcatcgagg cagaagtgcc 1140
gtggtttgat cataattcac cacagccctg aactcttgag tccaagccat cctttttgcct 1200
taatctccca accagttgga tctacaagca taaggcatca tgcgtggcta attttttcac 1260
gttttttttt tttttgtcga gattatggta tcactgtgtt gctctggctg atctcaaatg 1320
tttgacctca aggatctttt ctgccacagc ctcctaaagt gctaggatta tatgcatgat 1380
acaccatgcc tattgtagag tattacatta ttttcaaagt cttattgtaa gagccattta 1440
ttgcctttgg cctaaataac tcaatataat atctctgaaa cttttttttg acaaattttg 1500
gggcgtgatg atgagagaag gggggtttgaa actttctaat aagagttaac ttagagccat 1560
ttaagaaagg aaaaaacaca aattatcaga aaaacaacag taagatcaag tgcaaaagtt 1620
ctgtggcaaa gatgatgaga gtaaagaata tatgtttgtg actcatggtg gcttttactt 1680
tgttcttgaa tttctgagta cgggttaaca tttaaagaat ctacattata gataacattt 1740
tattgcaagt aaatgtattt caaaatttgt tattggtttt gtatgagatt attctcagcc 1800
tacttcatta tcaagctata ttattttatt aatgtagttc gatgatctta cagcaaagct 1860
gaaagctgta tcttcaaaat atgtctattt gactaaaaag ttattcaaca ggagttatta 1920
tctataaaaa aatacaacag gaatataaaa aacttgagga taaaaagatg ttggaaaaag 1980
taatattaaa tcttaaaaaa catatggaaa ctacacaatg gtgaagacac attggtgaag 2040
tacaaaaata taaattggat ctagaagaaa gggcaatgca ggcaatagaa aaattagtag 2100
aaatcccttt aaaggttagt ttgtaaaatc aggtaagttt atttataatt tgctttcatt 2160
tatttcactg caaattatat tttggatatg tatatatatt gtgcttcctc tgcctgtctt 2220
acagcaattt gccttgcaga gttctaggaa aaaggtggca tgtgttttta ctttcaaaat 2280
atttaaattt ccatcattat aacaaaatca atttttcaga gtaatgattc tcactgtgga 2340
gtcatttgat tattaagacc cgttggcata agattacatc ctctgactat aaaaatcctg 2400
gaagaaaacc taggaaatat tcgtctggac attgcacttg gcaatgaatt tatgggcgct 2460
ttggaatcct gcagatataa taatgataat taaacaaaac actcagagaa actgccaacc 2520
ctaggatgaa gtatattgtt actgtgcttt gggattaaaa taagtaacta cagtttatag 2580
aacttttata ctgatacaca gacactaaaa agggaaaggg tttagatgag aagctctgct 2640
atgcaatcaa gaatctcagc cactcatttc tgtaggggct gcaggagctc cctgtaaaga 2700
gaggttatgg agtctgtagc ttcaggtaag atacttaaaa cccttcagag tttctccatt 2760
ttttcccata gtttccccaa aaaggttatg acactttata agaatgcttc acttgtgaaa 2820
aacaaatatc aaagtcttct tgtagattat ttttaaggac aaatctttat tccatgttta 2880
atttatttag ctttccctgt agctaatatt tcatgctgaa cacattttaa atgctgtaaa 2940
tgtagataat gtaatttatg tatcattaat gcctctttag tagtttagag aaaacgtcaa 3000
aagaaatggc cccagaataa gcttcttgat ttgtaaaatt ctatgtcatt ggctcaaatt 3060
tgtatagtat ctcaaaatat aaatatatag acatctcaga taatatattt gaaatagcaa 3120
attcctgtta gaaaataata gtacttaact agatgagaat aacaggtcgc cattatttga 3180
attgtctcct attcgttttt catttgttgt gttactcatg ttttacttat gggggatat 3240
atataacttc cgctgttttc agaagtattg tatgcagtca gtatgagaat gcaatttaag 3300
tttccttgat gctttttcac acttctatta ctagaaataa gaatacagta atattggcaa 3360
agaaaattga ccagttcaat aaaatttttt agtaaatctg attgaaaata aaaaaaaaaa 3420
aaaaaaaaaa aaaa                                                  3434
```

<210> 477
<211> 140
<212> PRT
<213> Homo sapiens

<400> 477
Met Asp Gly His Thr Asp Ile Trp Arg Asn His Met Asp Thr Pro Pro
5 10 15
His Tyr His Arg Asp Thr Asp Thr Arg Arg His His His Met Asp Thr
20 25 30
Leu Ser His Tyr His Arg Asp Thr Arg His His Thr Val Thr Trp Thr
35 40 45
His His His Thr His Glu His Thr Asp Thr Leu Pro Tyr Gly His Trp
50 55 60
His Thr His Cys His Thr Val Thr Trp Thr His Leu His Thr Ile Thr
65 70 75 80
Pro Pro His Thr Leu Pro Val Asp Thr Arg Thr His Arg His Cys His
85 90 95
Thr Asp Thr Gln Asn Thr Val Thr Arg Arg His His His Ala Asp Thr
100 105 110
Pro Pro Leu Trp Cys Arg Leu Asn Tyr Pro Ala Gly Gly Thr Ala Val
115 120 125
Ala Tyr Ser Cys Leu Ser Asp Trp Leu Ser Pro Gln
130 135 140

<210> 478
<211> 143
<212> PRT
<213> Homo sapiens

<400> 478
Met Tyr Arg His Thr Glu Thr Leu Pro His Gly Asp Thr Val Thr Gln
5 10 15
Ser His Gly His Thr Gly Ile Val Thr Trp Thr Asp Thr Gln Thr Tyr
20 25 30
Gly Glu Ile Thr Trp Thr His His His Thr Ile Thr Gly Thr Gln Thr
35 40 45
His Gly Asp Ile Thr Thr Trp Thr His Cys His Thr Thr Thr Gly Thr
50 55 60
Arg Asp Ile Thr Leu Ser His Gly His Thr Ile Thr His Met Asn Thr
65 70 75 80
Pro Thr His Cys His Met Asp Thr Gly Thr His Thr Ala Thr Leu Ser
85 90 95
His Gly His Thr Ser Thr Pro Ser His His His Thr His Cys Leu Trp
100 105 110
Thr Gln Gly His Thr Asp Thr Val Thr Gln Ile His Lys Thr Leu Ser
115 120 125
His Gly Asp Ile Thr Met Gln Ile His His His Ser Gly Ala Val
130 135 140

<210> 479
<211> 222
<212> PRT
<213> Homo sapiens

<400> 479
Met Tyr Arg His Thr Glu Thr Leu Pro His Gly Asp Thr Val Thr Gln
5 10 15
Ser His Glu His Thr Gly Ile Val Thr Trp Thr Asp Thr Gln Thr Tyr
20 25 30

```
Gly Glu Ile Thr Leu Thr His His His Thr Ile Thr Gly Thr Gln Thr
        35                  40                  45
His Gly Asp Ile Thr Thr Trp Thr His Cys His Thr Thr Thr Gly Thr
    50                  55                  60
Arg Asp Ile Thr Leu Ser His Gly His Thr Ile Thr His Met Asn Thr
65                  70                  75                  80
Pro Thr His Cys His Met Asp Thr Ala Thr His Thr Ala Thr Leu Ser
                85                  90                  95
His Gly His Thr Ser Ile Pro Ser His His His Thr His Cys His Val
            100                 105                 110
Asp Thr Arg Thr His Arg His Cys His Thr Asp Thr Gln Asn Thr Val
        115                 120                 125
Thr Arg Arg His His His Ala Asp Thr Pro Pro His Gly His Ser Thr
    130                 135                 140
Arg His Ser Ala Thr Gln Ile His His His Thr Glu Met Arg Thr His
145                 150                 155                 160
Cys His Thr Asp Thr Thr Thr Ser Leu Pro His Phe His Val Ser Ala
                165                 170                 175
Gly Gly Val Gly Pro Thr Thr Leu Gly Ser Asn Arg Glu Ile Thr Trp
            180                 185                 190
Thr Tyr Ser Glu Gly Lys Ile Phe Phe Tyr Phe Leu Gly Asn Gln Ala
        195                 200                 205
Arg Leu Cys Leu Lys Lys Arg Lys Lys Lys Gln Tyr Thr Val
    210                 215                 220
```

<210> 480
<211> 144
<212> PRT
<213> Homo sapiens

<400> 480

```
Met Glu Pro Tyr Arg Gly Asn Glu Gln Pro Ser Gln Glu Gln Gly Val
                5                   10                  15
Cys Cys Leu Trp Gly Leu Gln Ser Leu Pro Gln Gly Ser Tyr Val Thr
            20                  25                  30
Val Gly Phe Leu Val Val Lys Arg Gln Thr Ile Gly Arg Leu Glu Arg
        35                  40                  45
Asp Phe Met Phe Lys Cys Arg Lys Gln Pro Gly Leu Pro Pro Ser Gly
    50                  55                  60
Leu Cys Leu Leu Trp Pro Trp Pro Asn Leu Glu Phe Gly Arg Arg Gln
65                  70                  75                  80
Asp Arg Leu Thr Trp Ser Ser Val Ser Val Ala Gly Val Cys Ala Cys
                85                  90                  95
Arg Ala Arg Pro Gly Trp Leu Gly Glu Gln Pro Ala Thr Ser Ala Gly
            100                 105                 110
Val Arg Leu Glu Gln Val Glu Gln Pro Pro Ala His Pro Leu Gln Glu
        115                 120                 125
Ala Gly Val Ala Arg Phe Pro Arg Pro Glu Trp Val Pro Pro Asn Gly
    130                 135                 140
```

<210> 481
<211> 167
<212> PRT
<213> Homo sapiens

<400> 481

Met His Gly Pro Gln Val Leu Ala Arg Cys Ser Glu Cys Ala Cys Pro
5 10 15
Ala Leu Ala Ala Thr Ser Ala Gly Val Arg Leu Glu Gly Val Asp Arg
20 25 30
Pro Pro Thr Leu Pro Ser Gln Gly Ser Gly Trp Pro Cys Ser His Ser
35 40 45
Leu Ser Gly Cys His Leu Met Ala Asp Gly Ala Lys Ala Leu Gly Lys
50 55 60
Ala Asp Gly Pro Trp Pro Tyr Leu Phe Val Arg Arg Thr Asp Val Pro
65 70 75 80
Cys Pro Ala Ala Ser Glu Val Gly Gly Cys Ala Pro Ser Ser Trp Arg
85 90 95
Ala Leu Ala Glu Val Thr Gly Cys Ser Leu Gly Pro Leu Gly Leu Ala
100 105 110
Gln His Ala Gln Ala Ser Val Leu Leu Leu Cys Tyr Lys Trp Ser His
115 120 125
Ile Gly Glu Thr Ser Ser His Leu Arg Ser Lys Val Tyr Ala Ala Phe
130 135 140
Gly Gly Ser Ser Pro Cys Leu Lys Gly Leu Met Ser Leu Trp Ala Ser
145 150 155 160
Trp Leu Ser Arg Gly Arg Pro
165

<210> 482
<211> 143
<212> PRT
<213> Homo sapiens

<400> 482
Met Glu Pro Tyr Arg Gly Asn Lys Lys Gln Val Gln Glu Lys Gly Val
5 10 15
Pro Cys Leu Trp Gly Ser Ser Pro Cys Leu Arg Cys His Met Ala Leu
20 25 30
Arg Ala Ser Trp Leu Pro Gly Gly Gly Pro Gln Ala Ile Leu Gly Arg
35 40 45
Thr Leu Cys Ser Ser Ala Glu Ser Ser Gln Asp Cys His Pro Gly Gly
50 55 60
Pro Ser Ile Ala Leu Ala Lys Pro Cys Arg Gly Val Trp Leu Leu Phe
65 70 75 80
Glu Pro Ala Trp Pro Pro Trp His Ala Arg Ala Pro Gly Ala Gly Thr
85 90 95
Leu Leu Arg Val Cys Leu Ser Cys Leu Gly Cys His Leu Cys Gly Gly
100 105 110
Ala Ser Gly Gly Gly Gly Pro Ala Thr Asn Leu Thr Gln Ser Arg Lys
115 120 125
Trp Met Ala Met Phe Pro Gln Pro Glu Trp Leu Pro Pro Asp Gly
130 135 140

<210> 483
<211> 143
<212> PRT
<213> Homo sapiens

<400> 483
Met Glu Thr Gln Arg Gly Asn Lys Gln Arg Ala Gln Glu Gln Gly Val
5 10 15
Cys Cys Leu Trp Gly Ser Ser Pro Cys Leu Gly Ser Tyr Gly Thr Ala

```
            20                  25                  30
Gly Phe Leu Val Ala Lys Arg Arg Thr Thr Gly Leu Leu Glu Glu Asp
        35                  40                  45
Phe Thr Phe Lys Cys Arg Lys Gln Pro Lys Leu Pro Ser Met Arg Leu
    50                  55                  60
Ser Leu Leu Trp Pro Trp Arg Asp Leu Lys Phe Val Pro Arg Gln Asp
65                  70                  75                  80
Lys Leu Thr Arg Ser Ser Val Ser Val Ala Gly Ala Tyr Ala Cys Arg
                85                  90                  95
Ala Gly Pro Gly Trp Leu Lys Glu Gln Pro Ala Thr Ser Ala Arg Val
            100                 105                 110
Arg Leu Val Gln Ala Glu His Pro Pro Pro His Pro Leu Glu Glu Val
        115                 120                 125
Gly Met Ala Arg Phe Pro Gln Pro Glu Cys Leu Pro Pro Tyr Cys
    130                 135                 140

      <210> 484
      <211> 30
      <212> PRT
      <213> Homo Sapien

      <400> 484
Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe
1               5                   10                  15
Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile
            20                  25                  30

      <210> 485
      <211> 31
      <212> DNA
      <213> Artificial Sequence

      <220>
      <223> Made in a lab

      <400> 485
gggaagctta tcacctatgt gccgcctctg c                                  31

      <210> 486
      <211> 27
      <212> DNA
      <213> Artificial Sequence

      <220>
      <223> Made in a lab

      <400> 486
gcgaattctc acgctgagta tttggcc                                       27

      <210> 487
      <211> 36
      <212> DNA
      <213> Artificial Sequence

      <220>
      <223> Made in a lab

      <400> 487
```

cccgaattct tagctgccca tccgaacgcc ttcatc 36

<210> 488
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 488
gggaagcttc ttccccggct gcaccagctg tgc 33

<210> 489
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 489
Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg Ala Val Tyr Leu Ala
1 5 10 15
Ser Val Ala

<210> 490
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 490
Tyr Leu Ala Ser Val Ala Ala Phe Pro Val Ala Ala Gly Ala Thr Cys
1 5 10 15
Leu Ser His Ser
20

<210> 491
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 491
Thr Cys Leu Ser His Ser Val Ala Val Val Thr Ala Ser Ala Ala Leu
1 5 10 15
Thr Gly Phe Thr
20

<210> 492
<211> 20
<212> PRT

<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 492
Ala Leu Thr Gly Phe Thr Phe Ser Ala Leu Gln Ile Leu Pro Tyr Thr
1 5 10 15
Leu Ala Ser Leu
20

<210> 493
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 493
Tyr Thr Leu Ala Ser Leu Tyr His Arg Glu Lys Gln Val Phe Leu Pro
1 5 10 15
Lys Tyr Arg Gly
20

<210> 494
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 494
Leu Pro Lys Tyr Arg Gly Asp Thr Gly Gly Ala Ser Ser Glu Asp Ser
1 5 10 15
Leu Met Ile Ser
20

<210> 495
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 495
Asp Ser Leu Met Thr Ser Phe Leu Pro Gly Pro Lys Pro Gly Ala Pro
1 5 10 15
Phe Pro Asn Gly
20

<210> 496
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 496
Ala Pro Phe Pro Asn Gly His Val Gly Ala Gly Gly Ser Gly Leu Leu
1 5 10 15
Pro Pro Pro Pro Ala
20

<210> 497
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 497
Leu Leu Pro Pro Pro Pro Ala Leu Cys Gly Ala Ser Ala Cys Asp Val
1 5 10 15
Ser Val Arg Val
20

<210> 498
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 498
Asp Val Ser Val Arg Val Val Val Gly Glu Pro Thr Glu Ala Arg Val
1 5 10 15
Val Pro Gly Arg
20

<210> 499
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 499
Arg Val Val Pro Gly Arg Gly Ile Cys Leu Asp Leu Ala Ile Leu Asp
1 5 10 15
Ser Ala Phe Leu
20

<210> 500
<211> 20
<212> PRT
<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 500
Leu Asp Ser Ala Phe Leu Leu Ser Gln Val Ala Pro Ser Leu Phe Met
1 5 10 15
Gly Ser Ile Val
20

<210> 501
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 501
Phe Met Gly Ser Ile Val Gln Leu Ser Gln Ser Val Thr Ala Tyr Met
1 5 10 15
Val Ser Ala Ala
20

<210> 502
<211> 414
<212> DNA
<213> Homo Sapien

<220>
<221> misc_feature
<222> (1)...(414)
<223> n=A,T,C or G

<400> 502
caccatggag acaggcctgc gctggctttt cctggtcgct gtgctcaaag gtgtccaatg 60
tcagtcggtg gaggagtccg gggtcgcct ggtcacgcct gggacacctt tgacantcac 120
ctgtagagtt tttggaatng acctcagtag caatgcaatg agctgggtcc gccaggctcc 180
agggaagggg ctggaatgga tcggagccat tgataattgt ccacantacg cgacctgggc 240
gaaaggccga ttnatnattt ccaaaacctn gaccacggtg gatttgaaaa tgaccagtcc 300
gacaaccgag gacacggcca cctatttttg tggcagaatg aatactggta atagtggttg 360
gaagaatatt tggggcccag gcaccctggt caccgtntcc tcagggcaac ctaa 414

<210> 503
<211> 379
<212> DNA
<213> Homo Sapien

<220>
<221> misc_feature
<222> (1)...(379)
<223> n=A,T,C or G

<400> 503
atncgatggt gcttggtcaa aggtgtccag tgtcagtcgg tggaggagtc cgggggtcgc 60
ctggtcacgc ctgggacacc cctgacactc acctgcaccg tntctggatt ngacatcagt 120
agctatggag tgagctgggt ccgccaggct ccagggaagg ggctggnata catcggatca 180
ttagtagtag tggtacattt tacgcgagct gggcgaaagg ccgattcacc atttccaaaa 240
cctngaccac ggtggatttg aaaatcacca gtttgacaac cgaggacacg gccacctatt 300
tntgtgccag aggggggttt aattataaag acatttgggg cccaggcacc ctggtcaccg 360

tntccttagg gcaacctaa 379

<210> 504
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 504
Gly Phe Thr Asn Tyr Thr Asp Phe Glu Asp Ser Pro Tyr Phe Lys Glu
1 5 10 15
Asn Ser Ala

<210> 505
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 505
Lys Glu Asn Ser Ala Phe Pro Pro Phe Cys Cys Asn Asp Asn Val Thr
1 5 10 15
Asn Thr Ala Asn
20

<210> 506
<211> 407
<212> DNA
<213> Homo Sapien

<400> 506
atggagacag gcctgcgctg gcttctcctg gtcgctgcgc tcaaaggtgt ccagtgtcag 60
tcgctggagg agtccggggg tcgcctggtc acgcctggga cacccctgac actcacctgc 120
accgtctctg gattctccct cagtagcaat gcaatgatct gggtccgcca ggctccaggg 180
aaggggctgg aatacatcgg atacattagt tatggtggta gcgcatacta cgcgagctgg 240
gtgaaaggcc gattcaccat ctccaaaacc tcgaccacgg tggatctgag aatgaccagt 300
ctgacaaccg aggacacggc cacctatttc tgtgccagaa atagtgattt tagtggtatg 360
ttgtggggcc caggcaccct ggtcaccgtc tcctcagggc aacctaa 407

<210> 507
<211> 422
<212> DNA
<213> Homo Sapien

<400> 507
atggagacag gcctgcgctg gcttctcctg gtcgctgtgc tcaaaggtgt ccagtgtcag 60
tcggtggagg agtccggggg tcgcctggtc acgcctggga cacccctgac actcacctgt 120
acagtctctg gattctccct cagcaactac gacctgaact gggtccgcca ggctccaggg 180
aaggggctgg aatggatcgg gatcattaat tatgttggta ggacggacta cgcgaactgg 240
gcaaaaggcc ggttcaccat ctccaaaacc tcgaccaccg tggatctcaa gatcgccagt 300
ccgacaaccg aggacacggc cacctatttc tgtgccagag ggtggaagtg cgatgagtct 360
ggtccgtgct tgcgcatctg ggcccaggc accctggtca ccgtctcctt agggcaacct 420

aa 422

<210> 508
<211> 411
<212> DNA
<213> Homo Sapien

<220>
<221> misc_feature
<222> (1)...(411)
<223> n=A,T,C or G

<400> 508
atggagacag gcctcgctgg cttctcctgg tcgctgtgct caaaggtgtc cagtgtcagt 60
cggtggagga gtccgggggt cgcctggtca cgcctgggac acccctgaca ctcacctgca 120
cagtctctgg aatcgacctc agtagctact gcatgagctg ggtccgccag gctccaggga 180
aggggctgga atggatcgga atcattggta ctcctggtga cacatactac gcgaggtggg 240
cgaaaggccg attcaccatc tccaaaacct cgaccacggt gcatntgaaa atcnccagtc 300
cgacaaccga ggacacggcc acctatttct gtgccagaga tcttcgggat ggtagtagta 360
ctggttatta taaaatctgg ggcccaggca ccctggtcac cgtctccttg g 411

<210> 509
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 509
Leu Cys Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Ala Ser
1 5 10 15

<210> 510
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 510
Pro Glu Tyr Asn Arg Pro Leu Leu Ala Asn Asp Leu Met Leu Ile
1 5 10 15

<210> 511
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 511

Tyr His Pro Ser Met Phe Cys Ala Gly Gly Gly Gln Asp Gln Lys
1 5 10 15

<210> 512
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 512
```
Asp Ser Gly Gly Pro Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu
 1               5                  10                  15
```

<210> 513
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 513
```
Ala Pro Cys Gly Gln Val Gly Val Pro Asx Val Tyr Thr Asn Leu
 1               5                  10                  15
```

<210> 514
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 514
```
Leu Cys Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Ala Ser
 1               5                  10                  15
```

<210> 515
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 515
```
Met Val Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg
 1               5                  10                  15
```

<210> 516
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 516
```
Val Ser Glu Ser Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln
```

1 5 10 15

<210> 517
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 517
Glu Val Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met
1 5 10 15

<210> 518
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 518
Arg Ala Glu Pro Gly Thr Glu Ala Arg Arg His Tyr Asp Glu Gly
1 5 10 15

<210> 519
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 519
Arg Ala Glu Pro Gly Thr Glu Ala Arg Arg Asn Tyr Asp Glu Gly Cys
1 5 10 15
Gly

<210> 520
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 520
Val Gly Glu Gly Leu Tyr Gln Gly Val Pro Arg Ala Glu Pro Gly Thr
1 5 10 15
Glu Ala Arg Arg His Tyr Asp Glu Gly
20 25

<210> 521
<211> 21
<212> PRT
<213> Artificial Sequence

```
      <220>
      <223> Made in a lab

      <400> 521
Ala Pro Phe Pro Asn Gly His Val Gly Ala Gly Gly Ser Gly Leu Leu
 1               5                  10                  15
Pro Pro Pro Pro Ala
            20

      <210> 522
      <211> 20
      <212> PRT
      <213> Artificial Sequence

      <220>
      <223> Made in a lab

      <400> 522
Leu Leu Val Val Pro Ala Ile Lys Lys Asp Tyr Gly Ser Gln Glu Asp
 1               5                  10                  15
Phe Thr Gln Val
            20

      <210> 523
      <211> 254
      <212> PRT
      <213> Artificial Sequence

      <220>
      <223> Made in a lab

      <220>
      <221> VARIANT
      <222> (1)...(254)
      <223> Xaa = any amino acid

      <400> 523
Met Ala Thr Ala Gly Asn Pro Trp Gly Trp Phe Leu Gly Tyr Leu Ile
 1               5                  10                  15
Leu Gly Val Ala Gly Ser Leu Val Ser Gly Ser Cys Ser Gln Ile Ile
            20                  25                  30
Asn Gly Glu Asp Cys Ser Pro His Ser Gln Pro Trp Gln Ala Ala Leu
        35                  40                  45
Val Met Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln
    50                  55                  60
Trp Val Leu Ser Ala Thr His Cys Phe Gln Asn Ser Tyr Thr Ile Gly
65                  70                  75                  80
Leu Gly Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met
                85                  90                  95
Val Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro Leu
            100                 105                 110
Leu Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu
        115                 120                 125
Ser Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala
    130                 135                 140
Gly Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly Arg
145                 150                 155                 160
```

```
Met Pro Thr Val Leu Gln Cys Val Asn Val Ser Val Val Ser Glu Glu
                165                 170                 175
Val Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe Cys
            180                 185                 190
Ala Gly Gly Gly Gln Xaa Gln Xaa Asp Ser Cys Asn Gly Asp Ser Gly
        195                 200                 205
Gly Pro Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe Gly
    210                 215                 220
Lys Ala Pro Cys Gly Gln Val Gly Val Pro Gly Val Tyr Thr Asn Leu
225                 230                 235                 240
Cys Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Ala Ser
                245                 250
```

<210> 524
<211> 765
<212> DNA
<213> Homo sapien

<400> 524
```
atggccacag caggaaatcc ctggggctgg ttcctggggt acctcatcct tggtgtcgca      60
ggatcgctcg tctctggtag ctgcagccaa atcataaacg gcgaggactg cagcccgcac     120
tcgcagccct ggcaggcggc actggtcatg gaaaacgaat tgttctgctc gggcgtcctg     180
gtgcatccgc agtgggtgct gtcagccgca cactgtttcc agaactccta caccatcggg     240
ctgggcctgc acagtcttga ggccgaccaa gagccaggga gccagatggt ggaggccagc     300
ctctccgtac ggcacccaga gtacaacaga cccttgctcg ctaacgacct catgctcatc     360
aagttggacg aatccgtgtc cgagtctgac accatccgga gcatcagcat tgcttcgcag     420
tgccctaccg cggggaactc ttgcctcgtt tctggctggg gtctgctggc gaacggcaga     480
atgcctaccg tgctgcagtg cgtgaacgtg tcggtggtgt ctgaggaggt ctgcagtaag     540
ctctatgacc cgctgtacca ccccagcatg ttctgcgccg gcggagggca agaccagaag     600
gactcctgca acggtgactc tgggggggccc ctgatctgca acgggtactt gcagggcctt    660
gtgtctttcg gaaaagcccc gtgtggccaa gttggcgtgc caggtgtcta caccaacctc     720
tgcaaattca ctgagtggat agagaaaacc gtccaggcca gttaa                     765
```

<210> 525
<211> 254
<212> PRT
<213> Homo sapien

<400> 525
```
Met Ala Thr Ala Gly Asn Pro Trp Gly Trp Phe Leu Gly Tyr Leu Ile
 1               5                  10                  15
Leu Gly Val Ala Gly Ser Leu Val Ser Gly Ser Cys Ser Gln Ile Ile
            20                  25                  30
Asn Gly Glu Asp Cys Ser Pro His Ser Gln Pro Trp Gln Ala Ala Leu
        35                  40                  45
Val Met Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln
    50                  55                  60
Trp Val Leu Ser Ala Ala His Cys Phe Gln Asn Ser Tyr Thr Ile Gly
65                  70                  75                  80
Leu Gly Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met
                85                  90                  95
Val Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro Leu
            100                 105                 110
Leu Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu
        115                 120                 125
Ser Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala
    130                 135                 140
Gly Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly Arg
```

```
145                 150                 155                 160
Met Pro Thr Val Leu Gln Cys Val Asn Val Ser Val Val Ser Glu Glu
                165                 170                 175
Val Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe Cys
            180                 185                 190
Ala Gly Gly Gly Gln Asp Gln Lys Asp Ser Cys Asn Gly Asp Ser Gly
        195                 200                 205
Gly Pro Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe Gly
    210                 215                 220
Lys Ala Pro Cys Gly Gln Val Gly Val Pro Gly Val Tyr Thr Asn Leu
225                 230                 235                 240
Cys Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Ala Ser
                245                 250
```

<210> 526
<211> 963
<212> DNA
<213> Homo sapiens

<400> 526

```
atgagttcct gcaacttcac acatgccacc tttgtgctta ttggtatccc aggattagag 60
aaagcccatt tctgggttgg cttcccccctc ctttccatgt atgtagtggc aatgtttgga 120
aactgcatcg tggtcttcat cgtaaggacg gaacgcagcc tgcacgctcc gatgtacctc 180
tttctctgca tgcttgcagc cattgacctg gccttatcca catccaccat gcctaagatc 240
cttgcccttt tctggtttga ttcccgagag attagctttg aggcctgtct tacccagatg 300
ttctttattc atgccctctc agccattgaa tccaccatcc tgctggccat ggcctttgac 360
cgttatgtgg ccatctgcca cccactgcgc catgctgcag tgctcaacaa tacagtaaca 420
gcccagattg gcatcgtggc tgtggtccgc ggatccctct ttttttccc actgcctctg 480
ctgatcaagc ggctggcctt ctgccactcc aatgtcctct cgcactccta ttgtgtccac 540
caggatgtaa tgaagttggc ctatgcagac actttgccca atgtggtata tggtcttact 600
gccattctgc tggtcatggg cgtggacgta atgttcatct ccttgtccta ttttctgata 660
atacgaacgg ttctgcaact gccttccaag tcagagcggg ccaaggcctt tggaacctgt 720
gtgtcacaca ttggtgtggt actcgccttc tatgtgccac ttattggcct ctcagttgta 780
caccgctttg gaaacagcct tcatcccatt gtgcgtgttg tcatgggtga catctacctg 840
ctgctgcctc ctgtcatcaa tcccatcatc tatggtgcca aaaccaaaca gatcagaaca 900
cgggtgctgg ctatgttcaa gatcagctgt gacaaggact tgcaggctgt gggaggcaag 960
tga                                                               963
```

<210> 527
<211> 320
<212> PRT
<213> Homo sapiens

<400> 527

```
Met Ser Ser Cys Asn Phe Thr His Ala Thr Phe Val Leu Ile Gly Ile
                5                   10                  15
Pro Gly Leu Glu Lys Ala His Phe Trp Val Gly Phe Pro Leu Leu Ser
            20                  25                  30
Met Tyr Val Val Ala Met Phe Gly Asn Cys Ile Val Val Phe Ile Val
        35                  40                  45
Arg Thr Glu Arg Ser Leu His Ala Pro Met Tyr Leu Phe Leu Cys Met
    50                  55                  60
Leu Ala Ala Ile Asp Leu Ala Leu Ser Thr Ser Thr Met Pro Lys Ile
65                  70                  75                  80
Leu Ala Leu Phe Trp Phe Asp Ser Arg Glu Ile Ser Phe Glu Ala Cys
                85                  90                  95
Leu Thr Gln Met Phe Phe Ile His Ala Leu Ser Ala Ile Glu Ser Thr
            100                 105                 110
```

```
Ile Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile Cys His Pro
        115                 120                 125
Leu Arg His Ala Ala Val Leu Asn Asn Thr Val Thr Ala Gln Ile Gly
    130                 135                 140
Ile Val Ala Val Val Arg Gly Ser Leu Phe Phe Phe Pro Leu Pro Leu
145                 150                 155                 160
Leu Ile Lys Arg Leu Ala Phe Cys His Ser Asn Val Leu Ser His Ser
                165                 170                 175
Tyr Cys Val His Gln Asp Val Met Lys Leu Ala Tyr Ala Asp Thr Leu
            180                 185                 190
Pro Asn Val Val Tyr Gly Leu Thr Ala Ile Leu Leu Val Met Gly Val
        195                 200                 205
Asp Val Met Phe Ile Ser Leu Ser Tyr Phe Leu Ile Ile Arg Thr Val
    210                 215                 220
Leu Gln Leu Pro Ser Lys Ser Glu Arg Ala Lys Ala Phe Gly Thr Cys
225                 230                 235                 240
Val Ser His Ile Gly Val Val Leu Ala Phe Tyr Val Pro Leu Ile Gly
                245                 250                 255
Leu Ser Val Val His Arg Phe Gly Asn Ser Leu His Pro Ile Val Arg
            260                 265                 270
Val Val Met Gly Asp Ile Tyr Leu Leu Leu Pro Pro Val Ile Asn Pro
        275                 280                 285
Ile Ile Tyr Gly Ala Lys Thr Lys Gln Ile Arg Thr Arg Val Leu Ala
    290                 295                 300
Met Phe Lys Ile Ser Cys Asp Lys Asp Leu Gln Ala Val Gly Gly Lys
305                 310                 315                 320
```

<210> 528
<211> 20
<212> DNA
<213> Homo Sapien

<400> 528
actatggtcc agaggctgtg 20

<210> 529
<211> 20
<212> DNA
<213> Homo Sapien

<400> 529
atcacctatg tgccgcctct 20

<210> 530
<211> 1852
<212> DNA
<213> Homo sapiens

<400> 530
```
ggcacgagaa ttaaaaccct cagcaaaaca ggcatagaag ggacatacct taaagtaata 60
aaaaccacct atgacaagcc cacagccaac ataatactaa atggggaaaa gttagaagca 120
tttcctctga gaactgcaac aataaataca aggatgctgg attttgtcaa atgccttttc 180
tgtgtctgtt gagatgctta tgtgactttg cttttaattc tgtttatgtg attatcacat 240
ttattgactt gcctgtgtta gaccggaaga gctggggtgt ttctcaggag ccaccgtgtg 300
ctgcggcagc ttcgggataa cttgaggctg catcactggg gaagaaacac aytcctgtcc 360
gtggcgctga tggctgagga cagagcttca gtgtggcttc tctgcgactg gcttcttcgg 420
ggagttcttc cttcatagtt catccatatg gctccagagg aaaattatat tattttgtta 480
tggatgaaga gtattacgtt gtgcagatat actgcagtgt cttcatctct tgatgtgtga 540
```

ttgggtaggt tccaccatgt tgccgcagat gacatgattt cagtacctgt gtctggctga 600
aaagtgtttg tttgtgaatg gatattgtgg tttctggatc tcatcctctg tgggtggaca 660
gctttctcca ccttgctgga agtgacctgc tgtccagaag tttgatggct gaggagtata 720
ccatcgtgca tgcatctttc atttcctgca tttcttcctc cctggatgga caggggggagc 780
ggcaagagca acgtgggcac ttctggagac cacaacgact cctctgtgaa gacgcttggg 840
agcaagaggt gcaagtggtg ctgccactgc ttcccctgct gcagggggag cggcaagagc 900
aacgtggtcg cttggggaga ctacgatgac agcgccttca tggatcccag gtaccacgtc 960
catggagaag atctggacaa gctccacaga gctgcctggt ggggtaaagt ccccagaaag 1020
gatctcatcg tcatgctcag ggacacggat gtgaacaaga gggacaagca aaagaggact 1080
gctctacatc tggcctctgc caatgggaat tcagaagtag taaaactcgt gctggacaga 1140
cgatgtcaac ttaatgtcct tgacaacaaa aagaggacag ctctgacaaa ggccgtacaa 1200
tgccaggaag atgaatgtgc gttaatgttg ctggaacatg gcactgatcc aaatattcca 1260
gatgagtatg gaaataccac tctacactat gctgtctaca atgaagataa attaatggcc 1320
aaagcactgc tcttatacgg tgctgatatc gaatcaaaaa acaagcatgg cctcacacca 1380
ctgctacttg gtatacatga gcaaaaacag caagtggtga aatttttaat caagaaaaaa 1440
gcgaatttaa atgcgctgga tagatatgga agaactgctc tcatacttgc tgtatgttgt 1500
ggatcagcaa gtatagtcag ccctctactt gagcaaaatg ttgatgtatc ttctcaagat 1560
ctggaaagac ggccagagag tatgctgttt ctagtcatca tcatgtaatt tgccagttac 1620
tttctgacta caaagaaaaa cagatgttaa aaatctcttc tgaaaacagc aatccagaac 1680
aagacttaaa gctgacatca gaggaagagt cacaaaggct taaaggaagt gaaaacagcc 1740
agccagagct agaagattta tggctattga agaagaatga agaacacgga agtactcatg 1800
tgggattccc agaaaacctg actaacggtg ccgctgctgg caatggtgat ga 1852

<210> 531
<211> 879
<212> DNA
<213> Homo sapiens

<400> 531
atgcatcttt catttcctgc atttcttcct ccctggatgg acagggggag cggcaagagc 60
aacgtgggca cttctggaga ccacaacgac tcctctgtga agacgcttgg gagcaagagg 120
tgcaagtggt gctgccactg cttcccctgc tgcaggggga gcggcaagag caacgtggtc 180
gcttggggag actacgatga cagcgccttc atggatccca ggtaccacgt ccatggagaa 240
gatctggaca agctccacag agctgcctgg tggggtaaag tccccagaaa ggatctcatc 300
gtcatgctca gggacacgga tgtgaacaag agggacaagc aaaagaggac tgctctacat 360
ctggcctctg ccaatgggaa ttcagaagta gtaaaactcg tgctggacag acgatgtcaa 420
cttaatgtcc ttgacaacaa aaagaggaca gctctgacaa aggccgtaca atgccaggaa 480
gatgaatgtg cgttaatgtt gctggaacat ggcactgatc caaatattcc agatgagtat 540
ggaaatacca ctctacacta tgctgtctac aatgaagata aattaatggc caaagcactg 600
ctcttatacg gtgctgatat cgaatcaaaa aacaagcatg gcctcacacc actgctactt 660
ggtatacatg agcaaaaaca gcaagtggtg aaatttttaa tcaagaaaaa agcgaattta 720
aatgcgctgg atagatatgg aagaactgct ctcatacttg ctgtatgttg tggatcagca 780
agtatagtca gccctctact tgagcaaaat gttgatgtat cttctcaaga tctggaaaga 840
cggccagaga gtatgctgtt tctagtcatc atcatgtaa 879

<210> 532
<211> 292
<212> PRT
<213> Homo sapiens

<400> 532
Met His Leu Ser Phe Pro Ala Phe Leu Pro Pro Trp Met Asp Arg Gly
5 10 15
Ser Gly Lys Ser Asn Val Gly Thr Ser Gly Asp His Asn Asp Ser Ser
20 25 30
Val Lys Thr Leu Gly Ser Lys Arg Cys Lys Trp Cys Cys His Cys Phe
35 40 45
Pro Cys Cys Arg Gly Ser Gly Lys Ser Asn Val Val Ala Trp Gly Asp

```
    50                  55                  60
Tyr Asp Asp Ser Ala Phe Met Asp Pro Arg Tyr His Val His Gly Glu
 65                 70                  75                  80
Asp Leu Asp Lys Leu His Arg Ala Ala Trp Trp Gly Lys Val Pro Arg
                85                  90                  95
Lys Asp Leu Ile Val Met Leu Arg Asp Thr Asp Val Asn Lys Arg Asp
            100                 105                 110
Lys Gln Lys Arg Thr Ala Leu His Leu Ala Ser Ala Asn Gly Asn Ser
        115                 120                 125
Glu Val Val Lys Leu Val Leu Asp Arg Arg Cys Gln Leu Asn Val Leu
    130                 135                 140
Asp Asn Lys Lys Arg Thr Ala Leu Thr Lys Ala Val Gln Cys Gln Glu
145                 150                 155                 160
Asp Glu Cys Ala Leu Met Leu Leu Glu His Gly Thr Asp Pro Asn Ile
                165                 170                 175
Pro Asp Glu Tyr Gly Asn Thr Thr Leu His Tyr Ala Val Tyr Asn Glu
            180                 185                 190
Asp Lys Leu Met Ala Lys Ala Leu Leu Leu Tyr Gly Ala Asp Ile Glu
        195                 200                 205
Ser Lys Asn Lys His Gly Leu Thr Pro Leu Leu Leu Gly Ile His Glu
    210                 215                 220
Gln Lys Gln Gln Val Val Lys Phe Leu Ile Lys Lys Lys Ala Asn Leu
225                 230                 235                 240
Asn Ala Leu Asp Arg Tyr Gly Arg Thr Ala Leu Ile Leu Ala Val Cys
                245                 250                 255
Cys Gly Ser Ala Ser Ile Val Ser Pro Leu Leu Glu Gln Asn Val Asp
            260                 265                 270
Val Ser Ser Gln Asp Leu Glu Arg Arg Pro Glu Ser Met Leu Phe Leu
        275                 280                 285
Val Ile Ile Met
    290
```

```
&lt;210&gt; 533
&lt;211&gt; 801
&lt;212&gt; DNA
&lt;213&gt; Homo sapiens

&lt;400&gt; 533
atgtacaagc ttcagtgcaa caactgtgct acaaatggag ccacagagag gaaacaagca 60
gcaggctcag gagcagggta tgcgctgcct tcggctctcc aatccatgcc tcagggctcc 120
tatgccactg cacgattctt ggttgccaag aggccaacca caggccatct tgagaaggag 180
tttatgttcc actgcagaaa gcagccagga tcaccatcca ggggacttgg tcttctgtgg 240
ccctggccag acatagaatt tgtgccaagg caggacaagc tcactcagag cagcgtgtta 300
gtacctcaaa tctgtgcgtg ccagacaagg ccaaactggc tcaatgagca accagccacc 360
tctgcagggg tgcgtctgga ggaggtggac cagccaccaa ccttacccag tcaaggaagt 420
ggatggccat gttcccacag cctgagtggc tgccacctga tggctgatat agcaaaggcc 480
ttaggaaaag cagatggccc ttggccctac ctttttgtta gaagaactga tgttccatgt 540
cctgcagcga gtgaggttgg tggctgtgcc cccagctcct ggcacaccct cgcagaggtg 600
actggttgct ctttgagccc tcttagcctt gcccagcatg cacaagcctc agtgctacta 660
ctgtgctaca aatggagcca tataggggaa acgagcagcc atctcaggag caaggtgtat 720
gctgcctttg gggctccag tccttgcctc aagggtctta tgtcactgtg ggcttcttgg 780
ttgccaagag gcagaccata g                                          801

&lt;210&gt; 534
&lt;211&gt; 266
&lt;212&gt; PRT
&lt;213&gt; Homo sapiens
```

<400> 534
Met Tyr Lys Leu Gln Cys Asn Asn Cys Ala Thr Asn Gly Ala Thr Glu
                5   10   15
Arg Lys Gln Ala Ala Gly Ser Gly Ala Gly Tyr Ala Leu Pro Ser Ala
            20   25   30
Leu Gln Ser Met Pro Gln Gly Ser Tyr Ala Thr Ala Arg Phe Leu Val
        35   40   45
Ala Lys Arg Pro Thr Thr Gly His Leu Glu Lys Glu Phe Met Phe His
    50   55   60
Cys Arg Lys Gln Pro Gly Ser Pro Ser Arg Gly Leu Gly Leu Leu Trp
65   70   75   80
Pro Trp Pro Asp Ile Glu Phe Val Pro Arg Gln Asp Lys Leu Thr Gln
                85   90   95
Ser Ser Val Leu Val Pro Gln Ile Cys Ala Cys Gln Thr Arg Pro Asn
            100   105   110
Trp Leu Asn Glu Gln Pro Ala Thr Ser Ala Gly Val Arg Leu Glu Glu
        115   120   125
Val Asp Gln Pro Pro Thr Leu Pro Ser Gln Gly Ser Gly Trp Pro Cys
    130   135   140
Ser His Ser Leu Ser Gly Cys His Leu Met Ala Asp Ile Ala Lys Ala
145   150   155   160
Leu Gly Lys Ala Asp Gly Pro Trp Pro Tyr Leu Phe Val Arg Arg Thr
                165   170   175
Asp Val Pro Cys Pro Ala Ala Ser Glu Val Gly Gly Cys Ala Pro Ser
            180   185   190
Ser Trp His Thr Leu Ala Glu Val Thr Gly Cys Ser Leu Ser Pro Leu
        195   200   205
Ser Leu Ala Gln His Ala Gln Ala Ser Val Leu Leu Leu Cys Tyr Lys
    210   215   220
Trp Ser His Ile Gly Glu Thr Ser Ser His Leu Arg Ser Lys Val Tyr
225   230   235   240
Ala Ala Phe Gly Gly Ser Ser Pro Cys Leu Lys Gly Leu Met Ser Leu
                245   250   255
Trp Ala Ser Trp Leu Pro Arg Gly Arg Pro
            260   265

<210> 535
<211> 6082
<212> DNA
<213> Homo sapiens

<400> 535
cctccactat tacagcttat aggaaattac aatccacttt acaggcctca aaggttcatt 60
ctggccgagc ggacaggcgt ggcggccgga gccccagcat ccctgcttga ggtccaggag 120
cggagcccgc ggccactgcc gcctgatcag cgcgaccccg gcccgcgccc gccccgcccg 180
gcaagatgct gcccgtgtac caggaggtga agcccaaccc gctgcaggac gcgaacctct 240
gctcacgcgt gttcttctgg tggctcaatc ccttgtttaa aattggccat aaacggagat 300
tagaggaaga tgatatgtat tcagtgctgc cagaagaccg ctcacagcac cttggagagg 360
agttgcaagg gttctgggat aaagaagttt taagagctga gaatgacgca cagaagcctt 420
ctttaacaag agcaatcata aagtgttact ggaaatctta tttagttttg ggaattttta 480
cgttaattga ggaaagtgcc aaagtaatcc agcccatatt tttgggaaaa attattaatt 540
attttgaaaa ttatgatccc atggattctg tggctttgaa cacagcgtac gcctatgcca 600
cggtgctgac tttttgcacg ctcattttgg ctatactgca tcacttatat ttttatcacg 660
ttcagtgtgc tgggatgagg ttacgagtag ccatgtgcca tatgatttat cggaaggcac 720
ttcgtcttag taacatggcc atggggaaga caaccacagg ccagatagtc aatctgctgt 780
ccaatgatgt gaacaagttt gatcaggtga cagtgttctt acacttcctg tgggcaggac 840

cactgcaggc gatcgcagtg actgccctac tctggatgga gataggaata tcgtgccttg 900
ctgggatggc agttctaatc attctcctgc ccttgcaaag ctgttttggg aagttgttct 960
catcactgag gagtaaaact gcaactttca cggatgccag gatcaggacc atgaatgaag 1020
ttataactgg tataaggata ataaaaatgt acgcctggga aaagtcattt tcaaatctta 1080
ttaccaattt gagaaagaag gagatttcca agattctgag aagttcctgc ctcaggggga 1140
tgaatttggc ttcgtttttc agtgcaagca aaatcatcgt gtttgtgacc ttcaccacct 1200
acgtgctcct cggcagtgtg atcacagcca gccgcgtgtt cgtggcagtg acgctgtatg 1260
gggctgtgcg gctgacggtt accctcttct tcccctcagc cattgagagg gtgtcagagg 1320
caatcgtcag catccgaaga atccagacct tttgctact tgatgagata tcacagcgca 1380
accgtcagct gccgtcagat ggtaaaaaga tggtgcatgt gcaggatttt actgcttttt 1440
gggataaggc atcagagacc ccaactctac aaggcctttc ctttactgtc agacctggcg 1500
aattgttagc tgtggtcggc cccgtgggag cagggaagtc atcactgtta agtgccgtgc 1560
tcggggaatt ggccccaagt cacgggctgg tcagcgtgca tggaagaatt gcctatgtgt 1620
ctcagcagcc ctgggtgttc tcgggaactc tgaggagtaa tattttattt gggaagaaat 1680
acgaaaagga acgatatgaa aaagtcataa aggcttgtgc tctgaaaaag gatttacagc 1740
tgttggagga tggtgatctg actgtgatag gagatcgggg aaccacgctg agtggagggc 1800
agaaagcacg ggtaaacctt gcaagagcag tgtatcaaga tgctgacatc tatctcctgg 1860
acgatcctct cagtgcagta gatgcggaag ttagcagaca cttgttcgaa ctgtgtattt 1920
gtcaaatttt gcatgagaag atcacaattt tagtgactca tcagttgcag tacctcaaag 1980
ctgcaagtca gattctgata ttgaaagatg gtaaaatggt gcagaagggg acttacactg 2040
agttcctaaa atctggtata gattttggct ccctttttaa gaaggataat gaggaaagtg 2100
aacaacctcc agttccagga actcccacac taaggaatcg taccttctca gagtcttcgg 2160
tttggtctca acaatcttct agaccctcct tgaaagatgg tgctctggag agccaagata 2220
cagagaatgt cccagttaca ctatcagagg agaaccgttc tgaaggaaaa gttggttttc 2280
aggcctataa gaattacttc agagctggtg ctcactggat tgtcttcatt ttccttattc 2340
tcctaaacac tgcagctcag gttgcctatg tgcttcaaga ttggtggctt tcatactggg 2400
caaacaaaca aagtatgcta aatgtcactg taaatggagg aggaaatgta accgagaagc 2460
tagatcttaa ctggtactta ggaatttatt caggtttaac tgtagctacc gttctttttg 2520
gcatagcaag atctctattg gtattctacg tccttgttaa ctcttcacaa actttgcaca 2580
acaaaatgtt tgagtcaatt ctgaaagctc cggtattatt ctttgataga aatccaatag 2640
gaagaatttt aaatcgtttc tccaaagaca ttggacactt ggatgatttg ctgccgctga 2700
cgtttttaga tttcatccag acattgctac aagtggttgg tgtggtctct gtggctgtgg 2760
ccgtgattcc ttggatcgca atacccttgg ttccccttgg aatcatttc attttcttc 2820
ggcgatattt tttggaaacg tcaagagatg tgaagcgcct ggaatctaca actcggagtc 2880
cagtgttttc ccacttgtca tcttctctcc aggggctctg gaccatccgg gcatacaaag 2940
cagaagagag gtgtcaggaa ctgtttgatg cacaccagga tttacattca gaggcttggt 3000
tcttgttttt gacaacgtcc cgctggttcg ccgtccgtct ggatgccatc tgtgccatgt 3060
ttgtcatcat cgttgccttt gggtccctga ttctggcaaa aactctggat gccgggcagg 3120
ttggtttggc actgtcctat gccctcacgc tcatggggat gtttcagtgg tgtgttcgac 3180
aaagtgctga agttgagaat atgatgatct cagtagaaag ggtcattgaa tacacagacc 3240
ttgaaaaaga agcaccttgg gaatatcaga aacgcccacc accagcctgg ccccatgaag 3300
gagtgataat ctttgacaat gtgaacttca tgtacagtcc aggtgggcct ctggtactga 3360
agcatctgac agcactcatt aaatcacaag aaaaggttgg cattgtggga agaaccggag 3420
ctggaaaaag ttccctcatc tcagcccttt ttagattgtc agaacccgaa ggtaaaattt 3480
ggattgataa gatcttgaca actgaaattg gacttcacga tttaaggaag aaaatgtcaa 3540
tcatacctca ggaacctgtt ttgttcactg gaacaatgag gaaaaacctg gatcccttta 3600
atgagcacac ggatgaggaa ctgtggaatg ccttacaaga ggtacaactt aaagaaacca 3660
ttgaagatct tcctggtaaa atggatactg aattagcaga atcaggatcc aattttagtg 3720
ttggacaaag acaactggtg tgccttgcca gggcaattct caggaaaaat cagatattga 3780
ttattgatga agcgacggca aatgtggatc caagaactga tgagttaata caaaaaaaat 3840
ccgggagaaa tttgcccact gcaccgtgct aaccattgca cacagattga acaccattat 3900
tgacagcgac aagataatgg ttttagattc aggaagactg aaagaatatg atgagccgta 3960
tgttttgctg caaaataaag agagcctatt ttacaagatg gtgcaacaac tgggcaaggc 4020
agaagccgct gccctcactg aaacagcaaa acaggtatac ttcaaaagaa attatccaca 4080
tattggtcac actgaccaca tggttacaaa cacttccaat ggacagccct cgaccttaac 4140
tattttcgag acagcactgt gaatccaacc aaaatgtcaa gtccgttccg aaggcatttg 4200
ccactagttt ttggactatg taaaccacat tgtacttttt tttactttgg caacaaatat 4260
ttatacatac aagatgctag ttcatttgaa tatttctccc aacttatcca aggatctcca 4320

gctctaacaa aatggtttat ttttatttaa atgtcaatag ttgtttttta aaatccaaat 4380
cagaggtgca ggccaccagt taaatgccgt ctatcaggtt ttgtgcctta agagactaca 4440
gagtcaaagc tcatttttaa aggagtagga cagagttgtc acaggttttt gttgttgttt 4500
ttattgcccc caaaattaca tgttaatttc catttatatc aggattcta tttacttgaa 4560
gactgtgaag ttgccatttt gtctcattgt tttctttgac ataactagga tccattattt 4620
cccctgaagg cttcttgtta gaaaatagta cagttacaac caataggaac aacaaaaaga 4680
aaaagtttgt gacattgtag tagggagtgt gtacccctta ctccccatca aaaaaaaaaa 4740
tggatacatg gttaaaggat agaagggcaa tattttatca tatgttctaa aagagaagga 4800
agagaaaata ctactttctc aaaatggaag cccttaaagg tgctttgata ctgaaggaca 4860
caaatgtgac cgtccatcct cctttagagt tgcatgactt ggacacggta actgttgcag 4920
ttttagactc agcattgtga cacttcccaa gaaggccaaa cctctaaccg acattcctga 4980
aatacgtggc attattcttt tttggatttc tcatttatgg aaggctaacc ctctgttgac 5040
tgtaagcctt ttggtttggg ctgtattgaa atcctttcta aattgcatga ataggctctg 5100
ctaacgtgat gagacaaact gaaaattatt gcaagcattg actataatta tgcagtacgt 5160
tctcaggatg catccagggg ttcattttca tgagcctgtc caggttagtt tactcctgac 5220
cactaatagc attgtcattt gggctttctg ttgaatgaat caacaaacca caatacttcc 5280
tgggaccttt tgtactttat ttgaactatg agtctttaat ttttcctgat gatggtggct 5340
gtaatatgtt gagttcagtt tactaaaggt tttactatta tggtttgaag tggagtctca 5400
tgacctctca gaataaggtg tcacctccct gaaattgcat atatgtatat agacatgcac 5460
acgtgtgcat ttgtttgtat acatatattt gtccttcgta tagcaagttt tttgctcatc 5520
agcagagagc aacagatgtt ttattgagtg aagccttaaa aagcacacac cacacacagc 5580
taactgccaa aatacattga ccgtagtagc tgttcaactc ctagtactta gaaatacacg 5640
tatggttaat gttcagtcca acaaaccaca cacagtaaat gtttattaat agtcatggtt 5700
cgtattttag gtgactgaaa ttgcaacagt gatcataatg aggtttgtta aaatgatagc 5760
tatattcaaa atgtctatat gtttatttgg acttttgagg ttaaagacag tcatataaac 5820
gtcctgtttc tgttttaatg ttatcataga atttttaat gaaactaaat tcaattgaaa 5880
taaatgatag ttttcatctc caaaaaaaaa aaaaaaaagg gcggccgctc gagtctagag 5940
ggcccgttta aacccgctga tcagcctcga ctgtgccttc tagttgccag ccatctgttg 6000
tttgcccctc ccccgtgcct tccttgaccc tggaaggtgc cactcccact gtcctttcct 6060
aataaaatga ggaaattgca tc 6082

<210> 536
<211> 6140
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(6140)
<223> n=A,T,C or G

<400> 536
cagtggcgca gtctcagctc actgcagcct ccacctcctg tgttcaagca gtcctcctgc 60
ctcagccacc agactagcag gtctcccccg cctctttctt ggaaggacac ttgccattgg 120
atttaggacc cacttggata atccaggatg atgtcttcac tccaacatcc tcagtttaat 180
tccatgtgca aataccсttt tcccaaataa cattcaattc tttaccagga aaggtggctc 240
aatcccttgt ttaaaattgg ccataaacgg agattagagg aagatgatat gtattcagtg 300
ctgccagaag accgctcaca gcaccttgga gaggagttgc aagggttctg ggataaagaa 360
gttttaagag ctgagaatga cgcacagaag ccttctttaa caagagcaat cataaagtgt 420
tactggaaat cttatttagt tttgggaatt tttacgttaa ttgaggaaag tgccaaagta 480
atccagccca tatttttggg aaaaattatt aattattttg aaaattatga tcccatggat 540
tctgtggctt tgaacacagc gtacgcctat gccacggtgc tgacttttg cacgctcatt 600
ttggctatac tgcatcactt atatttttat cacgttcagt gtgctgggat gaggttacga 660
gtagccatgt gccatatgat ttatcggaag gcacttcgtc ttagtaacat ggccatgggg 720
aagacaacca caggccagat agtcaatctg ctgtccaatg atgtgaacaa gtttgatcag 780
gtgacagtgt tcttacactt cctgtgggca ggaccactgc aggcgatcgc agtgactgcc 840
ctactctgga tggagatagg aatatcgtgc cttgctggga tggcagttct aatcattctc 900
ctgcccttgc aaagctgttt tgggaagttg ttctcatcac tgaggagtaa aactgcaact 960

```
ttcacggatg ccaggatcag gaccatgaat gaagttataa ctggtataag gataataaaa 1020
atgtacgcct gggaaaagtc attttcaaat cttattacca atttgagaaa gaaggagatt 1080
tccaagattc tgagaagttc ctgcctcagg gggatgaatt tggcttcgtt tttcagtgca 1140
agcaaaatca tcgtgtttgt gaccttcacc acctacgtgc tcctcggcag tgtgatcaca 1200
gccagccgcg tgttcgtggc agtgacgctg tatggggctg tgcggctgac ggttaccctc 1260
ttcttcccct cagccattga gagggtgtca gaggcaatcg tcagcatccg aagaatccag 1320
accttttgc tacttgatga gatatcacag cgcaaccgtc agctgccgtc agatggtaaa 1380
aagatggtgc atgtgcagga ttttactgct tttgggata aggcatcaga gaccccaact 1440
ctacaaggcc tttcctttac tgtcagacct ggcgaattgt tagctgtggt cggccccgtg 1500
ggagcaggga agtcatcact gttaagtgcc gtgctcgggg aattggcccc aagtcacggg 1560
ctggtcagcg tgcatggaag aattgcctat gtgtctcagc agccctgggt gttctcggga 1620
actctgagga gtaatatttt atttgggaag aaatacgaaa aggaacgata tgaaaaagtc 1680
ataaaggctt gtgctctgaa aaaggattta cagctgttgg aggatggtga tctgactgtg 1740
ataggagatc ggggaaccac gctgagtgga gggcagaaag cacgggtaaa ccttgcaaga 1800
gcagtgtatc aagatgctga catctatctc ctggacgatc ctctcagtgc agtagatgcg 1860
gaagttagca gacacttgtt cgaactgtgt atttgtcaaa ttttgcatga gaagatcaca 1920
attttagtga ctcatcagtt gcagtacctc aaagctgcaa gtcagattct gatattgaaa 1980
gatggtaaaa tggtgcagaa ggggacttac actgagttcc taaaatctgg tatagatttt 2040
ggctcccttt taaagaagga taatgaggaa agtgaacaac ctccagttcc aggaactccc 2100
acactaagga atcgtacctt ctcagagtct tcggtttggt ctcaacaatc ttctagaccc 2160
tccttgaaag atggtgctct ggagagccaa gatacagaga atgtcccagt tacactatca 2220
gaggagaacc gttctgaagg aaaagttggt tttcaggcct ataagaatta cttcagagct 2280
ggtgctcact ggattgtctt cattttcctt attctcctaa acactgcagc tcaggttgcc 2340
tatgtgcttc aagattggtg gctttcatac tgggcaaaca aacaaagtat gctaaatgtc 2400
actgtaaatg gaggaggaaa tgtaaccgag aagctagatc ttaactggta cttaggaatt 2460
tattcaggtt taactgtagc taccgttctt tttggcatag caagatctct attggtattc 2520
tacgtccttg ttaactcttc acaaactttg cacaacaaaa tgtttgagtc aattctgaaa 2580
gctccggtat tattctttga tagaaatcca ataggaagaa ttttaaatcg tttctccaaa 2640
gacattggac acttggatga tttgctgccg ctgacgtttt tagatttcat ccagacattg 2700
ctacaagtgg ttggtgtggt ctctgtggct gtggccgtga ttccttggat cgcaataccc 2760
ttggttcccc ttggaatcat tttcattttt cttcggcgat atttttggaa aacgtcaaga 2820
gatgtgaagc gcctggaatc tacaactcgg agtccagtgt tttcccactt gtcatcttct 2880
ctccaggggc tctggaccat ccgggcatac aaagcagaag agaggtgtca ggaactgttt 2940
gatgcacacc aggatttaca ttcagaggct tggttcttgt ttttgacaac gtcccgctgg 3000
ttcgccgtcc gtctggatgc catctgtgcc atgtttgtca tcatcgttgc ctttgggtcc 3060
ctgattctgg caaaaactct ggatgccggg caggttggtt tggcactgtc ctatgccctc 3120
acgctcatgg ggatgtttca gtggtgtgtt cgacaaagtg ctgaagttga gaatatgatg 3180
atctcagtag aaagggtcat tgaatacaca gaccttgaaa aagaagcacc ttgggaatat 3240
cagaaacgcc caccaccagc ctggccccat gaaggagtga taatctttga caatgtgaac 3300
ttcatgtaca gtccaggtgg gcctctggta ctgaagcatc tgacagcact cattaaatca 3360
caagaaaagg ttggcattgt gggaagaacc ggagctggaa aagttccct catctcagcc 3420
ctttttagat tgtcagaacc cgaaggtaaa atttggattg ataagatctt gacaactgaa 3480
attggacttc acgatttaag gaagaaaatg tcaatcatac ctcaggaacc tgttttgttc 3540
actggaacaa tgaggaaaaa cctggatccc tttaatgagc acacggatga ggaactgtgg 3600
aatgccttac aagaggtaca acttaaagaa accattgaag atcttcctgg taaaatggat 3660
actgaattag cagaatcagg atccaatttt agtgttggac aaagacaact ggtgtgcctt 3720
gccagggcaa ttctcaggaa aaatcagata ttgattattg atgaagcgac ggcaaatgtg 3780
gatccaagaa ctgatgagtt aatacaaaaa aaaatccggg agaaatttgc ccactgcacc 3840
gtgctaacca ttgcacacag attgaacacc attattgaca gcgacaagat aatggtttta 3900
gattcaggaa gactgaaaga atatgatgag ccgtatgttt tgctgcaaaa taaagagagc 3960
ctattttaca agatggtgca acaactgggc aaggcagaag ccgctgccct cactgaaaca 4020
gcaaaacaga gatggggttt caccatgttg gccaggctgg tctcaaactc ctgacctcaa 4080
gtgatccacc tgccttggcc tcccaaactg ctgagattac aggtgtgagc caccacgccc 4140
agcctgagta tacttcaaaa gaaattatcc acatattggt cacactgacc acatggttac 4200
aaacacttcc aatggacagc cctcgacctt aactattttc gagacagcac tgtgaatcca 4260
accaaaatgt caagtccgtt ccgaaggcat ttgccactag tttttggact atgtaaacca 4320
cattgtactt ttttttactt tggcaacaaa tatttataca tacaagatgc tagttcattt 4380
gaatatttct cccaacttat ccaaggatct ccagctctaa caaaatggtt tatttttatt 4440
```

```
taaatgtcaa tagtkgkttt ttaaaatcca aatcagaggt gcaggccacc agttaaatgc 4500
cgtctatcag gttttgtgcc ttaagagact acagnagtca gaagctcatt tttaaaggag 4560
taggacagag ttgtcacagg tttttgttgg tgtttktatt gcccccaaaa ttacatgtta 4620
atttccattt atatcagggg attctattta cttgaagact gtgaagttgc cattttgtct 4680
cattgttttc tttgacatam ctaggatcca ttatttcccc tgaaggcttc ttgkagaaaa 4740
tagtacagtt acaaccaata ggaactamca aaaagaaaaa gtttgtgaca ttgtagtagg 4800
gagtgtgtac cccttactcc ccatcaaaaa aaaaaatgga tacatggtta aaggatagaa 4860
gggcaatatt ttatcatatg ttctaaaaga gaaggaagag aaaatactac tttctcaaaa 4920
tggaagccct taaaggtgct ttgatactga aggacacaaa tgtgaccgtc catcctcctt 4980
tagagttgca tgacttggac acggtaactg ttgcagtttt agactcagca ttgtgacact 5040
tcccaagaag gccaaacctc taaccgacat tcctgaaata cgtggcatta ttcttttttg 5100
gatttctcat ttaggaaggc taaccctctg ttgamtgtam kcctttttggt ttgggctgta 5160
ttgaaatcct ttctaaattg catgaatagg ctctgctaac cgtgatgaga caaactgaaa 5220
attattgcaa gcattgacta taattatgca gtacgttctc aggatgcatc caggggttca 5280
ttttcatgag cctgtccagg ttagtttact cctgaccact aatagcattg tcatttgggc 5340
tttctgttga atgaatcaac aaaccacaat acttcctggg acctttttgta ctttatttga 5400
actatgagtc tttaattttt cctgatgatg gtggctgtaa tatgttgagt tcagtttact 5460
aaaggtttta ctattatggt ttgaagggag tctcatgacc tctcagaaaa ggtgcacctc 5520
cctgaaattg catatatgta tatagacatg cacacgtgtg catttgtttg tatacatata 5580
tttgtccttc gtatagcaag ttttttgctc atcagcagag agcaacagat gttttattga 5640
gtgaagcctt aaaaagcaca caccacacac agctaactgc caaaatacat tgaccgtagt 5700
agctgttcaa ctcctagtac ttagaaatac acgtatggtt aatgttcagt ccaacaaacc 5760
acacacagta aatgtttatt aatagtcatg gttcgtattt taggtgactg aaattgcaac 5820
agtgatcata atgaggtttg ttaaaatgat agctatattc aaaatgtcta tatgtttatt 5880
tggacttttg aggttaaaga cagtcatata aacgtcctgt ttctgtttta atgttatcat 5940
agaatttttt aatgaaacta aattcaattg aaataaatga tagttttcat ctccaaaaaa 6000
aaaaaaaaag ggcggcccgc tcgagtctag agggcccggt ttaaacccgc tgatcagcct 6060
cgactgtgcc ttctagttgc cagccatctg ttgtttggcc ctcccccgtg ccttccttga 6120
ccctggaagg ggccactccc                                             6140
```

<210> 537
<211> 1228
<212> PRT
<213> Homo sapiens

<400> 537

```
Met Leu Pro Val Tyr Gln Glu Val Lys Pro Asn Pro Leu Gln Asp Ala
                5                   10                  15
Asn Leu Cys Ser Arg Val Phe Phe Trp Trp Leu Asn Pro Leu Phe Lys
            20                  25                  30
Ile Gly His Lys Arg Arg Leu Glu Glu Asp Asp Met Tyr Ser Val Leu
        35                  40                  45
Pro Glu Asp Arg Ser Gln His Leu Gly Glu Glu Leu Gln Gly Phe Trp
    50                  55                  60
Asp Lys Glu Val Leu Arg Ala Glu Asn Asp Ala Gln Lys Pro Ser Leu
65                  70                  75                  80
Thr Arg Ala Ile Ile Lys Cys Tyr Trp Lys Ser Tyr Leu Val Leu Gly
                85                  90                  95
Ile Phe Thr Leu Ile Glu Glu Ser Ala Lys Val Ile Gln Pro Ile Phe
            100                 105                 110
Leu Gly Lys Ile Ile Asn Tyr Phe Glu Asn Tyr Asp Pro Met Asp Ser
        115                 120                 125
Val Ala Leu Asn Thr Ala Tyr Ala Tyr Ala Thr Val Leu Thr Phe Cys
    130                 135                 140
Thr Leu Ile Leu Ala Ile Leu His His Leu Tyr Phe Tyr His Val Gln
145                 150                 155                 160
Cys Ala Gly Met Arg Leu Arg Val Ala Met Cys His Met Ile Tyr Arg
                165                 170                 175
```

```
Lys Ala Leu Arg Leu Ser Asn Met Ala Met Gly Lys Thr Thr Thr Gly
            180                 185                 190
Gln Ile Val Asn Leu Leu Ser Asn Asp Val Asn Lys Phe Asp Gln Val
        195                 200                 205
Thr Val Phe Leu His Phe Leu Trp Ala Gly Pro Leu Gln Ala Ile Ala
    210                 215                 220
Val Thr Ala Leu Leu Trp Met Glu Ile Gly Ile Ser Cys Leu Ala Gly
225                 230                 235                 240
Met Ala Val Leu Ile Ile Leu Leu Pro Leu Gln Ser Cys Phe Gly Lys
                245                 250                 255
Leu Phe Ser Ser Leu Arg Ser Lys Thr Ala Thr Phe Thr Asp Ala Arg
            260                 265                 270
Ile Arg Thr Met Asn Glu Val Ile Thr Gly Ile Arg Ile Ile Lys Met
        275                 280                 285
Tyr Ala Trp Glu Lys Ser Phe Ser Asn Leu Ile Thr Asn Leu Arg Lys
    290                 295                 300
Lys Glu Ile Ser Lys Ile Leu Arg Ser Ser Cys Leu Arg Gly Met Asn
305                 310                 315                 320
Leu Ala Ser Phe Phe Ser Ala Ser Lys Ile Ile Val Phe Val Thr Phe
                325                 330                 335
Thr Thr Tyr Val Leu Leu Gly Ser Val Ile Thr Ala Ser Arg Val Phe
            340                 345                 350
Val Ala Val Thr Leu Tyr Gly Ala Val Arg Leu Thr Val Thr Leu Phe
        355                 360                 365
Phe Pro Ser Ala Ile Glu Arg Val Ser Glu Ala Ile Val Ser Ile Arg
    370                 375                 380
Arg Ile Gln Thr Phe Leu Leu Leu Asp Glu Ile Ser Gln Arg Asn Arg
385                 390                 395                 400
Gln Leu Pro Ser Asp Gly Lys Lys Met Val His Val Gln Asp Phe Thr
                405                 410                 415
Ala Phe Trp Asp Lys Ala Ser Glu Thr Pro Thr Leu Gln Gly Leu Ser
            420                 425                 430
Phe Thr Val Arg Pro Gly Glu Leu Leu Ala Val Val Gly Pro Val Gly
        435                 440                 445
Ala Gly Lys Ser Ser Leu Leu Ser Ala Val Leu Gly Glu Leu Ala Pro
    450                 455                 460
Ser His Gly Leu Val Ser Val His Gly Arg Ile Ala Tyr Val Ser Gln
465                 470                 475                 480
Gln Pro Trp Val Phe Ser Gly Thr Leu Arg Ser Asn Ile Leu Phe Gly
                485                 490                 495
Lys Lys Tyr Glu Lys Glu Arg Tyr Glu Lys Val Ile Lys Ala Cys Ala
            500                 505                 510
Leu Lys Lys Asp Leu Gln Leu Leu Glu Asp Gly Asp Leu Thr Val Ile
        515                 520                 525
Gly Asp Arg Gly Thr Thr Leu Ser Gly Gly Gln Lys Ala Arg Val Asn
    530                 535                 540
Leu Ala Arg Ala Val Tyr Gln Asp Ala Asp Ile Tyr Leu Leu Asp Asp
545                 550                 555                 560
Pro Leu Ser Ala Val Asp Ala Glu Val Ser Arg His Leu Phe Glu Leu
                565                 570                 575
Cys Ile Cys Gln Ile Leu His Glu Lys Ile Thr Ile Leu Val Thr His
            580                 585                 590
Gln Leu Gln Tyr Leu Lys Ala Ala Ser Gln Ile Leu Ile Leu Lys Asp
        595                 600                 605
Gly Lys Met Val Gln Lys Gly Thr Tyr Thr Glu Phe Leu Lys Ser Gly
    610                 615                 620
Ile Asp Phe Gly Ser Leu Leu Lys Lys Asp Asn Glu Glu Ser Glu Gln
625                 630                 635                 640
```

```
Pro Pro Val Pro Gly Thr Pro Thr Leu Arg Asn Arg Thr Phe Ser Glu
                645                 650                 655
Ser Ser Val Trp Ser Gln Gln Ser Ser Arg Pro Ser Leu Lys Asp Gly
            660                 665                 670
Ala Leu Glu Ser Gln Asp Thr Glu Asn Val Pro Val Thr Leu Ser Glu
        675                 680                 685
Glu Asn Arg Ser Glu Gly Lys Val Gly Phe Gln Ala Tyr Lys Asn Tyr
    690                 695                 700
Phe Arg Ala Gly Ala His Trp Ile Val Phe Ile Phe Leu Ile Leu Leu
705                 710                 715                 720
Asn Thr Ala Ala Gln Val Ala Tyr Val Leu Gln Asp Trp Trp Leu Ser
                725                 730                 735
Tyr Trp Ala Asn Lys Gln Ser Met Leu Asn Val Thr Val Asn Gly Gly
            740                 745                 750
Gly Asn Val Thr Glu Lys Leu Asp Leu Asn Trp Tyr Leu Gly Ile Tyr
        755                 760                 765
Ser Gly Leu Thr Val Ala Thr Val Leu Phe Gly Ile Ala Arg Ser Leu
    770                 775                 780
Leu Val Phe Tyr Val Leu Val Asn Ser Ser Gln Thr Leu His Asn Lys
785                 790                 795                 800
Met Phe Glu Ser Ile Leu Lys Ala Pro Val Leu Phe Phe Asp Arg Asn
                805                 810                 815
Pro Ile Gly Arg Ile Leu Asn Arg Phe Ser Lys Asp Ile Gly His Leu
            820                 825                 830
Asp Asp Leu Leu Pro Leu Thr Phe Leu Asp Phe Ile Gln Thr Leu Leu
        835                 840                 845
Gln Val Val Gly Val Val Ser Val Ala Val Ala Val Ile Pro Trp Ile
    850                 855                 860
Ala Ile Pro Leu Val Pro Leu Gly Ile Ile Phe Ile Phe Leu Arg Arg
865                 870                 875                 880
Tyr Phe Leu Glu Thr Ser Arg Asp Val Lys Arg Leu Glu Ser Thr Thr
                885                 890                 895
Arg Ser Pro Val Phe Ser His Leu Ser Ser Ser Leu Gln Gly Leu Trp
            900                 905                 910
Thr Ile Arg Ala Tyr Lys Ala Glu Glu Arg Cys Gln Glu Leu Phe Asp
        915                 920                 925
Ala His Gln Asp Leu His Ser Glu Ala Trp Phe Leu Phe Leu Thr Thr
    930                 935                 940
Ser Arg Trp Phe Ala Val Arg Leu Asp Ala Ile Cys Ala Met Phe Val
945                 950                 955                 960
Ile Ile Val Ala Phe Gly Ser Leu Ile Leu Ala Lys Thr Leu Asp Ala
                965                 970                 975
Gly Gln Val Gly Leu Ala Leu Ser Tyr Ala Leu Thr Leu Met Gly Met
            980                 985                 990
Phe Gln Trp Cys Val Arg Gln Ser Ala Glu Val Glu Asn Met Met Ile
        995                 1000                1005
Ser Val Glu Arg Val Ile Glu Tyr Thr Asp Leu Glu Lys Glu Ala Pro
    1010                1015                1020
Trp Glu Tyr Gln Lys Arg Pro Pro Pro Ala Trp Pro His Glu Gly Val
1025                1030                1035                1040
Ile Ile Phe Asp Asn Val Asn Phe Met Tyr Ser Pro Gly Gly Pro Leu
                1045                1050                1055
Val Leu Lys His Leu Thr Ala Leu Ile Lys Ser Gln Glu Lys Val Gly
            1060                1065                1070
Ile Val Gly Arg Thr Gly Ala Gly Lys Ser Ser Leu Ile Ser Ala Leu
        1075                1080                1085
Phe Arg Leu Ser Glu Pro Glu Gly Lys Ile Trp Ile Asp Lys Ile Leu
    1090                1095                1100
```

```
Thr Thr Glu Ile Gly Leu His Asp Leu Arg Lys Lys Met Ser Ile Ile
1105                1110                1115                1120
Pro Gln Glu Pro Val Leu Phe Thr Gly Thr Met Arg Lys Asn Leu Asp
                1125                1130                1135
Pro Phe Asn Glu His Thr Asp Glu Glu Leu Trp Asn Ala Leu Gln Glu
            1140                1145                1150
Val Gln Leu Lys Glu Thr Ile Glu Asp Leu Pro Gly Lys Met Asp Thr
        1155                1160                1165
Glu Leu Ala Glu Ser Gly Ser Asn Phe Ser Val Gly Gln Arg Gln Leu
    1170                1175                1180
Val Cys Leu Ala Arg Ala Ile Leu Arg Lys Asn Gln Ile Leu Ile Ile
1185                1190                1195                1200
Asp Glu Ala Thr Ala Asn Val Asp Pro Arg Thr Asp Glu Leu Ile Gln
                1205                1210                1215
Lys Lys Ser Gly Arg Asn Leu Pro Thr Ala Pro Cys
            1220                1225

<210> 538
<211> 1261
<212> PRT
<213> Homo sapiens

<400> 538
Met Tyr Ser Val Leu Pro Glu Asp Arg Ser Gln His Leu Gly Glu Glu
                5                   10                  15
Leu Gln Gly Phe Trp Asp Lys Glu Val Leu Arg Ala Glu Asn Asp Ala
            20                  25                  30
Gln Lys Pro Ser Leu Thr Arg Ala Ile Ile Lys Cys Tyr Trp Lys Ser
        35                  40                  45
Tyr Leu Val Leu Gly Ile Phe Thr Leu Ile Glu Glu Ser Ala Lys Val
    50                  55                  60
Ile Gln Pro Ile Phe Leu Gly Lys Ile Ile Asn Tyr Phe Glu Asn Tyr
65                  70                  75                  80
Asp Pro Met Asp Ser Val Ala Leu Asn Thr Ala Tyr Ala Tyr Ala Thr
                85                  90                  95
Val Leu Thr Phe Cys Thr Leu Ile Leu Ala Ile Leu His His Leu Tyr
            100                 105                 110
Phe Tyr His Val Gln Cys Ala Gly Met Arg Leu Arg Val Ala Met Cys
        115                 120                 125
His Met Ile Tyr Arg Lys Ala Leu Arg Leu Ser Asn Met Ala Met Gly
    130                 135                 140
Lys Thr Thr Thr Gly Gln Ile Val Asn Leu Leu Ser Asn Asp Val Asn
145                 150                 155                 160
Lys Phe Asp Gln Val Thr Val Phe Leu His Phe Leu Trp Ala Gly Pro
                165                 170                 175
Leu Gln Ala Ile Ala Val Thr Ala Leu Leu Trp Met Glu Ile Gly Ile
            180                 185                 190
Ser Cys Leu Ala Gly Met Ala Val Leu Ile Ile Leu Leu Pro Leu Gln
        195                 200                 205
Ser Cys Phe Gly Lys Leu Phe Ser Ser Leu Arg Ser Lys Thr Ala Thr
    210                 215                 220
Phe Thr Asp Ala Arg Ile Arg Thr Met Asn Glu Val Ile Thr Gly Ile
225                 230                 235                 240
Arg Ile Ile Lys Met Tyr Ala Trp Glu Lys Ser Phe Ser Asn Leu Ile
                245                 250                 255
Thr Asn Leu Arg Lys Lys Glu Ile Ser Lys Ile Leu Arg Ser Ser Cys
            260                 265                 270
Leu Arg Gly Met Asn Leu Ala Ser Phe Phe Ser Ala Ser Lys Ile Ile
```

```
        275                 280                 285
Val Phe Val Thr Phe Thr Thr Tyr Val Leu Leu Gly Ser Val Ile Thr
    290                 295                 300
Ala Ser Arg Val Phe Val Ala Val Thr Leu Tyr Gly Ala Val Arg Leu
305                 310                 315                 320
Thr Val Thr Leu Phe Phe Pro Ser Ala Ile Glu Arg Val Ser Glu Ala
                325                 330                 335
Ile Val Ser Ile Arg Arg Ile Gln Thr Phe Leu Leu Leu Asp Glu Ile
            340                 345                 350
Ser Gln Arg Asn Arg Gln Leu Pro Ser Asp Gly Lys Lys Met Val His
        355                 360                 365
Val Gln Asp Phe Thr Ala Phe Trp Asp Lys Ala Ser Glu Thr Pro Thr
    370                 375                 380
Leu Gln Gly Leu Ser Phe Thr Val Arg Pro Gly Glu Leu Leu Ala Val
385                 390                 395                 400
Val Gly Pro Val Gly Ala Gly Lys Ser Ser Leu Leu Ser Ala Val Leu
                405                 410                 415
Gly Glu Leu Ala Pro Ser His Gly Leu Val Ser Val His Gly Arg Ile
            420                 425                 430
Ala Tyr Val Ser Gln Gln Pro Trp Val Phe Ser Gly Thr Leu Arg Ser
        435                 440                 445
Asn Ile Leu Phe Gly Lys Lys Tyr Glu Lys Glu Arg Tyr Glu Lys Val
    450                 455                 460
Ile Lys Ala Cys Ala Leu Lys Lys Asp Leu Gln Leu Leu Glu Asp Gly
465                 470                 475                 480
Asp Leu Thr Val Ile Gly Asp Arg Gly Thr Thr Leu Ser Gly Gly Gln
                485                 490                 495
Lys Ala Arg Val Asn Leu Ala Arg Ala Val Tyr Gln Asp Ala Asp Ile
            500                 505                 510
Tyr Leu Leu Asp Asp Pro Leu Ser Ala Val Asp Ala Glu Val Ser Arg
        515                 520                 525
His Leu Phe Glu Leu Cys Ile Cys Gln Ile Leu His Glu Lys Ile Thr
    530                 535                 540
Ile Leu Val Thr His Gln Leu Gln Tyr Leu Lys Ala Ala Ser Gln Ile
545                 550                 555                 560
Leu Ile Leu Lys Asp Gly Lys Met Val Gln Lys Gly Thr Tyr Thr Glu
                565                 570                 575
Phe Leu Lys Ser Gly Ile Asp Phe Gly Ser Leu Leu Lys Lys Asp Asn
            580                 585                 590
Glu Glu Ser Glu Gln Pro Pro Val Pro Gly Thr Pro Thr Leu Arg Asn
        595                 600                 605
Arg Thr Phe Ser Glu Ser Ser Val Trp Ser Gln Gln Ser Ser Arg Pro
    610                 615                 620
Ser Leu Lys Asp Gly Ala Leu Glu Ser Gln Asp Thr Glu Asn Val Pro
625                 630                 635                 640
Val Thr Leu Ser Glu Glu Asn Arg Ser Glu Gly Lys Val Gly Phe Gln
                645                 650                 655
Ala Tyr Lys Asn Tyr Phe Arg Ala Gly Ala His Trp Ile Val Phe Ile
            660                 665                 670
Phe Leu Ile Leu Leu Asn Thr Ala Ala Gln Val Ala Tyr Val Leu Gln
        675                 680                 685
Asp Trp Trp Leu Ser Tyr Trp Ala Asn Lys Gln Ser Met Leu Asn Val
    690                 695                 700
Thr Val Asn Gly Gly Gly Asn Val Thr Glu Lys Leu Asp Leu Asn Trp
705                 710                 715                 720
Tyr Leu Gly Ile Tyr Ser Gly Leu Thr Val Ala Thr Val Leu Phe Gly
                725                 730                 735
Ile Ala Arg Ser Leu Leu Val Phe Tyr Val Leu Val Asn Ser Ser Gln
```

```
            740                 745                 750
Thr Leu His Asn Lys Met Phe Glu Ser Ile Leu Lys Ala Pro Val Leu
        755                 760                 765
Phe Phe Asp Arg Asn Pro Ile Gly Arg Ile Leu Asn Arg Phe Ser Lys
    770                 775                 780
Asp Ile Gly His Leu Asp Asp Leu Leu Pro Leu Thr Phe Leu Asp Phe
785                 790                 795                 800
Ile Gln Thr Leu Leu Gln Val Val Gly Val Val Ser Val Ala Val Ala
                805                 810                 815
Val Ile Pro Trp Ile Ala Ile Pro Leu Val Pro Leu Gly Ile Ile Phe
            820                 825                 830
Ile Phe Leu Arg Arg Tyr Phe Leu Glu Thr Ser Arg Asp Val Lys Arg
        835                 840                 845
Leu Glu Ser Thr Thr Arg Ser Pro Val Phe Ser His Leu Ser Ser Ser
    850                 855                 860
Leu Gln Gly Leu Trp Thr Ile Arg Ala Tyr Lys Ala Glu Glu Arg Cys
865                 870                 875                 880
Gln Glu Leu Phe Asp Ala His Gln Asp Leu His Ser Glu Ala Trp Phe
                885                 890                 895
Leu Phe Leu Thr Thr Ser Arg Trp Phe Ala Val Arg Leu Asp Ala Ile
            900                 905                 910
Cys Ala Met Phe Val Ile Ile Val Ala Phe Gly Ser Leu Ile Leu Ala
        915                 920                 925
Lys Thr Leu Asp Ala Gly Gln Val Gly Leu Ala Leu Ser Tyr Ala Leu
    930                 935                 940
Thr Leu Met Gly Met Phe Gln Trp Cys Val Arg Gln Ser Ala Glu Val
945                 950                 955                 960
Glu Asn Met Met Ile Ser Val Glu Arg Val Ile Glu Tyr Thr Asp Leu
                965                 970                 975
Glu Lys Glu Ala Pro Trp Glu Tyr Gln Lys Arg Pro Pro Pro Ala Trp
            980                 985                 990
Pro His Glu Gly Val Ile Ile Phe Asp Asn Val Asn Phe Met Tyr Ser
        995                 1000                1005
Pro Gly Gly Pro Leu Val Leu Lys His Leu Thr Ala Leu Ile Lys Ser
    1010                1015                1020
Gln Glu Lys Val Gly Ile Val Gly Arg Thr Gly Ala Gly Lys Ser Ser
1025                1030                1035                1040
Leu Ile Ser Ala Leu Phe Arg Leu Ser Glu Pro Glu Gly Lys Ile Trp
                1045                1050                1055
Ile Asp Lys Ile Leu Thr Thr Glu Ile Gly Leu His Asp Leu Arg Lys
            1060                1065                1070
Lys Met Ser Ile Ile Pro Gln Glu Pro Val Leu Phe Thr Gly Thr Met
        1075                1080                1085
Arg Lys Asn Leu Asp Pro Phe Asn Glu His Thr Asp Glu Glu Leu Trp
    1090                1095                1100
Asn Ala Leu Gln Glu Val Gln Leu Lys Glu Thr Ile Glu Asp Leu Pro
1105                1110                1115                1120
Gly Lys Met Asp Thr Glu Leu Ala Glu Ser Gly Ser Asn Phe Ser Val
                1125                1130                1135
Gly Gln Arg Gln Leu Val Cys Leu Ala Arg Ala Ile Leu Arg Lys Asn
            1140                1145                1150
Gln Ile Leu Ile Ile Asp Glu Ala Thr Ala Asn Val Asp Pro Arg Thr
        1155                1160                1165
Asp Glu Leu Ile Gln Lys Lys Ile Arg Glu Lys Phe Ala His Cys Thr
    1170                1175                1180
Val Leu Thr Ile Ala His Arg Leu Asn Thr Ile Ile Asp Ser Asp Lys
1185                1190                1195                1200
Ile Met Val Leu Asp Ser Gly Arg Leu Lys Glu Tyr Asp Glu Pro Tyr
```

```
                1205                1210                1215
Val Leu Leu Gln Asn Lys Glu Ser Leu Phe Tyr Lys Met Val Gln Gln
            1220                1225                1230
Leu Gly Lys Ala Glu Ala Ala Ala Leu Thr Glu Thr Ala Lys Gln Arg
        1235                1240                1245
Trp Gly Phe Thr Met Leu Ala Arg Leu Val Ser Asn Ser
    1250                1255                1260
```

<210> 539
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 539

```
Cys Leu Ser His Ser Val Ala Val Val Thr
 1               5                  10
```

<210> 540
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 540

```
Ala Val Val Thr Ala Ser Ala Ala Leu
 1               5
```

<210> 541
<211> 14
<212> PRT
<213> Homo sapiens

<400> 541

```
Leu Ala Gly Leu Leu Cys Pro Asp Pro Arg Pro Leu Glu Leu
                 5                  10
```

<210> 542
<211> 15
<212> PRT
<213> Homo sapiens

<400> 542

```
Thr Gln Val Val Phe Asp Lys Ser Asp Leu Ala Lys Tyr Ser Ala
                 5                  10                  15
```

<210> 543
<211> 12
<212> PRT
<213> Homo sapiens

<400> 543

```
Phe Met Gly Ser Ile Val Gln Leu Ser Gln Ser Val
                 5                  10
```

<210> 544
<211> 18
<212> PRT
<213> Homo sapiens

<400> 544
Thr Tyr Val Pro Pro Leu Leu Leu Glu Val Gly Val Glu Glu Lys Phe
5 10 15
Met Thr

<210> 545
<211> 18
<212> PRT
<213> Homo sapiens

<400> 545
Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg Ala Val Tyr Leu Ala
5 10 15
Ser Val

<210> 546
<211> 29
<212> PRT
<213> Homo sapiens

<400> 546
Phe Val Gly Glu Gly Leu Tyr Gln Gly Val Pro Arg Ala Glu Pro Gly
5 10 15
Thr Glu Ala Arg Arg His Tyr Asp Glu Gly Val Arg Met
20 25

<210> 547
<211> 58
<212> PRT
<213> Homo sapiens

<400> 547
Val Ala Glu Glu Ala Ala Leu Gly Pro Thr Glu Pro Ala Glu Gly Leu
5 10 15
Ser Ala Pro Ser Leu Ser Pro His Cys Cys Pro Cys Arg Ala Arg Leu
20 25 30
Ala Phe Arg Asn Leu Gly Ala Leu Leu Pro Arg Leu His Gln Leu Cys
35 40 45
Cys Arg Met Pro Arg Thr Leu Arg Arg Leu
50 55

<210> 548
<211> 18
<212> PRT
<213> Homo sapiens

<400> 548
Ile Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu Gly Thr Gln Glu

5 10 15
Glu Cys

<210> 549
<211> 18
<212> PRT
<213> Homo sapiens

<400> 549
Leu Glu Ala Leu Leu Ser Asp Leu Phe Arg Asp Pro Asp His Cys Arg
5 10 15
Gln Ala

<210> 550
<211> 14
<212> PRT
<213> Homo sapiens

<400> 550
Ser Asp His Trp Arg Gly Arg Tyr Gly Arg Arg Arg Pro Phe
5 10

<210> 551
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 551
Phe Asp Lys Ser Asp Leu Ala Lys Tyr Ser Ala
5 10

<210> 552
<211> 2577
<212> DNA
<213> Homo sapiens

<400> 552
agcatatgta acatgacctg tgcttcagtg ttcttttgtg atcaaaaatt ccttactttt 60
agttttttat ctatggtaga accacccaga gcaggggtcc tcaactccca ggccacagac 120
tcataccagt ccacggacta ttatgaacca caccacacag gaggaggtga gcactaggca 180
agccaaggaa gcttcacctg tacttacagc cacacgccat ggctcatatt acagcctgaa 240
ctctgcctcc actcagatca gtgataacat tagaaactca ttggagcacg aaccctgttg 300
tgaactgcct atccgaagga tctaggttgt gtgcttcgta tgagaatcta atgccagatg 360
atctatcatt gtctcacttt gcccccagat aagaccatct agttgcagaa aaataagctc 420
agagcttcca ctgattctac attatggata tgtgccgccg aagcaagcac aaagccctac 480
ttttacacat gcctagtgat gcttcatgga caaggcttgg ctctgttgag tccaactaac 540
ctacctgaga ttctgagatt tctcttcaat ggcttcctgt gagctagagt ttgaaaatat 600
cttaaaatct tgagctagag atggaagtag cttggacgat tttcattatc atgtaaatcg 660
ggtcactcaa ggggccaacc acagctggga gccactgctc aggggaaggt tcatatggga 720
ctttctactg cccaaggttc tatacaggat ataaaggtgc ctcacagtat agatctggta 780
gcaaagaaga agaaacaaac actgatctct ttctgccacc cctctgaccc tttggaactc 840
ctctgaccct ttagaacaag cctacctaat atctgctaga gaaaagacca acaacggcct 900
caaaggatct cttaccatga aggtctcagc taattcttgg ctaagatgtg ggttccacat 960

```
taggttctga atatgggggg aagggtcaat ttgctcattt tgtgtgtgga taaagtcagg 1020
atgcccaggg gccagagcag ggggctgctg ctttgggaac aatggctgag catataacca 1080
taggtatggg aacaaaaaac atcaaagtca ctgtatcaat tgccatgaag actcgaggga 1140
cctgaatcta ccgattcatc ttaaggcagc aggaccagtt tgagtggcaa caatgcagca 1200
gcagaatcaa tggaaacaac agaatgattg caatgtcctt ttttttctcc tccttctgac 1260
ttgataaaag ggaccgtctt ccttggattt agtgaacccc tttggttcct gaaaaattca 1320
aggagtatct aggacatagt ccccagaaga cagtacaaga ctttctgata aactggacat 1380
ttcaagrccc aaataactaa tcagaaaaat caaagatgtg atactatttt ttatcccatg 1440
cataggtgct acacttggat caaatgaaca atgttgggat ctytatggat aaaggtctta 1500
aaagtcctga gataaagaat cctgcaccca ctggtacttc taacttgtct tgttttttgt 1560
ctgwtttctg gctgatgcag gggactaact cactgccacg cgaaaactac ctgaactgaa 1620
ctatgacatc tcacctgata tgtaagatgt aactgttata attattttaa acctcaattt 1680
agcattaact agccttttaa tgtaaacact tacacattat gaygactaga aacagcatac 1740
tctctggccg tctgtccaga tagatcttga gaagatacat caatgttttg ctcaagtaga 1800
aggctgacta tacttgccga tccacaacat acagcaagta tgagagcagt tctaaaatga 1860
cagagatagg aacagtaata aagttattkt aaaagctaat ttgatatact ttaccaattt 1920
aacatcttgc ctgtccgtgc agaatcaaac atttacatgc actaaaagac ataagcatct 1980
tcagtgctca agtgttcatc tttgtaaaat accaccaagg ttaaaaggaa gggacaaaaa 2040
aaaaaaaccc tcttatctca gtggggtatt gcatagcaga agctactaat ttgaagtcct 2100
ttgatggaca agaaacaata ttagggccac ttatctgaaa tgaacaaaga tttaagtgaa 2160
gatttcatca cagcttccct agactgatat gctgtaatag aaaatcagct agggggtaaa 2220
ataaataaga gctctctgca tgctgaaagc aagtaagatt aataataatg gtaagaatag 2280
tagtcacagg agtttcagtt aatgatgcca ataagcatgt gctaggcact gaattaaatg 2340
ccacatatat ctttcttatg cgcagcaaac tttgaaggat atattctcct acttttcata 2400
tatgacaaca tatttggtgg taaataacgt tcccaaggtc acacacctag caagtaagaa 2460
agttaggaat taaacccagt attgtgtgaa tctaaagcct aacttttttc tctttatcac 2520
ccacctacgg cttgtcttca ttaaaggaaa agtgtatcca cttaaaaaaa aaaaaaa    2577
```

<210> 553
<211> 58
<212> PRT
<213> Homo sapiens

<400> 553

```
Ser Ile Cys Asn Met Thr Cys Ala Ser Val Phe Phe Cys Asp Gln Lys
                5                   10                  15
Phe Leu Thr Phe Ser Phe Leu Ser Met Val Glu Pro Pro Arg Ala Gly
            20                  25                  30
Val Leu Asn Ser Gln Ala Thr Asp Ser Tyr Gln Ser Thr Asp Tyr Tyr
        35                  40                  45
Glu Pro His His Thr Gly Gly Gly Glu His
    50                  55
```

<210> 554
<211> 59
<212> PRT
<213> Homo sapiens

<400> 554

```
Leu Gln Lys Asn Lys Leu Arg Ala Ser Thr Asp Ser Thr Leu Trp Ile
                5                   10                  15
Cys Ala Ala Glu Ala Ser Thr Lys Pro Tyr Phe Tyr Thr Cys Leu Val
            20                  25                  30
Met Leu His Gly Gln Gly Leu Ala Leu Leu Ser Pro Thr Asn Leu Pro
        35                  40                  45
Glu Ile Leu Arg Phe Leu Phe Asn Gly Phe Leu
    50                  55
```

<210> 555
<211> 71
<212> PRT
<213> Homo sapiens

<400> 555
```
Leu Gly Arg Phe Ser Leu Ser Cys Lys Ser Gly His Ser Arg Gly Gln
                5                   10                  15
Pro Gln Leu Gly Ala Thr Ala Gln Gly Lys Val His Met Gly Leu Ser
            20                  25                  30
Thr Ala Gln Gly Ser Ile Gln Asp Ile Lys Val Pro His Ser Ile Asp
        35                  40                  45
Leu Val Ala Lys Lys Lys Lys Gln Thr Leu Ile Ser Phe Cys His Pro
    50                  55                  60
Ser Asp Pro Leu Glu Leu Leu
65                  70
```

<210> 556
<211> 81
<212> PRT
<213> Homo sapiens

<400> 556
```
Asn His Pro Glu Gln Gly Ser Ser Thr Pro Arg Pro Gln Thr His Thr
                5                   10                  15
Ser Pro Arg Thr Ile Met Asn His Thr Thr Gln Glu Glu Val Ser Thr
            20                  25                  30
Arg Gln Ala Lys Glu Ala Ser Pro Val Leu Thr Ala Thr Arg His Gly
        35                  40                  45
Ser Tyr Tyr Ser Leu Asn Ser Ala Ser Thr Gln Ile Ser Asp Asn Ile
    50                  55                  60
Arg Asn Ser Leu Glu His Glu Pro Cys Cys Glu Leu Pro Ile Arg Arg
65                  70                  75                  80
Ile
```

<210> 557
<211> 54
<212> PRT
<213> Homo sapiens

<400> 557
```
Ser Leu Ser Ala Thr Pro Leu Thr Leu Trp Asn Ser Ser Asp Pro Leu
                5                   10                  15
Glu Gln Ala Tyr Leu Ile Ser Ala Arg Glu Lys Thr Asn Asn Gly Leu
            20                  25                  30
Lys Gly Ser Leu Thr Met Lys Val Ser Ala Asn Ser Trp Leu Arg Cys
        35                  40                  45
Gly Phe His Ile Arg Phe
    50
```

<210> 558
<211> 77
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (1)...(77)
<223> Xaa = Any amino acid

<400> 558
Asn Asp Arg Asp Arg Asn Ser Asn Lys Val Ile Xaa Lys Ala Asn Leu
5 10 15
Ile Tyr Phe Thr Asn Leu Thr Ser Cys Leu Ser Val Gln Asn Gln Thr
20 25 30
Phe Thr Cys Thr Lys Arg His Lys His Leu Gln Cys Ser Ser Val His
35 40 45
Leu Cys Lys Ile Pro Pro Arg Leu Lys Gly Arg Asp Lys Lys Lys Lys
50 55 60
Pro Ser Tyr Leu Ser Gly Val Leu His Ser Arg Ser Tyr
65 70 75

<210> 559
<211> 50
<212> PRT
<213> Homo sapiens

<400> 559
Thr Leu Pro Pro Leu Arg Ser Val Ile Thr Leu Glu Thr His Trp Ser
5 10 15
Thr Asn Pro Val Val Asn Cys Leu Ser Glu Gly Ser Arg Leu Cys Ala
20 25 30
Ser Tyr Glu Asn Leu Met Pro Asp Asp Leu Ser Leu Ser His Phe Ala
35 40 45
Pro Arg
50

<210> 560
<211> 56
<212> PRT
<213> Homo sapiens

<400> 560
Ile Gly Ser Leu Lys Gly Pro Thr Thr Ala Gly Ser His Cys Ser Gly
5 10 15
Glu Gly Ser Tyr Gly Thr Phe Tyr Cys Pro Arg Phe Tyr Thr Gly Tyr
20 25 30
Lys Gly Ala Ser Gln Tyr Arg Ser Gly Ser Lys Glu Glu Glu Thr Asn
35 40 45
Thr Asp Leu Phe Leu Pro Pro Leu
50 55

<210> 561
<211> 57
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT

<222> (1)...(57)
<223> Xaa = Any amino acid

<400> 561
Val Leu His Leu Asp Gln Met Asn Asn Val Gly Ile Xaa Met Asp Lys
5 10 15
Gly Leu Lys Ser Pro Glu Ile Lys Asn Pro Ala Pro Thr Gly Thr Ser
20 25 30
Asn Leu Ser Cys Phe Leu Ser Xaa Phe Trp Leu Met Gln Gly Thr Asn
35 40 45
Ser Leu Pro Arg Glu Asn Tyr Leu Asn
50 55

<210> 562
<211> 59
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (1)...(59)
<223> Xaa = Any amino acid

<400> 562
Asp Leu Tyr Pro Xaa Arg Ser Gln His Cys Ser Phe Asp Pro Ser Val
5 10 15
Ala Pro Met His Gly Ile Lys Asn Ser Ile Thr Ser Leu Ile Phe Leu
20 25 30
Ile Ser Tyr Leu Xaa Leu Glu Met Ser Ser Leu Ser Glu Ser Leu Val
35 40 45
Leu Ser Ser Gly Asp Tyr Val Leu Asp Thr Pro
50 55

<210> 563
<211> 79
<212> PRT
<213> Homo sapiens

<400> 563
Cys Phe Leu Phe Pro Tyr Leu Trp Leu Tyr Ala Gln Pro Leu Phe Pro
5 10 15
Lys Gln Gln Pro Pro Ala Leu Ala Pro Gly His Pro Asp Phe Ile His
20 25 30
Thr Gln Asn Glu Gln Ile Asp Pro Ser Pro His Ile Gln Asn Leu Met
35 40 45
Trp Asn Pro His Leu Ser Gln Glu Leu Ala Glu Thr Phe Met Val Arg
50 55 60
Asp Pro Leu Arg Pro Leu Leu Val Phe Ser Leu Ala Asp Ile Arg
65 70 75

<210> 564
<211> 64
<212> PRT
<213> Homo sapiens

<400> 564

```
Ala Cys Ser Lys Gly Ser Glu Glu Phe Gln Arg Val Arg Gly Val Ala
                5                   10                  15
Glu Arg Asp Gln Cys Leu Phe Leu Leu Leu Cys Tyr Gln Ile Tyr Thr
            20                  25                  30
Val Arg His Leu Tyr Ile Leu Tyr Arg Thr Leu Gly Ser Arg Lys Ser
        35                  40                  45
His Met Asn Leu Pro Leu Ser Ser Gly Ser Gln Leu Trp Leu Ala Pro
    50                  55                  60


<210> 565
<211> 57
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (1)...(57)
<223> Xaa = Any amino acid

<400> 565
Leu Tyr Tyr Cys Ser Tyr Leu Cys His Phe Arg Thr Ala Leu Ile Leu
                5                   10                  15
Ala Val Cys Cys Gly Ser Ala Ser Ile Val Ser Leu Leu Leu Glu Gln
            20                  25                  30
Asn Ile Asp Val Ser Ser Gln Asp Leu Ser Gly Gln Thr Ala Arg Glu
        35                  40                  45
Tyr Ala Val Ser Ser Xaa His Asn Val
    50                  55


<210> 566
<211> 55
<212> PRT
<213> Homo sapiens

<400> 566
Ile Leu Leu Glu Phe Phe Arg Asn Gln Arg Gly Ser Leu Asn Pro Arg
                5                   10                  15
Lys Thr Val Pro Phe Ile Lys Ser Glu Gly Gly Glu Lys Lys Gly His
            20                  25                  30
Cys Asn His Ser Val Val Ser Ile Asp Ser Ala Ala Ala Leu Leu Pro
        35                  40                  45
Leu Lys Leu Val Leu Leu Pro
    50                  55


<210> 567
<211> 51
<212> PRT
<213> Homo sapiens

<400> 567
Tyr Ser Asp Phe Asp Val Phe Cys Ser His Thr Tyr Gly Tyr Met Leu
                5                   10                  15
Ser His Cys Ser Gln Ser Ser Ser Pro Leu Leu Trp Pro Leu Gly Ile
            20                  25                  30
Leu Thr Leu Ser Thr His Lys Met Ser Lys Leu Thr Leu Pro Pro Ile
```

```
        35                    40                    45
Phe Arg Thr
    50

<210> 568
<211> 75
<212> PRT
<213> Homo sapiens

<400> 568
Lys Val Gly Glu Tyr Ile Leu Gln Ser Leu Leu Arg Ile Arg Lys Ile
                    5                   10                  15
Tyr Val Ala Phe Asn Ser Val Pro Ser Thr Cys Leu Leu Ala Ser Leu
            20                  25                  30
Thr Glu Thr Pro Val Thr Thr Ile Leu Thr Ile Ile Ile Asn Leu Thr
        35                  40                  45
Cys Phe Gln His Ala Glu Ser Ser Tyr Leu Phe Tyr Pro Leu Ala Asp
    50                  55                  60
Phe Leu Leu Gln His Ile Ser Leu Gly Lys Leu
65                  70                  75


<210> 569
<211> 4809
<212> DNA
<213> Homo sapiens

<400> 569
gcatccagag tggtggactg gttacaggct atgaacctac actgatgcgg caccaccacc 60
cagagtccac rggttatgtt ggttcacatt tactcttgct gtggtatggt ctataggttt 120
ggacagatgt ccgataatcc tttttacatt ttggcatcct tgggtagctc gtcttgtagg 180
aatggacttg cttcaaagtg gaggcaggca gatccttcag acgggtatat ggagccctgt 240
tttcagttgc ttttctaatt ctctcttatc gtttacctca aaatcttcct gaggtctcgc 300
ttccttttaa aatccttgtc tactttgcag catcactctg acactcccat tgattcctca 360
gcacctactg actacacggt taggagtgca agggtagaat tcatgtttta ttcatctttg 420
ggtctgtagc acccagcaaa gtgctcagta aatgcgcagt aattgatttg acctctgaac 480
aaatacacac tgtactaaga atctacacac cgaaagacaa aaacaagaca aatttgagtg 540
ctacaggtgt cacgcttggc atcacacatg tgcctgtgta ttcctctagg tggttaccag 600
gagctctgcc actgcatgtc cactagtgac gggttcgctc caccacccca gctgggtagc 660
cgctgctctc acataagggg tccaattaaa attgccagga ataaattccc ccggactttg 720
acttctcaag agctaagaag gtttgctgag tattctggca tgatgtttgg tgatcaaaca 780
actgctggcc aaaaatgatg agtatttccc cctcttgctg aagatgtgct ccatacaata 840
gtccatcaca ttcatcattc atcagtctgg aagtgtgcag aacaacatgt aatagataat 900
atgattggct gcacacttcc agactgatga atgatgaatg tgatggacta ttgtatggag 960
cacatcttca gcaagagggg gaaatactca tcattttatc tattacatgt tgttctggtt 1020
tttttttttt tccaatgtcc agcctaaact ataaagtact ttgagaacgc acagtgagcc 1080
ataagcttgc caataaagag tcctctgtgg tatggaactg gcttatttca tacacaatct 1140
gcaaacaatg agggcactat tggaaacata ctgtgctgca cagagcattt acaccgctta 1200
tctttaatct tccccagcaa tccttgcttt gtgcgcattt atgatccttg ctctcagaag 1260
tccacatact tttccccaac cgtaacaaat tatttaactc atctaatgta tgtatgtccg 1320
cgcagtctga aaacagtaat tgtccttggg aagaagtgag tttaagagag ctctagggca 1380
ctcatcacaa ctccagccct gccctccatg tggtagcagc tctttggact ggggctaagt 1440
gcttattctt gtgcttcatt cctggtaagc tcaatttctt taccttagga taactttgct 1500
ggaaaagggc tcagattcag ccgaccattg tggcctctgt ggctgtcaca gcttgtccct 1560
gacatgctat gatgttgggt cccttctca tcccccttggg atttcttctg ctggcccaca 1620
gccagaacaa ctaggccttt tactccacca tccctttgtt ttcttttgtt tcgttggtaa 1680
aaatcaatcc ttctaccatc catgcatagc aatttctaaa aactgaattt caagagcagt 1740
atctgaagaa acaaacatga tttggtcctt ttagtaaaca gaataaattt taataaatca 1800
```

actttgaaat agttgtaaga gttaagaaaa agcacaaaac tgagatcatc agagcagctt 1860
ggcctcaaag gacaggcagc aggattctac agggtttgag ccttcctaag tgaagctgtt 1920
tcctgcaggc tccctgctcc aagctcctag ctaacagccc cttctcccac gattggcaac 1980
aaagagcaaa aataactttg tacttgatgc tgagtcagtg taaaaagcca taaaaaattc 2040
cctctaaatg tcaaaatgtt tgcctccttt gaggcttctc tcctcctact gggtctggat 2100
aaattagcac tgggcttata ttgagtcaca gatctgggcc ctgccacaga gagcttcctc 2160
ctagtgtgtg atgctttttc tccaaactat tgatacaaaa tgcactggaa tagaaatcaa 2220
cagaaactgg tcaaaggtgt ggcatacaca ttctcatgta gatgtaaagc tgtgcttaga 2280
attcctttgt ggagtctggt ttggtcttgg ttttcttggt gtttgattca ttttttttacg 2340
taaattacaa aaaccctcca catttcttca tggattgtat tagtccatgt tctccagaga 2400
agcagaacga gttggatgta tgttttggaa gagattatga ggaaccggct catgtgatga 2460
aggaggttga gaggtcctgt gctctgccat ctgcaagctg aagacctgga aagctgaggg 2520
tgtggctcca gtctgagtct gaaggcccaa gaaccagggg aaccaacggt gtagattcca 2580
ggttgaaggc aggagaagat ggatgtccca gctcagcagg caggcaggaa gcaaatgggg 2640
taaattcctc cttcctccac cttttgttcc attcaggcct tcaacagatt ggatgagcgc 2700
ccccccaccc ccacactagg gagggccatc tgctttactg agtcggctga gtcaagtgcc 2760
agcctcatcc caaaacactc tccagacaca cgcagaaatg tttcatctgg gcaccctgtg 2820
gccagtcatg ctgacacaca gaactaacca tgacatggat tcttcttaaa gcagtgatag 2880
gagcgaacag aaacattttc ataattttca attattttta atgaaaacta tatctgatgg 2940
aattgtttaa acctagtctg gccacacatt atttcctggg accgcccctc cttcaatccc 3000
ttggacactg atgactttat gcccagatta cactggaggc ctgtgctgat tttctaacac 3060
atacctgcaa ctgagctggc aaaaagaaaa ctaggcaagt atgacagata catgatgcac 3120
aggctaagtg caaaggaaag aaaaacacca actgcaggga tgagggactc acccctttag 3180
aagtttctac ttgagcagct agaagactac aatgccactc atcaaaacag tgactcaggg 3240
ggagtatttg ggataaagga ggaatctgat gttggaggtc aaatttgaag tgtctttaag 3300
acctacaggt aacgagacag ctggacaaac acatggaact caggacaaag gctctaagga 3360
cagcacagca gctgacatcc tgtgtgacag ccttgaaagc agcaggcccg ccgctcacat 3420
tttggaaggg aaaatgggta caatgttgtc tgccactttg ggccttcttt gggtcacatg 3480
cattttacat ttatgcagtt gatatattta tgtttcctgg gtcttttata cattagacac 3540
catgattctc aatcctttgt tattttgtat tacaaaaagc tgaattatta tttcaaatat 3600
gggcaaatta gagccttcca tattgccaag gtgtatcaac cacactgata ycaygatctc 3660
tcttttgaat tagttttcca gttcacacct accatttatt tcatgattgg tttcagactt 3720
gttcctcctg gaaacactcc ctaacaagca cccttgcagg aatgaagaca caccacacac 3780
atctacccca ttactgcatg tactcaagag tcagctttta tatgatctct cccaagtgct 3840
cctataatgg ggatctttca ctcaccctaa agtgaggaca aaatacttga aagcatgagc 3900
ccagtgcctg taggtgtgca attaacctca gaccaaggaa gtgccgaacg catctggctt 3960
ttagcaaggc acctgacaaa gtccttcagg atgtttttgt acatgagcta gagaaatgta 4020
cctggagaac agcttctact gccagatgat cttactcaaa agatgcagat taagcaaaat 4080
atcaacccaa agggtggtcc ctgatggccc accagcccct gtgcctggct cgtttcctat 4140
gtttcctaga tttggtttca gacttgctcc tcctgcagac actccctaac cagcatcctt 4200
gcagaaaact ggtgaactag aaaaggcctg tgtgggtcac gtggccaccc aacaccacag 4260
cagtgtctaa ggtatgcgtg ggagcctgca cagcaggagc ggggtcttct ggagacccgc 4320
atgagatgca aagggcagtg gacaaggagc caagggaggt ggctctagtc acgctggtat 4380
ggtgccagct tgaggatgct gggcaagtcc cgagccgtct gccttcctag taccacagtt 4440
accactgtct gttacctcgc gagttcaagt gcttcacgtg agacagctac gagacaggcc 4500
cctggaaact ggaaaatgcy aagtaaatgt catgcacaat tgttgttcac attttatctc 4560
aatcactttt accaaatcag gctaaaccct gggtattcat aacgtcttgg gctgtacaaa 4620
ttgttccttg aaatgactca gagacatttt ctgaattggc ttccatcagc caagcatttc 4680
ttcagaactg gaaaaatgct ttaaatttgg ctttgtcatg attattaaaa cactctgtac 4740
attttttatt attgaaatta acacattgcc tactttttaa aaattggaaa aagaaaaaaa 4800
aaaaaaaaa 4809

<210> 570
<211> 951
<212> DNA
<213> Homo sapiens

<400> 570

```
aaaattgaat attgagatac cattctttag tgttaccttt tttacccaca tgtgtttctg 60
aaaatattgg aattttattc atcttaaaaa ttggacccgg ccttatttac catctttaat 120
ccattttagt actatgggtg agtacatgga attgaagtct ggcttaaatc ttcagaaagt 180
tatatatcta ttttatttta tttttttgag acagagtctc gctgtgtcac ccaggctgga 240
gtgcggtgcc acaatcttgg ctcactgcaa cctctgagtc ccaggttcaa gcgatactca 300
tgcctcggcc tcctgagtag ctgggactac aggcgtgcac caccacatct ggctaatctt 360
tttttgtatt tttagtagag acggggtttc actgtggtct ccatctcctg acctcgtgat 420
ccgcctgcct cccaaagtgc tgggattaca ggcatgagcc accgcacaca gctgggactg 480
ggtaatttat aaagaaaaga ggtttaatga ctcacagttc cgcatggctg gagaggcctc 540
aggaaactta caatcatggt ggaaggcgaa ggggaagcaa ggcacgtctt acatggtggc 600
aggagagaac gagtgagggg ggagactgcc acaaactttt tttttttgag acaagagtct 660
ggccctgttg cccaggctgg agtgcagtgg catgatctca gctcactgca acctctgcct 720
cacaggttca agcaattctc atgcctcagc ctcccgcata gctgggacca caggtatgca 780
ccaccacacc tagctaattt ttgtagtttt agtagagatg gggtctcact atgttgctca 840
ggctggtcta aaactcctgg gctccagcaa tccgcctgcc ttggcctccc aaagtgctgg 900
ggttacaggc ataagccacc acatccagcc tgccacatac ttttaaacta t          951
```

<210> 571
<211> 819
<212> DNA
<213> Homo sapiens

<400> 571

```
cagcttaaaa atggtttctt gaaatcagtg attagcattc actcaccagt acccctacta 60
aggggtaggc actggtttgt actcctggga atacaggagt acaccagaat ttatttctgc 120
ttattgcttt tgttgcaaat gccgtggctt catctgagga attctagaat tcagagggtg 180
tagccctcca ctctgctgtc ttgctatctg ctctcattgc atccgtttaa cctgcattct 240
gaaagatgtt tctcaggttt ttccttgacg atttcttctt tttctgattc tgacaatgtt 300
ttaaatcatt gtactgtggt tatcatttct ctgcatttat tttacccatc ttcctttgta 360
acttgtccta ttgtctttta atttctgcct gttctttatg gctttcaact tcataaataa 420
catgttttct caaatctctt tgtgaattcc agagagggcc aggcacggtg gctcacatct 480
gtaatcccag cactttgggg aggctgagac gggtggatca cttgaggtca ggagtttgag 540
accagcctgg ccaacatggt gaaatcccgt ttcactaaaa atacaaaaat tacccaggca 600
tggtggcggg cgcctgtaat cccaggtact cgggaggctg agggaggaga atcgcttgaa 660
cctgggaggc tgagggagga gaatcgcttg aacccgggag gcagaggttg cagtgaaccg 720
agatcatgtt gctgcactcc agcctggtca acagagcaag actctgcctc aaaaacaaac 780
aaataaacaa acaaacaaac aaaacagaga gattttgct                        819
```

<210> 572
<211> 203
<212> DNA
<213> Homo sapiens

<400> 572

```
tatagaatac tcaagctatg catcaagctt ggtaccgagc tcggatccac tatttacggc 60
cgccagtgtg ctggaattcg cccttagctc ggatccacta gtccagtgtg gtggaattcc 120
attgtgttgg gcccaacaca atggagccac cacatccagc ctgccacata cttttaaact 180
atcaggtctc atgagaactc atg                                         203
```

<210> 573
<211> 132
<212> PRT
<213> Homo sapiens

<400> 573

```
Met Val Glu Gly Glu Gly Glu Ala Arg His Val Leu His Gly Gly Arg
                    5                   10                  15
Arg Glu Arg Val Arg Gly Glu Thr Ala Thr Asn Phe Phe Phe Leu Arg
```

```
                20                  25                  30
Gln Glu Ser Gly Pro Val Ala Gln Ala Gly Val Gln Trp His Asp Leu
            35                  40                  45
Ser Ser Leu Gln Pro Leu Pro His Arg Phe Lys Gln Phe Ser Cys Leu
        50                  55                  60
Ser Leu Pro His Ser Trp Asp His Arg Tyr Ala Pro Pro His Leu Ala
65                  70                  75                  80
Asn Phe Cys Ser Phe Ser Arg Asp Gly Val Ser Leu Cys Cys Ser Gly
                85                  90                  95
Trp Ser Lys Thr Pro Gly Leu Gln Gln Ser Ala Cys Leu Gly Leu Pro
            100                 105                 110
Lys Cys Trp Gly Tyr Arg His Lys Pro Pro His Pro Ala Cys His Ile
        115                 120                 125
Leu Leu Asn Tyr
    130


<210> 574
<211> 62
<212> PRT
<213> Homo sapiens

<400> 574
Met Thr His Ser Ser Ala Trp Leu Glu Arg Pro Gln Glu Thr Tyr Asn
                5                   10                  15
His Gly Gly Arg Arg Arg Gly Ser Lys Ala Arg Leu Thr Trp Trp Gln
            20                  25                  30
Glu Arg Thr Ser Glu Gly Gly Asp Cys His Lys Leu Phe Phe Phe Glu
        35                  40                  45
Thr Arg Val Trp Pro Cys Cys Pro Gly Trp Ser Ala Val Ala
    50                  55                  60


<210> 575
<211> 76
<212> PRT
<213> Homo sapiens

<400> 575
Met Val Lys Ser Arg Phe Thr Lys Asn Thr Lys Ile Thr Gln Ala Trp
                5                   10                  15
Trp Arg Ala Pro Val Ile Pro Gly Thr Arg Glu Ala Glu Gly Gly Glu
            20                  25                  30
Ser Leu Glu Pro Gly Arg Leu Arg Glu Glu Asn Arg Leu Asn Pro Gly
        35                  40                  45
Gly Arg Gly Cys Ser Glu Pro Arg Ser Cys Cys Cys Thr Pro Ala Trp
    50                  55                  60
Ser Thr Glu Gln Asp Ser Ala Ser Lys Thr Asn Lys
65                  70                  75


<210> 576
<211> 68
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
```

<222> (1)...(68)
<223> Xaa = Any Amino Acid

<400> 576
Met Leu Gly Lys Ser Arg Ala Val Cys Leu Pro Ser Thr Thr Val Thr
5 10 15
Thr Val Cys Tyr Leu Ala Ser Ser Ser Ala Ser Arg Glu Thr Ala Thr
20 25 30
Arg Gln Ala Pro Gly Asn Trp Lys Met Xaa Ser Lys Cys His Ala Gln
35 40 45
Leu Leu Phe Thr Phe Tyr Leu Asn His Phe Tyr Gln Ile Arg Leu Asn
50 55 60
Pro Gly Tyr Ser
65

<210> 577
<211> 57
<212> PRT
<213> Homo sapiens

<400> 577
Met Tyr Leu Glu Asn Ser Phe Tyr Cys Gln Met Ile Leu Leu Lys Arg
5 10 15
Cys Arg Leu Ser Lys Ile Ser Thr Gln Arg Val Val Pro Asp Gly Pro
20 25 30
Pro Ala Pro Val Pro Gly Ser Phe Pro Met Phe Pro Arg Phe Gly Phe
35 40 45
Arg Leu Ala Pro Pro Ala Asp Thr Pro
50 55

<210> 578
<211> 51
<212> PRT
<213> Homo sapiens

<400> 578
Met Gln Leu Ile Tyr Leu Cys Phe Leu Gly Leu Leu Tyr Ile Arg His
5 10 15
His Asp Ser Gln Ser Phe Val Ile Leu Tyr Tyr Lys Lys Leu Asn Tyr
20 25 30
Tyr Phe Lys Tyr Gly Gln Ile Arg Ala Phe His Ile Ala Lys Val Tyr
35 40 45
Gln Pro His
50

<210> 579
<211> 56
<212> PRT
<213> Homo sapiens

<400> 579
Met His Phe Thr Phe Met Gln Leu Ile Tyr Leu Cys Phe Leu Gly Leu
5 10 15
Leu Tyr Ile Arg His His Asp Ser Gln Ser Phe Val Ile Leu Tyr Tyr
20 25 30
Lys Lys Leu Asn Tyr Tyr Phe Lys Tyr Gly Gln Ile Arg Ala Phe His
35 40 45
Ile Ala Lys Val Tyr Gln Pro His

50 55

<210> 580
<211> 67
<212> PRT
<213> Homo sapiens

<400> 580
Met Glu Leu Arg Thr Lys Ala Leu Arg Thr Ala Gln Gln Leu Thr Ser
5 10 15
Cys Val Thr Ala Leu Lys Ala Ala Gly Pro Pro Leu Thr Phe Trp Lys
20 25 30
Gly Lys Trp Val Gln Cys Cys Leu Pro Leu Trp Gly Leu Leu Gly Ser
35 40 45
His Ala Phe Tyr Ile Tyr Ala Val Asp Ile Phe Met Phe Pro Gly Ser
50 55 60
Phe Ile His
65

<210> 581
<211> 77
<212> PRT
<213> Homo sapiens

<400> 581
Met Leu Glu Val Lys Phe Glu Val Ser Leu Arg Pro Thr Gly Asn Glu
5 10 15
Thr Ala Gly Gln Thr His Gly Thr Gln Asp Lys Gly Ser Lys Asp Ser
20 25 30
Thr Ala Ala Asp Ile Leu Cys Asp Ser Leu Glu Ser Ser Arg Pro Ala
35 40 45
Ala His Ile Leu Glu Gly Lys Met Gly Thr Met Leu Ser Ala Thr Leu
50 55 60
Gly Pro Ser Trp Val Thr Cys Ile Leu His Leu Cys Ser
65 70 75

<210> 582
<211> 51
<212> PRT
<213> Homo sapiens

<400> 582
Met Leu Phe Leu Gln Thr Ile Asp Thr Lys Cys Thr Gly Ile Glu Ile
5 10 15
Asn Arg Asn Trp Ser Lys Val Trp His Thr His Ser His Val Asp Val
20 25 30
Lys Leu Cys Leu Glu Phe Leu Cys Gly Val Trp Phe Gly Leu Gly Phe
35 40 45
Leu Gly Val
50

<210> 583
<211> 60
<212> PRT
<213> Homo sapiens

<400> 583
Met Ser Thr Ser Asp Gly Phe Ala Pro Pro Pro Gln Leu Gly Ser Arg

```
                5                   10                  15
Cys Ser His Ile Arg Gly Pro Ile Lys Ile Ala Arg Asn Lys Phe Pro
            20                  25                  30
Arg Thr Leu Thr Ser Gln Glu Leu Arg Arg Phe Ala Glu Tyr Ser Gly
        35                  40                  45
Met Met Phe Gly Asp Gln Thr Thr Ala Gly Gln Lys
    50                  55                  60
```

<210> 584
<211> 76
<212> PRT
<213> Homo sapiens

<400> 584

```
Met Cys Leu Cys Ile Pro Leu Gly Gly Tyr Gln Glu Leu Cys His Cys
                5                   10                  15
Met Ser Thr Ser Asp Gly Phe Ala Pro Pro Pro Gln Leu Gly Ser Arg
            20                  25                  30
Cys Ser His Ile Arg Gly Pro Ile Lys Ile Ala Arg Asn Lys Phe Pro
        35                  40                  45
Arg Thr Leu Thr Ser Gln Glu Leu Arg Arg Phe Ala Glu Tyr Ser Gly
    50                  55                  60
Met Met Phe Gly Asp Gln Thr Thr Ala Gly Gln Lys
65                  70                  75
```

<210> 585
<211> 50
<212> PRT
<213> Homo sapiens

<400> 585

```
Met Val Tyr Arg Phe Gly Gln Met Ser Asp Asn Pro Phe Tyr Ile Leu
                5                   10                  15
Ala Ser Leu Gly Ser Ser Ser Cys Arg Asn Gly Leu Ala Ser Lys Trp
            20                  25                  30
Arg Gln Ala Asp Pro Ser Asp Gly Tyr Met Glu Pro Cys Phe Gln Leu
        35                  40                  45
Leu Phe
    50
```

<210> 586
<211> 60
<212> PRT
<213> Homo sapiens

<400> 586

```
Met Leu Val His Ile Tyr Ser Cys Cys Gly Met Val Tyr Arg Phe Gly
                5                   10                  15
Gln Met Ser Asp Asn Pro Phe Tyr Ile Leu Ala Ser Leu Gly Ser Ser
            20                  25                  30
Ser Cys Arg Asn Gly Leu Ala Ser Lys Trp Arg Gln Ala Asp Pro Ser
        35                  40                  45
Asp Gly Tyr Met Glu Pro Cys Phe Gln Leu Leu Phe
    50                  55                  60
```

<210> 587
<211> 1408
<212> DNA

<213> Homo sapiens

<400> 587
ctggacactt tgcgagggct tttgctggct gctgctgctg cccgtcatgc tactcatcgt 60
agcccgcccg gtgaagctcg ctgctttccc tacctcctta agtgactgcc aaacgcccac 120
cggctggaat tgctctggtt atgatgacag agaaaatgat ctcttcctct gtgacaccaa 180
cacctgtaaa tttgatgggg aatgtttaag aattggagac actgtgactt gcgtctgtca 240
gttcaagtgc aacaatgact atgtgcctgt gtgtggctcc aatggggaga gctaccagaa 300
tgagtgttac ctgcgacagg ctgcatgcaa acagcagagt gagatacttg tggtgtcaga 360
aggatcatgt gccacagatg caggatcagg atctggagat ggagtccatg aaggctctgg 420
agaaactagt caaaaggaga catccacctg tgatatttgc cagtttggtg cagaatgtga 480
cgaagatgcc gaggatgtct ggtgtgtgtg taatattgac tgttctcaaa ccaacttcaa 540
tcccctctgc gcttctgatg ggaaatctta tgataatgca tgccaaatca aagaagcatc 600
gtgtcagaaa caggagaaaa ttgaagtcat gtctttgggt cgatgtcaag ataacacaac 660
tacaactact aagtctgaag atgggcatta tgcaagaaca gattatgcag agaatgctaa 720
caaattagaa gaaagtgcca gagaacacca catactttgt ccggaacatt acaatggctt 780
ctgcatgcat gggaagtgtg agcattctat caatatgcag gagccatctt gcaggtgtga 840
tgctggttat actggacaac actgtgaaaa aaaggactac agtgttctat acgttgttcc 900
cggtcctgta cgatttcagt atgtcttaat cgcagctgtg attggaacaa ttcagattgc 960
tgtcatctgt gtggtggtcc tctgcatcac aaggaaatgc cccagaagca acagaattca 1020
cagacagaag caaaatacag ggcactacag ttcagacaat acaacaagag cgtccacgag 1080
gttaatctaa agggagcatg tttcacagtg gctggactac cgagagcttg gactacacaa 1140
tacagtatta tagacaaaag aataagacaa gagatctaca catgttgcct tgcatttgtg 1200
gtaatctaca ccaatgaaaa catgtactac agctatattt gattatgtat ggatatattt 1260
gaaatagtat acattgtctt gatgtttttt ctgtaatgta aataaactat ttatatcaca 1320
caatawagtt ttttctttcc catgtatttg ttatatataa taaatactca gtgatgagaa 1380
aaaaaaaaaa aaaaaaaaaa rwmgaccc 1408

<210> 588
<211> 81
<212> PRT
<213> Homo sapiens

<400> 588
Met Pro Gln Lys Gln Gln Asn Ser Gln Thr Glu Ala Lys Tyr Arg Ala
5 10 15
Leu Gln Phe Arg Gln Tyr Asn Lys Ser Val His Glu Val Asn Leu Lys
20 25 30
Gly Ala Cys Phe Thr Val Ala Gly Leu Pro Arg Ala Trp Thr Thr Gln
35 40 45
Tyr Ser Ile Ile Asp Lys Arg Ile Arg Gln Glu Ile Tyr Thr Cys Cys
50 55 60
Leu Ala Phe Val Val Ile Tyr Thr Asn Glu Asn Met Tyr Tyr Ser Tyr
65 70 75 80
Ile

<210> 589
<211> 157
<212> PRT
<213> Homo sapiens

<400> 589
Met Thr Met Cys Leu Cys Val Ala Pro Met Gly Arg Ala Thr Arg Met
5 10 15
Ser Val Thr Cys Asp Arg Leu His Ala Asn Ser Arg Val Arg Tyr Leu
20 25 30
Trp Cys Gln Lys Asp His Val Pro Gln Met Gln Asp Gln Asp Leu Glu

```
        35                  40                  45
Met Glu Ser Met Lys Ala Leu Glu Lys Leu Val Lys Arg Arg His Pro
    50                  55                  60
Pro Val Ile Phe Ala Ser Leu Val Gln Asn Val Thr Lys Met Pro Arg
65                  70                  75                  80
Met Ser Gly Val Cys Val Ile Leu Thr Val Leu Lys Pro Thr Ser Ile
                85                  90                  95
Pro Ser Ala Leu Leu Met Gly Asn Leu Met Ile Met His Ala Lys Ser
            100                 105                 110
Lys Lys His Arg Val Arg Asn Arg Arg Lys Leu Lys Ser Cys Leu Trp
        115                 120                 125
Val Asp Val Lys Ile Thr Gln Leu Gln Leu Leu Ser Leu Lys Met Gly
    130                 135                 140
Ile Met Gln Glu Gln Ile Met Gln Arg Met Leu Thr Asn
145                 150                 155


<210> 590
<211> 347
<212> PRT
<213> Homo sapiens

<400> 590
Met Leu Leu Ile Val Ala Arg Pro Val Lys Leu Ala Ala Phe Pro Thr
                5                   10                  15
Ser Leu Ser Asp Cys Gln Thr Pro Thr Gly Trp Asn Cys Ser Gly Tyr
            20                  25                  30
Asp Asp Arg Glu Asn Asp Leu Phe Leu Cys Asp Thr Asn Thr Cys Lys
        35                  40                  45
Phe Asp Gly Glu Cys Leu Arg Ile Gly Asp Thr Val Thr Cys Val Cys
    50                  55                  60
Gln Phe Lys Cys Asn Asn Asp Tyr Val Pro Val Cys Gly Ser Asn Gly
65                  70                  75                  80
Glu Ser Tyr Gln Asn Glu Cys Tyr Leu Arg Gln Ala Ala Cys Lys Gln
                85                  90                  95
Gln Ser Glu Ile Leu Val Val Ser Glu Gly Ser Cys Ala Thr Asp Ala
            100                 105                 110
Gly Ser Gly Ser Gly Asp Gly Val His Glu Gly Ser Gly Glu Thr Ser
        115                 120                 125
Gln Lys Glu Thr Ser Thr Cys Asp Ile Cys Gln Phe Gly Ala Glu Cys
    130                 135                 140
Asp Glu Asp Ala Glu Asp Val Trp Cys Val Cys Asn Ile Asp Cys Ser
145                 150                 155                 160
Gln Thr Asn Phe Asn Pro Leu Cys Ala Ser Asp Gly Lys Ser Tyr Asp
                165                 170                 175
Asn Ala Cys Gln Ile Lys Glu Ala Ser Cys Gln Lys Gln Glu Lys Ile
            180                 185                 190
Glu Val Met Ser Leu Gly Arg Cys Gln Asp Asn Thr Thr Thr Thr Thr
        195                 200                 205
Lys Ser Glu Asp Gly His Tyr Ala Arg Thr Asp Tyr Ala Glu Asn Ala
    210                 215                 220
Asn Lys Leu Glu Glu Ser Ala Arg Glu His His Ile Pro Cys Pro Glu
225                 230                 235                 240
His Tyr Asn Gly Phe Cys Met His Gly Lys Cys Glu His Ser Ile Asn
                245                 250                 255
Met Gln Glu Pro Ser Cys Arg Cys Asp Ala Gly Tyr Thr Gly Gln His
            260                 265                 270
Cys Glu Lys Lys Asp Tyr Ser Val Leu Tyr Val Val Pro Gly Pro Val
```

```
        275                 280                 285
Arg Phe Gln Tyr Val Leu Ile Ala Ala Val Ile Gly Thr Ile Gln Ile
    290                 295                 300
Ala Val Ile Cys Val Val Val Leu Cys Ile Thr Arg Lys Cys Pro Arg
305                 310                 315                 320
Ser Asn Arg Ile His Arg Gln Lys Gln Asn Thr Gly His Tyr Ser Ser
                325                 330                 335
Asp Asn Thr Thr Arg Ala Ser Thr Arg Leu Ile
            340                 345
```

<210> 591
<211> 565
<212> DNA
<213> Homo sapien

<400> 591

```
actaaagcaa atgaacaagc tgacttgcta gtatcatctg cattcattga agcacaagaa      60
cttcatgcct tgactcatgt aaatgcaata ggattaaaaa ataaatttga tatcacatgg     120
aaacagacaa aaaatattgt acaacattgc acccagtgtc agattctaca cctggccact     180
caggaagcaa gagttaatcc cagaggtcta tgtcctaatg tgttatggca aatggatgtc     240
atgcacgtac cttcatttgg aaaattgtca tttgtccatg tgacagttga tacttattca     300
catttcatat gggcaacctg ccagacagga gaaagtactt cccatgttaa aagacattta     360
ttatcttgtt ttcctgtcat gggagttcca gaaaaagtta aaacagacaa tgggccaggt     420
tactgtagta aagcatttca aaaattctta aatcagtgga aaattacaca tacaatagga     480
attctctata attcccaagg acaggccata attgaaggaa ctaatagaac actcaaagct     540
caattggtta aacaaaaaaa aaaaa                                           565
```

<210> 592
<211> 188
<212> PRT
<213> Homo sapien

<400> 592

```
Thr Lys Ala Asn Glu Gln Ala Asp Leu Leu Val Ser Ser Ala Phe Ile
 1               5                  10                  15
Glu Ala Gln Glu Leu His Ala Leu Thr His Val Asn Ala Ile Gly Leu
            20                  25                  30
Lys Asn Lys Phe Asp Ile Thr Trp Lys Gln Thr Lys Asn Ile Val Gln
        35                  40                  45
His Cys Thr Gln Cys Gln Ile Leu His Leu Ala Thr Gln Glu Ala Arg
    50                  55                  60
Val Asn Pro Arg Gly Leu Cys Pro Asn Val Leu Trp Gln Met Asp Val
65                  70                  75                  80
Met His Val Pro Ser Phe Gly Lys Leu Ser Phe Val His Val Thr Val
                85                  90                  95
Asp Thr Tyr Ser His Phe Ile Trp Ala Thr Cys Gln Thr Gly Glu Ser
            100                 105                 110
Thr Ser His Val Lys Arg His Leu Leu Ser Cys Phe Pro Val Met Gly
        115                 120                 125
Val Pro Glu Lys Val Lys Thr Asp Asn Gly Pro Gly Tyr Cys Ser Lys
    130                 135                 140
Ala Phe Gln Lys Phe Leu Asn Gln Trp Lys Ile Thr His Thr Ile Gly
145                 150                 155                 160
Ile Leu Tyr Asn Ser Gln Gly Gln Ala Ile Ile Glu Gly Thr Asn Arg
                165                 170                 175
Thr Leu Lys Ala Gln Leu Val Lys Gln Lys Lys Lys
            180                 185
```

<210> 593
<211> 271
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(271)
<223> n = A,T,C or G

<400> 593
actttatgtt cnagtgcana aanccncctg gattgccacc ntactctcag ggctgtgant 60
tgtgcnccca nagcaacctg ggcacgcggg gacagggggg ccnacaattg agggagcggt 120
gtccctagct ggggtctata catgncnggg naagggcngc tgagtnccat nagcaaagga 180
nctagnatnt gcgggggtgc ggcctgggcc taccctttna agcatccntn gatccactcc 240
angaanccng gggtagncag gtttnccaac a 271

<210> 594
<211> 376
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(376)
<223> n = A,T,C or G

<400> 594
cctttggggg ngggggggaac ctttaccatt gtnccccttt atttcatttg gttngggttc 60
gcgccctcnn gggccaacaa agttatcgtn nttgaagaga anattttttt ggnttngncc 120
cgattaagcg ncaaatgtgt agcaaaangc cgtgccactt gtggcgtagc tncgtcgggt 180
cgattcgacg acaaggcgtn gcgcgntanc gttagtctcn aatngacccn gtggcatgag 240
cccacgangg nttcgtgtcg tcacatggnc tctagacata acgcncnccn ttttttncag 300
agggggntgc cgcccttagg gaggnagggg tggggacact agccaancca nantctnacc 360
ccattgaaga aaaggn 376

<210> 595
<211> 242
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(242)
<223> n = A,T,C or G

<400> 595
agnctgctgn tcgtnccctn tatgtggctt catnntgagg acaanagtng cactgaggct 60
tgngnatgcc aggcaaggnc aagctggctc aaaaagcatc cacccacctc tgnaangggt 120
atgccangag cangtgcacc agtcccaact angagncccn ggcatgntac atcttcttcc 180
acccctnaaa ntttgngcta caangnccat ttttcttttt ctcttaaggg ncncntggct 240
tc 242

<210> 596
<211> 535
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(535)
<223> n = A,T,C or G

<400> 596
accagttgga tactgctaaa nagatattta tgcagcctca tatgttaagt cgtatatttt 60
gaaagctttt taaatttttt ctttaagaag atttagatg cttatcactg agtaccagag 120
ggatgtaggc tgatgccctt atcaacaaag tcagggactg tggcacacaa ggattgacta 180
ctgcagacac ggccacaatg ctacctctag agggcctgaa tccccctgcc ctctctggtg 240
gggagaaggg ctggcagagc cattagcatg ggctccggcc aatcctggcc actttgacac 300
tcctggtgct gacccagggt cctggaggaa gggatgaggt gggcagtaga gatgctcagg 360
gcagtggccc ctttccatcc acactggaac tatttcagta ttttaccacc aattcagcca 420
ttcccttgtg cgctggctga acatcagccc tgctccaggt ctcagtttcc cctttgtaaa 480
gggaaagctc tggattcagg gagtgatgaa gaggtcatca tggtcttgag aattc 535

<210> 597
<211> 257
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(257)
<223> n = A,T,C or G

<400> 597
tttcnatacc caaaantacc ccatattang accanacatt tgtctnggaa aaattaccat 60
tntntaacnt ttgggccacc tgagannaaa tgggtgtaat ncatgataag atggancagn 120
attnctctta agatnngatn agaccccgtt tttcacggaa catatccaag nacccaatag 180
gnaacaagcc acgggnggag tcacaaacat atattcttta ctctcataat ccgtnncaca 240
naactnttgn acttgac 257

<210> 598
<211> 222
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(222)
<223> n = A,T,C or G

<400> 598
nntggntacc gtcnaaactt nncttggtac ccgagctcgg atccactagt ccagtgtggt 60
ggaattccat tgtgttgggc tataagctgt aatagtggag ncgtgctngg ttcattgcan 120
nagnccctcc gcanncacnc ttgnnacaac ctgtgagnag gcnataaatt attcacataa 180
tcatcactgc atgaanctga ctcaaacgca tccacntaca cc 222

<210> 599
<211> 238
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(238)

<223> n = A,T,C or G

<400> 599
gcatgacatc ancgatgtnt ttggnnacct ganattngct aaaactngng natgccgggn 60
atgnaggttt ggtantgatc tatgcactca catctcatgg ggacgtttca tgtggagtgn 120
tcgacaangt tgctgnancn gagaagtgat gatctcagtt gaaagggtca tgtgaataca 180
cnttacactt gaaaaagaag cacattggga atatcacgaa acgnccacca acatcctg 238

<210> 600
<211> 232
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(232)
<223> n = A,T,C or G

<400> 600
cgaactattt agactaccta ggaaaattat tttagtatca gaagaatatc aggggtgtag 60
tactcatcag agctaaatga gagcgcttta aaaatgttag tttgtcttcc gccatttcta 120
cagaaagctg caatttcagg ttttcaacct aataggtgat atttaanaaa aaaaaaaagc 180
aatcgcaaat agccccactg cttttacaaa tcatttttc cccaacacaa tg 232

<210> 601
<211> 547
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(547)
<223> n = A,T,C or G

<400> 601
cattgtgttg gggaaaaaat gatttgtata agcagtgggg ctatttgcga ttgctttttt 60
tttttcttaa atatcaccta ttaggttgaa aacctgaaat tgcagctttc tgtagaaatg 120
gcggaagaca aactaacatt tttaaagcgc tctcatttag ctctgatgag tactacaccc 180
ctnatattct tctgatacta aaataatttt cctagtgtag tctaaacttt tttaaaaaga 240
catgtaatcc gcggagttag taactcaaaa cgagtgcatc tnggaagtat cgcagccgtt 300
nctggatnaa attcccagct tgctngcttg ctnagccggg gggcggtnaa aaaaacatct 360
gcagcccngg ggnaaaaacc ttcgcattgt tcttacgtgt ttacgttatt ttatttccct 420
nnagcaaggc ngggganttgg ggactcgaaa tggtacagtt gggctgggga tcgcccttgt 480
tacataaaag ncgtccagaa gagggacggt tacaggcngg ganctccaaa ggtcagtccc 540
tgccatt 547

<210> 602
<211> 826
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(826)
<223> n = A,T,C or G

<400> 602
cggggggnnt tacgtctctc tggacgcttt tattgtacca gggcgatccc agcccaactg 60

taccattcga gtccctactc ctgccttgct ctagggaaat aaaataacgt aaacacgtaa 120
gaacaatgcg aaagcgtttt cttccctagg ctgcagattg tcttcttcac cgcccctgct 180
tagctagcta gctagctggg aatttaatcc agaaacggct tgcgatacct cctagatgca 240
ctcgttttga gttacaaact ccgcggatta catgtctttt taaaaaagtt tagactacac 300
tagggaaaat tattttagta tcagaagaat atcagggggt gtagtactca tcagagctna 360
atgagagcgc tttaaaaatg ttagtttgtc ttccgccatt tctacagaaa gctgcaattt 420
caggttttca ncctaatagg tgatatntaa gaaaaaaaaa acaatcgcan atagcccact 480
gcttttacaa atcattttc tcttctaggt atagcctgtc aggtggccta atgtattttt 540
gacatctcta ggaattttaa tagaccagaa atgggtgcca gagatatgcc tgcactaatc 600
ttaagtgggg atttatgtat ttctcaanca agtgattaaa gcaaaactag gcacgaatga 660
aatcaagatc tttaggccag aaatcatgaa nantttana attattttan gaatctgtgg 720
cttctcttct taaaatngaa aaaaaaattg tttaaaccca naaggtctga atacccaagc 780
nccctgaacn anagaacaan gccggagcac cccctcccaa atcccc 826

<210> 603
<211> 817
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(817)
<223> n = A,T,C or G

<400> 603
nnangacttt tgtggtntta tacaattntt ttttctattt ctatgaagag aaagccacag 60
agtcctaaaa taattctaaa actcatcatg actttcttgc ctaaaagatc ttgatttcaa 120
tcgtgcctag ttttgcttta atcacttgct tgagaaatac ataaatcccc acttaagatt 180
agtgcaggca tatctctggc acccatttct ggttctatta aaattcctag agatgtcaaa 240
aattacatta ggccacctga caggctatac ctagaagaga aaaaatgatt tgtaaaagca 300
gtggggctat ttgcgattgc tttttttttt tcttaaatat cacctattag gttgaaaacc 360
tgaaattgca gctttctgta gaaatggcgg aagacaaact aacattttta aagcgctctc 420
atttagctct gatgagtact acacccctga tattcttctg atactaaaat aattttccta 480
gtgtagtcta aacttttttta aaaagacatg taatccgcgg agtttgtaac tcaaaacgag 540
tgcatctagg aggtatcgca agccgtttct ggattaaatt cccagctagc ttgcttgctt 600
agcaggggcg ggnaaanaag acatctgcag cctagggaag aaaacctttc gcattgttct 660
tacgtgttta cgttatttta tttcctanaa caaggcngaa ttgggactcg aatggttcag 720
ttgggggtggg ggatcccctg gtncataaaa ngtcanaaag anggtacagg cggaacncca 780
agggtcgtcc tgcatttana ctcggaattt tggtgcc 817

<210> 604
<211> 694
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(694)
<223> n = A,T,C or G

<400> 604
cttttcaaat catttttnct cttctaggta tancctgtca ggtggcctaa tgtaattttt 60
gacatctcta ngaattttaa tagaaccaga aatgggtgcc agagatatgc ctgcactaat 120
cttaagtggg gatttatgta tttctcaagc aagtgattaa agcaaaacta ggcacgattg 180
aaatcaagat ctttaggca anaaagtcat gatgagtttt agaattattt taggactctg 240
tggctttctc ttcatagaaa tagaaaaaaa aattgtataa aaccacaaaa ggtcctgaat 300
agccaaagca acactganca aaaagaacan agcagggaag caacacacta ccngaattca 360
aattatacta ccagggtgta gtaaccaaaa cagcattcta ttggcataaa atagacacca 420

agaccaatgg ancagaataa agaaccccac aaataaatcc atatatntac cgccanctga 480
ttatcaataa cnaacaccaa gaacatatnt taagggacnt nctattcaat aantagtgct 540
ggnaaaaact gggaaatcca tatgcagaaa naatgaaact agacccctat ccctcaccat 600
acgcaaannt caacttcgga atgggattac aaaacttaag acattccaac ccaagaaact 660
atnaaancta ctattaagaa aacagatcnc nccc 694

<210> 605
<211> 678
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(678)
<223> n = A,T,C or G

<400> 605
taaaaatcta gactacacta ggaaattatt ttantatcag aagaatatca ggggtgtagt 60
actcatcana gctaaatgag agcgctttaa aaatgttagt ttgtcttccg ccatttctac 120
agaaagctgc aatttcaggt tttcaaccta ataggtgata tttaagaaaa aaaaaaagca 180
atcgcaaata gccccactgc ttttacaaat catttttttct cttctaggta tagcctgtca 240
ggtggcctaa tgtaattttt gacatctcta ggaattttaa tagaaccaga aatgggtgcc 300
agagatatgc ctgcactaat cttaagtggg gatttatgta tttctcaagc aagtgattaa 360
agcaaaacta ggcacgattg aaatcaanat cttttaggca agaaagtcat gatgagtttt 420
anaattattt taggactctg tggctttctc ttcatagaaa tagaaaaaaa aaattgtata 480
aaaaccacaa aaggtcctga atagcccaaa gcaacactga acaaaangaa caaagcagga 540
agcaacacac taccggaatt caattatact accaaggtgt antaaccaaa acagcattct 600
attgggcata aaatagacca aagaccagtg ggaaacagaa taaagaancc caaaataaat 660
cctatattta cngcccnc 678

<210> 606
<211> 263
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(263)
<223> n = A,T,C or G

<400> 606
gtggggtcng cancagccaa ctcagcttcc tttcgggctt tgttagcaga cggatcatcc 60
tctagtccac tgtgntcaaa ttccattgtg tgggggccnc tcgcctcggc canagatctg 120
agtgancana cntgtcccca ctgaggtgcc ccacagcngn ttgtnttcag cangggctna 180
caactcgacc ggcagcgnan ggctggcaga antgngcgcc tnnctcattc ctacgcngtn 240
ngccgcagga aggangacag gcc 263

<210> 607
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 607
ccatgtgggt cccggttgtc tt 22

<210> 608
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 608
gataggggtg ctcaggggtt gg 22

<210> 609
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 609
gctggacagg gggcaaaagc tggggcagtg aaccatgtgc 40

<210> 610
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 610
ccttgtccag atagcccagt agctgac 27

<210> 611
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 611
gatagagaaa accgtccagg ccagtattgt gggaggctgg gagtgc 46

<210> 612
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 612
gcacatggtt cactgcccca gcttttgccc cctgtccagc 40

<210> 613
<211> 38
<212> DNA

<213> Artificial Sequence

<220>
<223> Primer

<400> 613
gccgctcgag ttagaattcg gggttggcca cgatggtg 38

<210> 614
<211> 53
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 614
cggcgggcat atgcatcacc atcaccatca catcataaac ggcgaggact gca 53

<210> 615
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 615
gcactcccag cctcccacaa tactggcctg gacggttttc tctatc 46

<210> 616
<211> 1350
<212> DNA
<213> Homo sapien

<400> 616
atgcatcacc atcaccatca catcataaac ggcgaggact gcagcccgca ctcgcagccc 60
tggcaggcgg cactggtcat ggaaaacgaa ttgttctgct cgggcgtcct ggtgcatccg 120
cagtgggtgc tgtcagccgc acactgtttc cagaactcct acaccatcgg gctgggcctg 180
cacagtcttg aggccgacca agagccaggg agccagatgg tggaggccag cctctccgta 240
cggcacccag agtacaacag acccttgctc gctaacgacc tcatgctcat caagttggac 300
gaatccgtgt ccgagtctga caccatccgg agcatcagca ttgcttcgca gtgccctacc 360
gcggggaact cttgcctcgt ttctggctgg ggtctgctgg cgaacggcag aatgcctacc 420
gtgctgcagt gcgtgaacgt gtcggtggtg tctgaggagg tctgcagtaa gctctatgac 480
ccgctgtacc accccagcat gttctgcgcc ggcggagggc aagaccagaa ggactcctgc 540
aacggtgact ctgggggccc cctgatctgc aacgggtact tgcagggcct tgtgtctttc 600
ggaaaagccc cgtgtggcca agttggcgtg ccaggtgtct acaccaacct ctgcaaattc 660
actgagtgga tagagaaaac cgtccaggcc agtattgtgg gaggctggga gtgcgagaag 720
cattcccaac cctggcaggt gcttgtggcc tctcgtggca gggcagtctg cggcggtgtt 780
ctggtgcacc cccagtgggt cctcacagct gcccactgca tcaggaacaa aagcgtgatc 840
ttgctgggtc ggcacagcct gtttcatcct gaagacacag gccaggtatt tcaggtcagc 900
cacagcttcc cacacccgct ctacgatatg agcctcctga agaatcgatt cctcaggcca 960
ggtgatgact ccagccacga cctcatgctg ctccgcctgt cagagcctgc cgagctcacg 1020
gatgctgtga aggtcatgga cctgcccacc caggagccag cactggggac cacctgctac 1080
gcctcaggct ggggcagcat tgaaccagag gagttcttga ccccaaagaa acttcagtgt 1140
gtggacctcc atgttatttc caatgacgtg tgtgcgcaag ttcaccctca gaaggtgacc 1200
aagttcatgc tgtgtgctgg acgctggaca gggggcaaaa gctggggcag tgaaccatgt 1260
gccctgcccg aaaggccttc cctgtacacc aaggtggtgc attaccggaa gtggatcaag 1320

gacaccatcg tggccaaccc cgaattctaa 1350

<210> 617
<211> 449
<212> PRT
<213> Homo sapien

<400> 617
Met His His His His His His Ile Ile Asn Gly Glu Asp Cys Ser Pro
1 5 10 15
His Ser Gln Pro Trp Gln Ala Ala Leu Val Met Glu Asn Glu Leu Phe
20 25 30
Cys Ser Gly Val Leu Val His Pro Gln Trp Val Leu Ser Ala Ala His
35 40 45
Cys Phe Gln Asn Ser Tyr Thr Ile Gly Leu Gly Leu His Ser Leu Glu
50 55 60
Ala Asp Gln Glu Pro Gly Ser Gln Met Val Glu Ala Ser Leu Ser Val
65 70 75 80
Arg His Pro Glu Tyr Asn Arg Pro Leu Leu Ala Asn Asp Leu Met Leu
85 90 95
Ile Lys Leu Asp Glu Ser Val Ser Glu Ser Asp Thr Ile Arg Ser Ile
100 105 110
Ser Ile Ala Ser Gln Cys Pro Thr Ala Gly Asn Ser Cys Leu Val Ser
115 120 125
Gly Trp Gly Leu Leu Ala Asn Gly Arg Met Pro Thr Val Leu Gln Cys
130 135 140
Val Asn Val Ser Val Val Ser Glu Glu Val Cys Ser Lys Leu Tyr Asp
145 150 155 160
Pro Leu Tyr His Pro Ser Met Phe Cys Ala Gly Gly Gly Gln Asp Gln
165 170 175
Lys Asp Ser Cys Asn Gly Asp Ser Gly Gly Pro Leu Ile Cys Asn Gly
180 185 190
Tyr Leu Gln Gly Leu Val Ser Phe Gly Lys Ala Pro Cys Gly Gln Val
195 200 205
Gly Val Pro Gly Val Tyr Thr Asn Leu Cys Lys Phe Thr Glu Trp Ile
210 215 220
Glu Lys Thr Val Gln Ala Ser Ile Val Gly Gly Trp Glu Cys Glu Lys
225 230 235 240
His Ser Gln Pro Trp Gln Val Leu Val Ala Ser Arg Gly Arg Ala Val
245 250 255
Cys Gly Gly Val Leu Val His Pro Gln Trp Val Leu Thr Ala Ala His
260 265 270
Cys Ile Arg Asn Lys Ser Val Ile Leu Leu Gly Arg His Ser Leu Phe
275 280 285
His Pro Glu Asp Thr Gly Gln Val Phe Gln Val Ser His Ser Phe Pro
290 295 300
His Pro Leu Tyr Asp Met Ser Leu Leu Lys Asn Arg Phe Leu Arg Pro
305 310 315 320
Gly Asp Asp Ser Ser His Asp Leu Met Leu Leu Arg Leu Ser Glu Pro
325 330 335
Ala Glu Leu Thr Asp Ala Val Lys Val Met Asp Leu Pro Thr Gln Glu
340 345 350
Pro Ala Leu Gly Thr Thr Cys Tyr Ala Ser Gly Trp Gly Ser Ile Glu
355 360 365
Pro Glu Glu Phe Leu Thr Pro Lys Lys Leu Gln Cys Val Asp Leu His
370 375 380
Val Ile Ser Asn Asp Val Cys Ala Gln Val His Pro Gln Lys Val Thr
385 390 395 400

```
Lys Phe Met Leu Cys Ala Gly Arg Trp Thr Gly Gly Lys Ser Trp Gly
                405                 410                 415
Ser Glu Pro Cys Ala Leu Pro Glu Arg Pro Ser Leu Tyr Thr Lys Val
            420                 425                 430
Val His Tyr Arg Lys Trp Ile Lys Asp Thr Ile Val Ala Asn Pro Glu
        435                 440                 445
Phe
```

<210> 618
<211> 385
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(385)
<223> n = A,T,C or G

<400> 618

```
ctgtgctgag aaccaaaagc tatgancact gcttttccaa atgtccataa naccaacatt      60
tttatcacta ccaccatcac ctgggagctc nttagaaagc tagtctcccg ggcaccaccc     120
tggcctactg aacctaatgt gcatttaaca agattnacgt ngaaatctgc aaagcacagg     180
ggcngataac agtaccacct gntctggttc ctanccccan gacccttaca gtctaactgg     240
gacacaaggg cttnaaatca aattgcctat cattaagata tacaanganc ntgagaaact     300
gctncactta tntattaagg ngctctaaga cttagaaacn aaangcantg ctgagangat     360
tcaaatatga nggggncac tttnc                                            385
```

<210> 619
<211> 869
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(869)
<223> n = A,T,C or G

<400> 619

```
gatatcccgg gaattcgcgg ccgcgtcgac ctctacttgt ttagacataa atgcagtcta      60
gcattaaaga tcctttaaaa aaatgttttc ccaatggtta aaagacaagc tcaaataaat     120
gaactctcat acatatgcca aaattgatga gtagataaat atttcagtag gtagttacta     180
gctttctgtg tatgagtaaa catatgggag aaatttaaaa cactaaagta gactcaatga     240
aagcatagta tcctatgtat tcgtttttca gaaatgtcta atgaaggaag gaaacaatga     300
atgaatgccc ttattcctct tagagtgctg ggacatggtt ttgcctgaaa acttcatgtg     360
aattttatat tttgctacac attacaccca tcttagactt atacgtataa gacataaggc     420
atatcttatg tcttacatgt ataataatct aagcagaaca aaaaataacg aaatattttc     480
ttccccaaat ttttgagaca gatggatttt ccggaaagat gtgtttagct tttaatcctg     540
tggttttgtg taccacctgg cacactagag tgttgctcta attcagtgag ttgtaactct     600
gggtgaacag tggaaatact agggtacatt ttaaaaatgc taatgctcgg gcctcgctga     660
agaccaaatt aattggaatc tctgngggng gnattgatct ttttataatc tttctanang     720
attctaatgg gcttccaggg atgaaaaccn ctgntggagc tnggaacctt cctttagttt     780
ggagaaaccc cgatgagggt ntnttaggcn ccgcctnttt ttggcctggg cttccccccct    840
tatnntnttt tggaanggnc cnaattttt                                       869
```

<210> 620
<211> 339
<212> DNA

<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(339)
<223> n = A,T,C or G

<400> 620
gngcgggcct cnccgtgctt gctctcgctg ccgacgctct ttttccacca gctgtaggan 60
aagcccgaag accactggtc ccccgggtag cccaagtacc actggtcctc ctggctcctg 120
acgctncggg tcttcctcgt ggcgtagact gccagcttcg gagacccctc agcccctccc 180
cgcttttctc caccccagga ggccatcagt agcgagctac tgcctcggcc acaacctccc 240
agcangatag cccgcggttt ccaatctgcg aaaggaggac cgccnagccc gaaatgccna 300
gcccagcnat cactgccacg ccgagccnag cgctcgtgc 339

<210> 621
<211> 267
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(267)
<223> n = A,T,C or G

<400> 621
ggggngcatg gtcccnggta gccaagtaca tggtcctcct ggctcctgac gctacgggtc 60
ttcctcgtgg cgtagactgc cagcttcgga gacccctcag cccctccccg cttttctcca 120
ccccaggagg ccatcagtag cgagctactg cctcggccac aacctcccag caggatngcc 180
cgcggtttcc aatctgcgaa aggaggaccg ccnagccaga aatgccnagc cnagcgatca 240
ctgccacgcc nagccnagcg ctcgtgc 267

<210> 622
<211> 847
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(847)
<223> n = A,T,C or G

<400> 622
cttangntgt cgactgacgt catgcatgan ttaaagcaga ggtttggtga aatttatgaa 60
aaatacaaaa ttccggcttg tcctgaggaa gagccactac ttgataactc tacaagagga 120
acagatgtga aggatattcc ctttaatttg acaaataaca tacctggttg tgaggaagaa 180
gatgcatctg aaatatctgt ctcagtggta ttcgagacat ttcctgaaca aaaagaaccc 240
agtctcaaaa atatcatcca tccatactat catccgtact ctgggtccca ggaacatgtt 300
tgccagtcat cttctaagct tcatttacat gaaaataaat tagactgcga caatgataac 360
aaactaggca ttggacatat ttttagtaca gataacaact ttcataatga tgcaagcact 420
aagaaagcaa ggaacccaga agtggttacg gttgaaatga aagaagacca agagtttgat 480
ttgcaaatga caaaaaatat gaaccaaaat agtgacagtg gcagtacaaa taactataaa 540
agcctgaaac ctaaattaga aaatctgagt tctttaccac cagattctga cagaacatca 600
ggaagtatat ctacatgaag aattacagca agacatgcca aaagtttaag aatgangtca 660
acacattaga aanaagantt ctgggctttg aagaaagaaa atgttccact tcataaagaa 720
ggttgaaaga agaatgggag agcccngaan tttttgcccn gaaattttcg ggaaccctac 780
tggatgggtc nactggttgg ccatgaatga ataatggact aatcnnccaa ttcctnggga 840
agggaat 847

<210> 623
<211> 681
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(681)
<223> n = A,T,C or G

<400> 623
aaaactgtac tcgcgcgctg catgtcgaca ctagtggatc caaagaatcg gcacgagcga 60
aaangctcan gcagcccggc tggccgccgc cgctcctccc cccaggaaag ccaangtgga 120
ngctgatgtg gctgcangag ctcgtttcac agcccctcan gtgganctgg ttgggccgcg 180
gctgccangg gcggaagtgg gtgtccccan gtctcagccc caaggctgcc cctcacaaag 240
cactggtggt ttgcctccac tgccaccttg ggctccgaac ccgctcccct gctgtggang 300
cccaccgtgg gaatccaggt ccccaggtgg actgcctgcc ttgccctcac tgcccactct 360
gcccacactt ccctgcctag anaccgggaa ggggctgtgt cggtantggt gcccacctgg 420
atgtggcagc accgactgtg gggtggacc tggccttgcc gggtgcaaaa gtgggggccc 480
ngggaaaagc acctgaagtg gccctgaaaa atcccccctt aattttnccc caatttgggg 540
ctcnaacaaa aggaaattgc tgaagccaan ggtaccaagg tcacccctaa ggccagggtg 600
aaaaggtccc aaaattccaa tncccaccnt ttgggcttnc ctcttggaac cccggccccc 660
tctcntgaan ttttaaaaaa n 681

<210> 624
<211> 661
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(661)
<223> n = A,T,C or G

<400> 624
attggtctta ctgtaccacc gggtggaaat cgatggccgc ggcgtctaaa tatccgattt 60
tttttttttt tcctcttctg actgtccatg gacaaatgaa actaacttaa tctaactaaa 120
aaacacaact atattttgaa gattttctat ctgcactcaa ggacactttc cacncggttg 180
ttgttacctt ttggtcttgt ctctgaacat gaaattnatc tcaagggatt ngatttctgg 240
acctcctatt cctgctatgg gtttgatatt tcttgggctc cagggccact gttgcattgg 300
gntgacagnt acctcctagc ccatanccctc ctatcttggg aaacaaacct aacaactacg 360
tgtaccttcc atagatctct gattgagtct cagtatncgc ttgctcatgg gcgattcact 420
tgaatccgtn attggtgcca acaatcctga ctcatgggnn aatggatcct atcacgttcc 480
cctgattngc aacccctgta tacatanatc taatcgcata gaatctagcn tnggntatgc 540
gcggctacgc tatcagggnt tgntaactat ngcatggcta cgaancctga tcatgatcna 600
gggtcatgga ctcttatcag gggggttggg ccgngcttct ttttcnnacc ttggtaaaac 660
c 661

<210> 625
<211> 181
<212> DNA
<213> Homo sapien

<400> 625
gcaacaatca gatcatgtta aagtaaatct ccattgccct ggatcacttc aggatttaat 60
tgtccaagga gagcagggtt ctcctgtgaa aaaaaggtgg ggaaatgttt gagagtaaaa 120
aatacaaaat tcaaccggtc gaaaatacac cactccattc agtgctctac ccccataagc 180

c 181

<210> 626
<211> 181
<212> DNA
<213> Homo sapien

<400> 626
gcaacaatca gatcatgtta aagtaaatct ccattgccct ggatcacttc aggatttaat 60
tgtccaagga gagcagggtt ctcctgtgaa aaaaaggtgg ggaaatgttt gagagtaaaa 120
aatacaaaat tcaaccggtc gaaaatacac cactccattc agtgctctac ccccataagc 180
c 181

<210> 627
<211> 813
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(813)
<223> n = A,T,C or G

<400> 627
accaagctgg agctcgcgcg cctgcaggtc gacactagtg gatccaaagt gaacgtgaag 60
gtgagcagag gagaacttgc gatggcaaag ttaaaaacaa gaggagatga tggtcttggt 120
gtggcacagg atgttaaaaa aattctcctg tccttaagga gttactgcta tttgagtaat 180
gtgccacttc cctacatagc cttctatgca gaaatgctat atttccactt cacaacccag 240
aacgtgcatt ttattttaca tttagaggag gaacaaacaa ccagaaggca aaaactggtg 300
cattattttt tgcaattctc ttggaaagag ttcgttttta acttctgctc agacagcaca 360
caactactgg gaatatattt taatttcaaa tctgatgtgt gacatctggt aactcattta 420
ttgctaatga agttttcaca ggaagcagca gtcaccagta gctcatctta tttttcagtt 480
ggcaaagtgt tgtttacctt ttattggcct gcatcggtgt ctcttatcac aggatattta 540
attagaaaac gcaagtagcc taacatagaa nagaaatgga gtggtagata atagtagata 600
gaatggctaa atatttttat tacagtgatg taatatcact gnaatttatg gttaaaaatt 660
atgtaatact caaaaggaat tctcagactg gcgaaacagc tggncaacag ctntcacagg 720
gctttnanct cctnttgagc tttccccctg ntggacttta gtcttccttt tacncccgna 780
gttnccattn nttaccaatt gtnccgggaa ana 813

<210> 628
<211> 646
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(646)
<223> n = A,T,C or G

<400> 628
tttgggnggn ggtgtctcnt ttgggtggac tttttgggtc gtagggcccc aaggccgtta 60
atcccgtaat aacggaagac gaagaagagt cagaagagtg cttctataag gatcgggacg 120
agactacctt agaggaataa aggaaaaaag cagaggagga agagtggtag aaggagtcag 180
aagaaaccca cacgtcgttc tgaacctgga gccttatcaa aaaggtctag ataaacgata 240
gcgatctcga tatcgagctc aagaggtagg tttagagact tctcgtcctc gagagcgaaa 300
tggaagatct cgacgacgat aagaagttaa agtgtagagg gtgcttgagg agcgcgtgga 360
aggattctgc ggagggaccc atcgacgtag agacttgaag gcctactaag gtccacaaga 420
agcccggctc tttctccgaa tggtcggagc gtacagtatg cgacgtcgat cggcagacaa 480

gctggcggta gactcgaagt gttcgggcga atcgacttat aatagtcgcg cgctagtaac 540
gtaggaacac gaagagtagt cgaaagaaaa cgtttagtga gggaaaagat tagggaaaaa 600
ggagaggctt aataactaag acacttggag cctaggccaa cgcgaa 646

<210> 629
<211> 617
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(617)
<223> n = A,T,C or G

<400> 629
gcccccnccc ccctcctngg gcttatnggg acagacccac gtagtactct aaatcttctc 60
ctacgccgga caacggaccc tataccaatt cgaatcttgg acactccgac cgccggattc 120
tcttcccctt tcggcttccc ctttctgtcg gtacccctcc ctagtcgtct cctacacctt 180
cgtaccgtcg atatatagtc gccgcggact agcctattta ggtgtcctag actcgttatt 240
gatccactca ttagtctagt actatgcgtc acgtatctta gttgcctaag agggagatta 300
aatcctccac aagttccgac gaattcctgg actctcgtac tagcaaactt tcttatgagg 360
cttccttgta tatcttctgg atgtttctcg tgtcccggtc ctccgctact actagagctc 420
cttgccctat ctctagaagt agaggactct cgggttcgtt ctccaaatct agcgctagag 480
ctatcgctac ccgctcgatt cccccagcgg aatcttgaaa cctgaggtag tacacaaacc 540
ctccncatct tccctcggtt gctccttctt ctcatccccc cttcccgcct tctcgggaan 600
gaatctactt tancttc 617

<210> 630
<211> 644
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(644)
<223> n = A,T,C or G

<400> 630
cnntcggcnt gggttttntt ctgagnnncc cccccccccc cccccccaaa cttacaccca 60
ccaaacactt tccgcccccct acctaggaga cattagaagg gtttaggctt cggcgtatag 120
taaagtcctc tacctcggaa gtagagaatt cggtatttaa attcagggtt agaggctcgc 180
tcgttagatt tatagtttag gtttagaatc ggaaaccttc gatcttcctt agaagggtaa 240
taagtgaggc cctaaatccg tctaaccaag gcgttaaggt ccgtacctaa acctagtctt 300
atcttctatc aggcgcacca atataggtag gttctacttt cgtataggcc ttaaggaata 360
gttcggtagt tatcgaaggc actcctctct aggctaggct tttctcagtc ttagtactcc 420
gggaccgtcg tcgcanaaat atcgatggac ggtaggtatc tccgcgttac gcgtcgggct 480
agggatatag agcgaattat cggcgagagg cggtcgctan gaatcggtat caatatgntg 540
ttctttaccc tacggatatc ggcagaaaac ataaaacctt ctnaccangg ataagggatt 600
atcggacccc taaaataaca gtaacattta gantactagt accc 644

<210> 631
<211> 526
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(526)

<223> n = A,T,C or G

<400> 631
ccntcggctt gggttttttt ctgagccccc cccccccccc cccccccccc cccccccggc 60
cccatagccc caccggnccc acccaaattt taacaaaata aatntaccta tcgntcacct 120
atcccncgta tcgngtaggt cggtaccggt accggngatc ncnacgattn ttcgggtcgt 180
cnccccttaan acggncccgt agccnccgga anaaatacta cgagngactc taatntagca 240
anacccgccg tcnattanta gcatccttag tcttccaatg ncgnggattn ngaatccttn 300
naagttatcg ggtagaacgg gtcccggtcc cccgccctct ttncaattaa cgccgggtac 360
aaantcggtt tctaaattcc ncacgaattt ngncggcaac attcncgggn ccttattanc 420
cntttccaac cccgatacnc nagctcgatc gggctttanc gaatccgggg tcncccccga 480
ngantccggg tcctttgagt ngctctagga cggttacgac ggagga 526

<210> 632
<211> 647
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(647)
<223> n = A,T,C or G

<400> 632
tttgggnggc gggngctcat ttgggtggac tttttgggtc gtaggaacct ggtatgaggg 60
gtgttttgag tttcttcttc gtcgtctctg ggaggttcgg tttcgattga gattcgggtt 120
cgtctttatc ttacgaggca ccctgatatt gttgcgcttt ggtttggttg tggagagttt 180
tgtcctactc tagcgggtca tgcggatgat atgtagcctg cgtggcctga tagtgatgtt 240
gtgagcttga gaggggagtt gtgggtgttg cgggcggagt aggaggggtt ggagcaccgg 300
gattgggaga tatagaatca taagtgttag gtataggtcg attgagcgag ttcgtggaat 360
tcgtgtggtc atcataatta gagtgaggat gggctctata tttcttagag gacgcacggt 420
cgtgattcgg ggtttgatgg gtgttcttct tgtgggcacg attagcttgt tcatgatggt 480
aaggaccata ctgtttcgaa tgaggattcg tgtcttcgga ttgttgtgga tattgtggnc 540
tanactattt agtgtaagcc ggaggtggtt tgccgtggtg gagtatccga nnttcattcg 600
ganggtatgc gtgcggagcg gtccttgtag acattccgga aaaatgg 647

<210> 633
<211> 630
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(630)
<223> n = A,T,C or G

<400> 633
tccttcggct tgggtttttt tctgaccccc cccccccccc cccccctcgga aggcctctag 60
gctcccaccc gtctctctaa tcctcaggaa ccgatccacc caaccaactt actaatgtcc 120
tacagtaaac acccgagaat ataaacccac acctaggcct ccaatcctac cagggaagca 180
agaagccgta gtctagcgta ttacgaaccc gagatagaga cggagatact tagttttatt 240
ctctcggaat aggaaagacg actggggagg gaatataggc tagcgcgggg ataggggcta 300
tggcggatat gggggcgggt cgctctctta ttcttctata ccacgtcaat aggaatgtag 360
atatacctag atgttcccgt agaaagagac gttagaggtc tccgaagcta taaaggagag 420
gcgcgaagaa acttcgtact ctagctttat ataggtagtc gctctagtcc cataagcgac 480
gagagatcta ctagatttcg gtatcgccgt cgtatgtatt cgaaatagtc ttcttcccct 540
tttcgatctc ctctctatac tacatggnga ttatagtcnt aagatagtca ggatattagg 600
atattagtta tatgacgttc gacgggacgg 630

<210> 634
<211> 647
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(647)
<223> n = A,T,C or G

<400> 634
ccntcggctt gggttttttt ctgacccccc cccccccccc cctccactaa gancttaacc 60
caaccctata gtttactcgt ataggggaat cgaggagaaa taggaacgaa gagcgggtga 120
taaagagaaa gtactttcct ttatatgtta agagcttagc gtaatgactt tcgttatatg 180
gctagttgat tttatccggc gttatagggc ttagttctgg ttatctcggg tctaattccc 240
ttagtatgct cgggagttta acgaggtcac gggatagcgc gtaccctttc taaggttctt 300
ggaaagctat tcgttattta tcgcgattct cgaggtcgaa aggatcaagg atcttccctt 360
ttactaccct agtcgggtta gcggtcggtc aaaactagtg tagtaccttt acctcctcga 420
aagttatagt cgaaacaacg tattagtcga aattatagcg gatagatcga gacggttctt 480
tctcgggttc tcagccggta atccctctat ttggggtct tctccctctt cccctttgtc 540
ttccgcctta gcttccaagg ttcctcggaa gcgaggggtt ctacttaagt cgntagcgtt 600
ccttataaac cncctacagg cagacccccct tgtaaacggc tcggggt 647

<210> 635
<211> 645
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(645)
<223> n = A,T,C or G

<400> 635
ccttcggctt gggttttttt ctgagccccc cccccccccc cccgaaactc gccttaccct 60
agatacccaa agaatagttc cactcaactt cgtctaagta aaactctaga acttccaaac 120
ataaaagact tcgcgcggtt agctacacag cctacgggaa tctcacgaat cccgattcaa 180
gtcccactct cgaccacacc ccggtatcgt cgttttccca taccaatgtc gaaaaataaa 240
ataaaatcca gtcaagcccc acggtaagcg ggggtagggc taggcgaaga ggcaggaacc 300
gttcgaggcc gggggctttc aaaatacaaa acaactactt aaagtttacc ccttctaaag 360
tcgggggcaa cggttaaagc acgcctctaa agtactactc gtttcgagaa ggggtagtca 420
tctcccgcat agagactctc gcgtatatca actcgcatcg cttctagcat tccgacggtc 480
gcccgcggct acatatcttg cggattagct ccgagggact atagggttaa ttagtctagt 540
aaattctctt agaggatagt cggggtcgta gttaggcagt acgaggggac atggnctgcg 600
tcgtgctcta ccttgacagc atactcttat aaacatcttt ttcct 645

<210> 636
<211> 643
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(643)
<223> n = A,T,C or G

<400> 636

```
ccttcggctt gggttttttt ctgaccccc ccccccccc cctagcggaa aacaatcccc     60
accgagattt tattaatcgt aaaactcgcc ttcggtacca agtcttcctc cttcccgtaa   120
cctggctccc tcctagnggc tttacgaacg tccctcctct tcttacggct cggaagtggt   180
tacggttaaa tccggaggng gggctaacga atccaaggct aactcctctt anagtttgtt   240
gtccncncgt ttagtaagga tccgtggagg gcgagtattt gncccccggc ctttattnta   300
tagttcccta gtacgataaa gntaccggct atcctattac agcggataaa agttatttan   360
agggccgacg tcnccgctag acaggctaca gctagnggag gtaccgcctc cgactantcc   420
gttgnttccg acaaggnagt ttcggttaac tccacaaact cctccgccga ctctanggtg   480
gggacggcag ttcccncgtt tagtgtgcgt tatagagaag ggcatttgag ttggacgtta   540
cnttttaaca taggttattc cgtttaggtt cttgcgggcc cgtgggggta gtncnccggc   600
gcgttnntat cggcgatttt ccgcagtttc cgtttccggn tnt                     643
```

<210> 637
<211> 631
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(631)
<223> n = A,T,C or G

<400> 637

```
gggttntctc atttgggtgg actttttggg tcgtaggaac cggtatgnag gagtaggagt    60
cgctgggaag actagaagtt agctacggac gattagtgtg attccactct taataacgag   120
taatcgttta cgtcgggttg gtgtttcggg gttttggaga gtaagcgtag ttgtggagtt   180
tcgcatatag gtccccttac ttcggcgatc tcgtcttctg tcggttaggt tattattgtt   240
catccttcgc attagtagta gggttggtcg gataaatcga tagctattct ttagaattcg   300
tagtcggaga attcgtgtac gaagtccttt aagttcttta agttcgcgag taagacgtgt   360
acggttattt tgtcgtcgac gtaggtgtcg tttacgggag tttcgtttta ggggtttacg   420
tagaacgtta ttaagcacgg taatacgata gaggattacg cgacgtattc gtcttagaac   480
gtcgattttt cgaaggcgca tttgttatcg aaggggagtc cttggagaat cgagatattc   540
caagaatatt acggagatta cagatcggaa ggctcccgag atcggacgta ttaccggtct   600
cgcccgaaac gagtaggtat cntccggata a                                  631
```

<210> 638
<211> 606
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(606)
<223> n = A,T,C or G

<400> 638

```
cccccccccc ctcaaccatc nattccccac ctcaacgcga attacggttt cgaaagtcga    60
caataagtcc ggtcgagtag agggaatcag gggctggtan aaaggaccac gggcggaaaa   120
taccggtctc cttccgggga gcgacgtcgg ggaaagggaa gagagcggtc tagttcgtag   180
gcaaacaggt cagaaaagtt aaggttaaag gtcggagggg agaggatagc tagtacgctt   240
agttcggggc tcgggcgcag ggccactttc ctctttcgcg ttcctttact ctgcttacga   300
gttcaggctc cggagttccg cgccggaggt cgtcgcgacg ctaggaatgg ggactcgctc   360
agtccccggt tatccttcgg gattctatgt tttcgccgat agacggagac cgggtagtag   420
ggttccgtcg taccgccact cgtcgccttg atccggcccg ctccgcttaa gggcgatgaa   480
agattaggta ttagggctct acgggacgag gcatagggcg ggagaagggg ggaggggtcg   540
ggggtcgaag ggantaagaa atcgcantcg cgcggggtcg gtagganccg aaatttttct   600
cnncgt                                                              606
```

<210> 639
<211> 592
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(592)
<223> n = A,T,C or G

<400> 639
tccntcggct tgggtttttt tctgagcccc cccccccccc cccccgggaa cgagaaaaca 60
atcccaccct accgcgggga gtgggttgna cgcttagttc tagaatcctc ggaatcgtcc 120
tccggcgttg gtagttccgg cgattccgag tatgccgaag tgtatcgctc cgtctagagg 180
ttggtatctg tttatcgcga tgacgctatt gactcggatg ctttcgaagt agggggatag 240
gcgcatagat acgcctccgc ggtgtcctct gaagtggccg catccgtgga cgcagcgtag 300
acagctctgg tggacgataa cggcttctcg tactcctact ccggctatta tgttagagag 360
gacttgtttc tgaacggata taccattagc gaaggggtac cctccgctaa cgcaggcgtt 420
tctaacagtt cttccgggcg ctccgaattt agattgacgc ctccgcagca ttgtgggatc 480
ctcttccgtt agccctcttt ataggatttc tcctccgccc cgaaagangg ctggtcgtcc 540
ccggcangta tgtctagctc gaacgctttg ttactccttt gttttcgaaa na 592

<210> 640
<211> 637
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(637)
<223> n = A,T,C or G

<400> 640
ctttgtggcg gtggntgtct catttgggtg gactttttgg gtcgtaggct tatccgggtn 60
gggctcccga agtagcttag gatcgccggc tagttccggt cccgcccgtc gaaagcgcgg 120
ttcggcgggc ggccccgcgt tcgttcgcgg gctttaccct catagagtgc caggtctcgg 180
ttcttacggg ttcgtcggcg atagatttta cggcgagagg tcggtatctt cgccgcttta 240
cgttcggtcg gcatctacgc ctagttcaca ggtagtttat gcgccggagc gcgtgacgga 300
gaggttatac gggacgcgga agaaccgcct ccaaatgact agtacaggct cgttcgggcg 360
tagatctcct cgctcggtcg gcggttctta cttctagggc cgctctacgg tttaaggcgg 420
tcgttagatc ttagaaacta tactcaagtt tcagtcggaa gaaaggaagt agagagaagg 480
gtaaacgatt acctccggtt ctagcccttt ttactcgcat aacgggagaa cggggtccgg 540
ctctcagata cgcctcgcga gacgtcgcga ttcaacttta acctccgcta gggcatccgt 600
atacggttaa cgcggtaaaa gcgacctcgg aaacctc 637

<210> 641
<211> 649
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(649)
<223> n = A,T,C or G

<400> 641
ctntgtggcg gtggttgtct cagtttgggt ggatttttgg gtcgtaggna acctggtatg 60
aggtctagtt tcttcaacga ttcttggttc agttacgcga ccctatcctt atcttacaat 120

gtcttctaca tcaggttcat caattaatat atcaattaca cattaacgac ggtgtgacgc 180
aatatgagaa agtatacatt aaggttatta tatattattc gcttaaaaag gttcctgaca 240
tgggacaact tcacccacca ttctagaagc ccccctcct gtaggacccc ctcgagttcc 300
ccattatctt agttcagttt tcatttttta accaggaggg tatcggtttt taataggtac 360
tattttgtca aacttttcag aagctttatc ttcaaatata cttgcaccat ctgtactagg 420
agcactaact attcgagtct attacagctc aacagaaaat aattgaaatt aaacaaccta 480
agtatcgtcc accataaccc catcgggctc tcaccccatt tcttcataag ttctagagca 540
tcctgagctc tttcctatta cccttgatgg tactcatggt ctaatacccc ccgcagttat 600
aggtccttat ggatcctatg ctaccaccgg tctaatccct tctatcacn 649

<210> 642
<211> 645
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(645)
<223> n = A,T,C or G

<400> 642
tccttcggct tgggtttttt ttcgtcgcgg gttactatta tcgattgtta cttgtaaagg 60
cgatactccc accgctcacg atattagacc tgctcctcta gaagcgaacg gcgataggtc 120
tactcggccg gcgaagacgg cgaacgggta ggaggagcca tatgcaaccc taacggagat 180
tataagtact gggaaaaata ctagtattaa ggtagcgggt taagataggt ggagagacac 240
tattcacgag cataagcact tagaaggtct tctcgaggag aggtaggcta cggactacgt 300
tccttcttcc tctagcctcg agagggagta tagatgattc gcaaaagaga atccctccta 360
tacgctggca taactagacg acgcgtcgtc gggaaatctc gccaacccta ttgcgacctc 420
caaaaggaag attgtcgttt catagaacgc taatactccg ggtcttcccg aatcatagcc 480
gcatatcggt aagaagacgg taaaatcgcg cgattctaac aagattctgt agacttaagg 540
ctaagcacta gaagcgatct cgattccgga tcttaagatc atactaatag ttcggtcaca 600
ccagacgacg attagccact agaagcccta ctccgtngaa accgg 645

<210> 643
<211> 586
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(586)
<223> n = A,T,C or G

<400> 643
ctttgtggcg gcggtgtctc atttgggtgg atttttgggt cgtaggaacc tggtatgcag 60
ggtccgcccg gaattaaaag cgggatcccc aaaacgnngn ttcgcaagaa gagaagaatc 120
atagcgatag anctttcata gtacaaaggt aactaagagg aaaataatgc agattcagaa 180
ctagttgcca aattagaact cgattaggcc aaggatccga gcctggcgct atcacttcgg 240
gacttaagct acggtagagc agtcggtcct gaagcatagc tcccgtagga cgtaggaaac 300
tagtccggca cggaggacat actctcgagt ctcggaacgt ctatttagaa tataaacgca 360
ttaacctcag aaggcgccga cgcggttact ctctagggaa ctatttcatt ccttccggag 420
ctcccctatt tttccaacac atataccggc aaaggaaaat cttntgtcct cggtctaaag 480
agagggaaaa aaaacgatat ctaggttcgg gtttatccat ttaaaaanat ngacgcgact 540
actccctttc aaagggagtt tccccctagg nagagttcaa cngaag 586

<210> 644
<211> 646
<212> DNA

<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(646)
<223> n = A,T,C or G

<400> 644
```
ctttgtggcg gtggttgtct catttgggtg gcatttttgg gtcgtaggaa cctggtatng     60
agggctattt gacttgtttc tcaaatccca tggtatggtg ggtggcgtgc ggggtggcgg    120
tcggttcggc gggggtgggg gtcgtcctcc aaaggagttg ctagagggct tttagtggtt    180
ttagggcggg aaggggttag agcggagaga cgtcgtcgtg gaagcttctg gcggagcgcg    240
agaaggtagt tagcgccggt tcggaagatt ctcagaattc gagaagaggt agtggggcgc    300
ggagagagag tttctaagtc taaacgtaga ggtcgtccta gtcgggccgg gagtagcttt    360
taagctagag gtcgaggtcc tcgtttaggc tccgggctct tcgggcagta tcctctttct    420
cgaggaacgg agcgaccgac gtcgtagccg gacccgtcta tccgtacgtt tagagatacg    480
ctcacctcca cgggcgtata tgcccgtata cgtataaacg cgtaatatac tcgcgcgtaa    540
aacacgtata cactatatac acgcatcgta cggaccgtat agcgttatac gcgcgcgtat    600
attaatttac acttatatac gcgttaacac gatatatcac acnccg                   646
```

<210> 645
<211> 654
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(654)
<223> n = A,T,C or G

<400> 645
```
nccntcggct tgggtttttt tctgaccccc cccccccccc cccccggtcg acaacgtgcc     60
caccgttgcc atcccagcat agctggttcg ttctgtttta ttcttagtag tttagttcgc    120
ctatagtccc tcgtctatcg tctatcattt aaggaggcgg ggctcgctct ttagggcggg    180
tatcttaggt attcttctgg tttcggctgc cgtctcggag tctggtcctt ttgctttcct    240
ttcttggtcg aacttcgtgt ttgatcgcgt tgtttctttg gggtcgtcat acctaagggc    300
cacttcgcca acaaacaagt ttgtgtagtc gtttctatta gggttcgctg gccggcgctc    360
ttactggttg gcgattttta acgcgtttgg ttttaatttg cttcctcccc tagggctcgc    420
tcggtcttct ctctgttcgc tgctctcgtc cggcctttgg tgcgggggata gctccggcta   480
ttancgtgcc gtgtccgtgt ggntttgtc caatgtgaag gcctaggggt gcgggcttct    540
ttggccatgg nttcccctct tgtgancctt aggggtaacg antcgtaatt naaggtcggg    600
ggttggnata cgttntangg gangcctgng tccgntattc cttgttttgg cctn          654
```

<210> 646
<211> 645
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(645)
<223> n = A,T,C or G

<400> 646
```
tccttcggct tgggtttttt tctgagcccc cccccccccc cccccacgcc aagtacacag     60
acccaccaaa aacaacgtca acacaacttc gggtatacgg accttaagag agaccccgta    120
gtagacccta ccacagccat ccaatagtca aacaacaagg gcgcacccaa tccatccata    180
gagctatcaa acaacggagg ggaaaggaaa gagcagggtc aacttagcag agatcgaagt    240
```

```
cggcactaat tcctttcaag tactcgctcg gcttgtagtt cggggtaaag tccgctctca     300
aagggccaac gaggttttaa agcgaccccc gtatcgagtc ttcttcgtat tcattaaggc     360
gttaaaggta cgagacctag aagagagtag aattagccca ccaaatcgcc taaaccggca     420
aaaacgacca aaagtcaaag acccttacaa atatcacctt aaaacgccaa ccccaaaaac     480
gcgatcagta acgcacgtac ctttcccacg cttttctttc tttcactctc caaaacaaac     540
ccgaatattt agcgcaaaaa atatccgagg gagaattaga agctattacc cgaaaaaaaa     600
ncgganangg antaaatngt ggggaatana cgtttggttt ttctg                     645
```

<210> 647
<211> 753
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(753)
<223> n = A,T,C or G

<400> 647

```
accttacctg gtaccgggcc ccccctcgag tttttttttt tccaaataca actcagattg      60
tatacgaaaa gctgataata cattgacttt tgctgtttaa atcccttgag cctttgataa     120
tgattttttt tgtgttaaca attgtagtat ataaaatcgg attcaccatc cttctgatgc     180
catattgatt agtttgattt tatggtgatg ggatcattgt gtgttaactg tattaagaag     240
aaatggattt gattgacttt gcatccattt ttatctgtgt tactttcatg ttttatttaa     300
aagcatttct ggaccagaat aagttaagtg gtataatttg ctttttacac gtttatataa     360
ttgaagttag caatgtggca aaatctctaa tggaaataaa atgcttcaga atgatgacat     420
aaatctgagc tatttcttgc ctggagaaca agtgttattc ataataattt aatagcttct     480
gaggtgtttt gttcatgtga tgaaggctta tccaccttgt atcaattcat gggctctgct     540
ttgtttaatg tagtcaggtt gttaatacna gacttaagag tcatcctact gtgataagtg     600
gtgagtgaag attacatgtc ttangaaaat tatactggga atatctctga cattaatggg     660
tttaaatgtt ttaaggctag ggatgatgc aatggananan atncttccaa angtttctgg     720
ttgtttatat ttgnggaagn catnaagana ccg                                  753
```

<210> 648
<211> 383
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(383)
<223> n = A,T,C or G

<400> 648

```
gatatcccgg ggaaatgcgg aggcctttng gcttacgtgt ttaccgcgta gggcaaagcc      60
ttgncaaatt cccggccagc ggagcggcga gggtggggac tcacgggaag ttaaacagcc     120
tcgtcggcgt cctcgaggct ccaaaaccag gctctaggcg gggacgactg cagccgttat     180
ggaggccacc gcggctacgg ccgcggctga ggcctcccca ggtggagcgg tggcctggag     240
gggaatcttg atcctgggcc agccacctgt caagaggagg cggagcgtca tgcctctgga     300
agactggatg aatattctcc aggagcctga cgaaggcgaa gaagtctttg cagaggaaat     360
tgaatgctgt ctgatgctac aat                                             383
```

<210> 649
<211> 349
<212> DNA
<213> Homo sapien

<220>

<221> misc_feature
<222> (1)...(349)
<223> n = A,T,C or G

<400> 649
cgattgtnta cnagtcttag agtaagctta agntcgntac cgagctcgga tccactagtc 60
cagtgtggtg ggaattccat tgtgttgggt cactagtaaa tggatttagc tagacanagg 120
anatttaccc tattccattt agcacagtga gganaggcta nacagctagg atgcaataaa 180
aaaaatttta atgagaaatg tgtgtggtag attaattcta ttaatctcaa gttatagatt 240
aaaaaattta agtaccncat aaatgccatt tgcctttgct aangntacat ttttatgaan 300
aangaccntg catacnnaat ganatactgg actttnggna cttgangga 349

<210> 650
<211> 306
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(306)
<223> n = A,T,C or G

<400> 650
cattgtgttg ggagcatcct tccatcagct cccatgagaa attctctgtt gggtttaagc 60
aatccccaaa tatatcatat tgacatgaat atatcatctc ctcaatgtcc agcattagca 120
gacaagatga gtgctgaaga tgatataact cctacctctt atgtaggcta gaggtaaagt 180
ctggctctgc tgactgtggg gacataccga aaaggaatgt gggttaatat cagangacct 240
ccctgcagat ccganantca gggnctggac tttctgggan aggaagcnna aagttatntc 300
tgaacc 306

<210> 651
<211> 769
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(769)
<223> n = A,T,C or G

<400> 651
cattgtgttg ggcagggtca tttctaaggc atgggctgga agcttttatt taaaacttta 60
catgtcttag aagcactctg gttgttgcta ggcagacaat tttacatctc ttgctatacc 120
agttgcatga agttcatcat gcatattggc tgtggaaaac cttaacagca tcatgtcata 180
aggtttcagt aaggtttaaa tgaaatcatg tattaagcac ttagtatagt gcaccttaaa 240
tgttagcttc aaaacaatga caacctaact aatgttgaaa gaagcttgtg tttgtaaatt 300
atgtcttatt gaaagatgtc atcaaatcct gttatttcta atcccttaaa gtctctcaat 360
gtatttcttt ttgccatatc caatgacagg accttagttt aagccagtgg ttctctcaac 420
ttctaatcca gagatacctg ggtgtcccca agaccttttc agagcatcct tgatgtcaaa 480
accattttca taataatatt aaaatattat ttgctcattg tactcttatt ctctcccaaa 540
tattcagcga gttttccaga agctatataa catgtggtaa catcttatca ctctgacgat 600
taatagaata tgngnttttg gattcttgng tttaaaattt tctcactttg gggttctaat 660
atggnnacga ttaatagata tggnctccat gaccagangg ctttaaagca ntcaataatt 720
tttaagagac taagnactat cctttaaaga tngngaactc catcttaat 769

<210> 652
<211> 267
<212> DNA

<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(267)
<223> n = A,T,C or G

<400> 652
nnangccctt taaccattgn ggcctccacg cnntggcggc cgctctacaa ctagnggatc 60
cgcnactcta gnanaangat tggctcttnt gggntgggcc ggncgggctg gggcgttaag 120
cggggctggg cgcgcgccgn ggttgnacna ggcgccgccg cccncacacn cccggagcac 180
cctcnttgcn gccntncccc gctcaccccg cgcgcgccgn tccgcttttt ccncacccan 240
agcnctnttt atctntgtct cctccgg 267

<210> 653
<211> 501
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(501)
<223> n = A,T,C or G

<400> 653
cccnttnacc cattgctgga ctccaccgcg gtggcggccg ctctanaact agtgggatcc 60
ttncnatgag atgngcgang gaggacnnat ttgctatnct ggatggggct gantcntnta 120
gctnctctag cancagatgg gttatcgagg aagatgactc caangggcta nantcctatg 180
cncatcctaa aanncanctg ctgtnttcag agtacgcgac acatcatcnc tnatgcattg 240
ntgancaaga cgggcangtg cttatcctca gcgangatgc ccttaaccan gagctcgaat 300
ggacntatca ccntanaggt acanntnccg caccacacac cngcttgcnn cctgacgctg 360
gactggatcn cttaggccac caatnccccg tttnccacat ncctgggacn ctananatac 420
tcganggggg gcccggtanc caattcgccc taatactgag ccttgntacg nacgctnact 480
nggngtccta ttanaacgtt g 501

<210> 654
<211> 710
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(710)
<223> n = A,T,C or G

<400> 654
gcgnctttan cncatgctgg gctccacgcg gtggcggccg ctctacacta gtggatccca 60
acactgagtc caccacagna aaactcanca ccaggcagac cccacaactg cagaatccag 120
gctgcaattc acagactaat cntctagacc cacctcagta ccagatggta ccacacagct 180
caaggnttta ggtttgcgtg gtanactcaa tctctatctt tcaccactgc cagcctgact 240
tcagagatcc tgngctctgg acagtcctca gtggcaggca actctcagga gcctcaggnt 300
tttggcacat cccagnacca gccagctgcc acaggccctg accttntanc aacactgccc 360
atgtattcca gacttctanc ataccacagt gccatgctga ttgcatctat agangctcag 420
gtgcncctca aanctgtgcc tgctgcagna ngccccacgt ctctggcatg ccccaatgcc 480
atgngtggna acanttgact tctgggcatg ntggaattcc ctaccactga ncctgaccat 540
aggnggganc ccattttttt cgaggggggg gcccggcccc caattccncc ntatagngag 600
ncgtanttac gcgcnnctta ctnggccngt ngtttaacaa cgtcnntgan ctggggaaaa 660
cccctggnng cnacccaaat taaacngcnt tgcannacat ccccctttcg 710

<210> 655
<211> 202
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(202)
<223> n = A,T,C or G

<400> 655
cccctttncc ctttcanccc ccccgttttg gcngccgccn acacctactn catccaccca 60
cantcgacca cccgagcttt tttccgatcc cancatcnat gcngattttn tctntgcntg 120
ctgngcctgc acctttgnta ggtcaagcct ggcccatctt cgacaacttc ctcatcacca 180
acgatgaggc atactctgac ga 202

<210> 656
<211> 308
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(308)
<223> n = A,T,C or G

<400> 656
gctgntgaaa gaccacaccg aaaaactctn ctttccgact tccacatgat gatcngcatg 60
tggtggtgag agacttatca tgacgacatc gcttccnacc atcgcanccn ctgcccaagc 120
ccattcatgg aggcctgggn anttctgtga ntgacntnga cnctanacnc tnccactgtn 180
tgctatccag acttgnttng aatatnttat tggcnaaana canttncgga atgctgtgnt 240
tgnncattga angatctgat cactatgaga gggtgaggac nncctgctng ctggcantnt 300
ntaacccn 308

<210> 657
<211> 696
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(696)
<223> n = A,T,C or G

<400> 657
accntttcca caatnctgnn ctcccccgcgg tggcggccgc gtcgaccagc aacctcagct 60
gtgggtcttg ttacagtaat gagttactgt aaggaaagtg tgacatttcg agcaatttga 120
tttgtttaaa aactagagca gtttcagggt tttccttgta aatctgtctt atgtgtcttc 180
aatgttcttt cttgaggagt agagaaagga attgttagga atgatgcata aaccatggct 240
tattttatct cgctgccacc cataatcaga gcagattctt gggactatga ccctcatgga 300
gacatgacaa ttgtgtgtgt ggtgggtggg agaaaagagc tgggaatttt tagggtctag 360
agggtccaat caggactatt ttatggagct ctgctcacca actttaagtg agcaccaggg 420
gtgngaaagc gaatcttggg ntcaaaanaa caatggnaag gggtaagttg gtatnctgaa 480
ctggccactt cggactctta tttaactggg tattctcant taaggaggcn ngggtggtct 540
tggcttgtna aggaaagcct gtgcaatgga atgactttaa aaccccccat taaaaaaaaa 600
angntataaa tcttgggtct taanaangaa gcctgggttc tnttanccca ttttnccccc 660
gggaaggnaa atnttcttag gnaanggaag ggaagg 696

<210> 658
<211> 698
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(698)
<223> n = A,T,C or G

<400> 658
ctggactccc cgcggtggcg gccgctctag aactagtgga tccgtgttgg ctcaattctc 60
aaggctgttg ctgtgcggcc tgttccccac acgtgctgct cagctcaggc aagcaccgag 120
cttgtgttgt ttcatgctca gcgtggaggc ccctcctcca ggtcgctgct ctgtggggtt 180
cccatacact caggctccta ggaggagtcc atttagaaag ccagggtttt tctcagagtc 240
ttagttcctt gtgctgtcat ccatttcaca cgacttgggc cctgctcggg gcaacacagc 300
aagagaaaag acagggaaaa taagagaggg accttgcaca cacacgctct ggaccacaga 360
gccctgtgcc cagctcctct gtcaatacag gtggaatctc gtgcaggatc gcaggggtct 420
gtgatgccac caaagagcag gccgggacag ggttaggaga gaaaggagag ggaagtgggg 480
gtttctccta cgcactctta tttgcagagg gaaaggcggg tttgtattgg ggttgtcggt 540
ctttgcaccc acngcacagt tgtgagacac ccccatcctn agatcaaagc cccacataca 600
gcttggggaa aaacaaaacn aaacaaaaca aaaacagtaa acctccatgc canttgttgg 660
gnaagttttn aatttncttc cccnacccan cttgcttc 698

<210> 659
<211> 750
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(750)
<223> n = A,T,C or G

<400> 659
ncaanctggn ctccaccgcg gtggcggccg ctctagacta gtggatcctc ctcatgggcc 60
tggatatctc tgaacatatg atgaacattg cttatgaaaa attatttgta ngaaaattgt 120
gaggcctaag aatgntattt tcttttagtg atggtctttg tttgcttctg taaggnactt 180
gtgggcactc gtaagcttgg atctctttaa tctaatacca gntttgagat tttcttggcc 240
ccatagatga attaaaactg gcgtacttct tgtttacaag anggataagt ctcctagggt 300
aagtcttttg gggtcccaag tcaaaaagat gagggattta ccagttctct aaccttggta 360
gccccagact ccaaactttg ccttctagtc ccaagaggct atcaaaaagc aaaggccatc 420
ttccaccttc ttttccanaa cagcacacat tccagacagt acttgaaagc aggaacctcc 480
ttatccctta aaaacctctt ggaancatct tccctctctt gcttctacta tgcttggccc 540
acctancatt cncnttttc tggaaaccgg aaaaancttn tgacttnngt tggctacatt 600
cagcttggcc ccctacaatn tggtttccat ctgccctaan gaaattttaa agggcacttt 660
ttttntggcc cctgactttc nntttttagg gctttccccc angctttgcc cctttggtta 720
aaggggttat tttccttccc cttttggaag 750

<210> 660
<211> 849
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(849)

<223> n = A,T,C or G

<400> 660
tcggatccac tagtccagtg tggtggaatt cgcggcccgc gtcgacgggc agtagtggta 60
tgcntntcta aatgttataa ttatttcaga attactctgc cagaaagtta tgatcataca 120
tagaagagtt tgtagctaac tttgaaagta gtggaaagtg gttttcatgt attgtttggg 180
ttaatttaat tttgattata tttggttttt agttcaggta atttttttgt tgaaaacttc 240
aaatgacaat ttcttcatgg ttactaaaga tcactcatgt ggagtagttt cagatttttt 300
tctgaataca tgtattactt ttagagatgt aaagatgtga aattactaag agagaaaccc 360
atgtgatttg tttagtggat caaaagtcgg tagctccttt gatcctaagt gccactgata 420
gttaaataga tactgaagct atgggcaggc tggattgata agaaaaaagg agacagagaa 480
atgggaaatt gggaaagaac tgtgcaaata ggaaaaggag agagcaacag aacagaatta 540
gtaccacagt gccgaagtgc cacctcaggt acttccatct cccatctcct gaagaattca 600
gtaacagttt gcaaatggtc aacacaatca tttagtgatc ctggttgata ttttcaatac 660
tttctgggga tttcttggct ggnttcaaaa gatgatgctg atagttttat tgcccctgaa 720
ggtattctga agnttancat aatttattgg tcagtaaaat atttgaataa aagngganga 780
aggaaaatct ggcntcttat tttgggatnt cngcnggggg aangaggata taattnaccc 840
cggccttgg 849

<210> 661
<211> 653
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(653)
<223> n = A,T,C or G

<400> 661
aacttaagct tggtaccgag ctcggatccc tagtccagtg tggtggaatt cgcggccgcg 60
tcgacctcca ttcgtttctt gtcctttttt ttcatttttt ctcatgttct attcacttta 120
ggtttctaag ataaatatta taaaataatt tttacttata aattattcac tgataccctg 180
tctttaacat gtgaaatgaa ttcaaaagga atcttaatga gaaataatat actcatgatg 240
tttaatagat ttgatttcga aataataagc cctctgaagt cctaagttaa aaataaagca 300
acttgtttga taatttttca tcaagaatgt atctgagtct ctgagtaatt attagtagga 360
atattccatt atcacaatta cacagtataa gctatttagt ctaactttac caaaaaaggg 420
agctacttca acactgtgtg agacttttaa tgggtttgca ttgggtatgc actattagca 480
agataaccta ttttacagca gtgtttntta acctttccca tttatttgaa aggcagctaa 540
gatatagtag ttaatntaan gggctgatgc atttatatta catgtagana atgggagata 600
cnaaagggag ngggggggana tnttttgnat tcnnaagctt cnttgncaat taa 653

<210> 662
<211> 646
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(646)
<223> n = A,T,C or G

<400> 662
aaacttaagc ttggtacccg agctcggatc cctagtccag tgtggtggaa ttcgcggccg 60
cgtcgaccca gggacaggca gccagngctg gggtcaccag ggtcccctct tgggccctcc 120
aanagcaaca gtactggcaa cagctgggat ttgctgagca cagactctgc agcaggctcg 180
gttgagctct ctgtgcctgt tccttcatac catcctcacg cccatccatg agatgggtcc 240
agctgttttc agatgagaaa atggcacagg aagctggtaa gtgacagtca gaaatgaatg 300

```
ctggcagctt antccttgga cccaccgcag tgcaggacct tgctcaacag ggatcaccct     360
tgtccgccac ctgttcatga ggccacccag ggtttgtgtg gtcatttgtc tcctttcatc     420
tgcttgcctt caaccagctg ggtcattagg gctggggaac ccagacccca cacagtcctt     480
ctcccagang ccagacacan nctncgccac agnaaggact tcagtccccg aancaaatgt     540
ncctgggcgt anaaactgna gggnccccaa tccctggtgg ggtactgctt tgcactggng     600
gaattcaccc ctcattgnna acctttccct nttnncaccc ctaaac                    646
```

<210> 663
<211> 650
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(650)
<223> n = A,T,C or G

<400> 663

```
aacttaagct tggtacccga gctcggatcc ctagtccagt gtggtggaat tcgcggccgc      60
gtcgacgtcg acgcggcgng ccgtttcgac gcagttgata catattatta tatactacat     120
nggttttcta gaattaaaaa attaatgtgt agtgccagcc ctagatgtaa gttacatata     180
tcaactctat ccaattttgt cagccataaa acttaccttt ttcacatact tctaactcta     240
acaatgtgag aaatgtagat cattgcaatt atacccacaa ggcagatggc tacatgcaga     300
atggatagca gaatctagct acttacgcta gccacatggt agacgttttt tcctttgttt     360
ttgcaaaatt gcaatataag ttgcatatcg ttagagtgaa aagatgtaaa gaacccatag     420
aagccagtga tgaaggacat ttatattttc acctttacaa angaccttaa aattgcctat     480
gtggagcaga aactggagga gggcnaancc atcngtaaaa aaaattttgn tnctatttgg     540
atttgggcac cattattacc tccccaggtn ccttttttgnt ttaacctttc ttttaaaaaa     600
aataattcnt aatttttggg caaaaaaaaa caaggttttt atttaaattt                650
```

<210> 664
<211> 678
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(678)
<223> n = A,T,C or G

<400> 664

```
taaaaatcta gactacacta ggaaattatt ttantatcag aagaatatca ggggtgtagt      60
actcatcana gctaaatgag agcgctttaa aaatgttagt ttgtcttccg ccatttctac     120
agaaagctgc aatttcaggt tttcaaccta ataggtgata tttaagaaaa aaaaaaagca     180
atcgcaaata gccccactgc ttttacaaat catttttct cttctaggta tagcctgtca     240
ggtggcctaa tgtaattttt gacatctcta ggaattttaa tagaaccaga aatgggtgcc     300
agagatatgc ctgcactaat cttaagtggg gatttatgta tttctcaagc aagtgattaa     360
agcaaaacta ggcacgattg aaatcaanat cttttaggca agaaagtcat gatgagtttt     420
anaattattt taggactctg tggctttctc ttcatagaaa tagaaaaaaa aaattgtata     480
aaaaccacaa aaggtcctga atagcccaaa gcaacactga acaaaangaa caaagcagga     540
agcaacacac taccggaatt caattatact accaaggtgt antaaccaaa acagcattct     600
attgggcata aaatagacca aagaccagtg ggaaacagaa taaagaancc caaaataaat     660
cctatattta cngcccnc                                                   678
```

<210> 665
<211> 694
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(694)
<223> n = A,T,C or G

<400> 665
```
cttttcaaat catttttnct cttctaggta tancctgtca ggtggcctaa tgtaattttt      60
gacatctcta ngaattttaa tagaaccaga aatgggtgcc agagatatgc ctgcactaat     120
cttaagtggg gatttatgta tttctcaagc aagtgattaa agcaaaacta ggcacgattg     180
aaatcaagat cttttaggca anaaagtcat gatgagtttt agaattattt taggactctg     240
tggctttctc ttcatagaaa tagaaaaaaa aattgtataa aaccacaaaa ggtcctgaat     300
agccaaagca acactganca aaaagaacan agcagggaag caacacacta ccngaattca     360
aattatacta ccagggtgta gtaaccaaaa cagcattcta ttggcataaa atagacacca     420
agaccaatgg ancagaataa agaaccccac aaataaatcc atatatntac cgccanctga     480
ttatcaataa cnaacaccaa gaacatatnt taagggacnt nctattcaat aantagtgct     540
ggnaaaaact gggaaatcca tatgcagaaa naatgaaact agacccctat ccctcaccat     600
acgcaaannt caacttcgga atgggattac aaaacttaag acattccaac ccaagaaact     660
atnaaancta ctattaagaa aacagatcnc nccc                                 694
```

<210> 666
<211> 705
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(705)
<223> n = A,T,C or G

<400> 666
```
tttaaaaatt tagatacact angaaaatta ttttagtatc agaagaatat caggggggtgt      60
agtactcatc agagctaaat gagagcgctt taaaaatgtt agtttgtctt ccgccatttc     120
tacagaaagc tgcaatttca ggttttcaac ctaataggtg atatttaaga aaaaaaaaaa     180
gcaatcgcaa atagccccac tgcttttaca aatcattttt tctcttctag gtatagcctg     240
tcaggtggcc taatgtaatt tttgacatct ctaggaattt taatagaacc agaaatgggt     300
gccagagata tgcctgcact aatcttaagt ggggatttat gtatttctca agcaagtgat     360
taaagcaaaa ctaggcacga ttgaaatcaa gatcttttag gcaagaaagt catgatgagt     420
tttanaatta ttttaggact ctgtggcttt ctcttcatag aaatagaaaa aaaaattgta     480
taaaaccaca aaaggtcctg aatagcccaa gcaacactga acaaaaagaa caaagcagga     540
agcaacacac taccagaatt caaattatac taccaaggtg tagtaaccaa aacagcattc     600
tattgggcnt aaaatagacc naagaccaat ggaacagaat aaagaaccca aaataaatcc     660
atatttttac agccagctna ttatcaataa aaacnccaag aacnt                     705
```

<210> 667
<211> 817
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(817)
<223> n = A,T,C or G

<400> 667
```
nnangacttt tgtggtntta tacaattntt ttttctattt ctatgaagag aaagccacag      60
agtcctaaaa taattctaaa actcatcatg actttcttgc ctaaaagatc ttgatttcaa     120
tcgtgcctag ttttgcttta atcacttgct tgagaaatac ataaatcccc acttaagatt     180
```

```
agtgcaggca tatctctggc acccatttct ggttctatta aaattcctag agatgtcaaa     240
aattacatta ggccacctga caggctatac ctagaagaga aaaaatgatt tgtaaaagca     300
gtggggctat ttgcgattgc tttttttttt tcttaaatat cacctattag gttgaaaacc     360
tgaaattgca gctttctgta gaaatggcgg aagacaaact aacattttta aagcgctctc     420
atttagctct gatgagtact acacccctga tattcttctg atactaaaat aattttccta     480
gtgtagtcta aactttttta aaaagacatg taatccgcgg agtttgtaac tcaaaacgag     540
tgcatctagg aggtatcgca agccgtttct ggattaaatt cccagctagc ttgcttgctt     600
agcaggggcg ggnaaaanaag acatctgcag cctagggaag aaaacctttc gcattgttct     660
tacgtgttta cgttatttta tttcctanaa caaggcngaa ttgggactcg aatggttcag     720
ttggggtggg ggatcccctg gtncataaaa ngtcanaaag anggtacagg cggaacncca     780
agggtcgtcc tgcatttana ctcggaattt tggtgcc                              817
```

<210> 668
<211> 826
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(826)
<223> n = A,T,C or G

<400> 668

```
cggggggnnt tacgtctctc tggacgcttt tattgtacca gggcgatccc agcccaactg      60
taccattcga gtccctactc ctgccttgct ctagggaaat aaaataacgt aaacacgtaa     120
gaacaatgcg aaagcgtttt cttccctagg ctgcagattg tcttcttcac cgcccctgct     180
tagctagcta gctagctggg aatttaatcc agaaacggct tgcgatacct cctagatgca     240
ctcgttttga gttacaaact ccgcggatta catgtctttt taaaaaagtt tagactacac     300
tagggaaaat tattttagta tcagaagaat atcagggggt gtagtactca tcagagctna     360
atgagagcgc tttaaaaatg ttagtttgtc ttccgccatt tctacagaaa gctgcaattt     420
caggttttca ncctaatagg tgatatntaa gaaaaaaaaa acaatcgcan atagcccact     480
gcttttacaa atcatttttc tcttctaggt atagcctgtc aggtggccta atgtattttt     540
gacatctcta ggaattttaa tagaccagaa atgggtgcca gagatatgcc tgcactaatc     600
ttaagtgggg atttatgtat ttctcaanca agtgattaaa gcaaaactag gcacgaatga     660
aatcaagatc tttaggccag aaatcatgaa nantttttana attattttan gaatctgtgg     720
cttctcttct taaaatngaa aaaaaaattg tttaaaccca naaggtctga atacccaagc     780
nccctgaacn anagaacaan gccggagcac cccctcccaa atcccc                     826
```

<210> 669
<211> 547
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(547)
<223> n = A,T,C or G

<400> 669

```
cattgtgttg gggaaaaaat gatttgtata agcagtgggg ctatttgcga ttgctttttt      60
tttttcttaa atatcaccta ttaggttgaa aacctgaaat tgcagctttc tgtagaaatg     120
gcggaagaca aactaacatt tttaaagcgc tctcatttag ctctgatgag tactacaccc     180
ctnatattct tctgatacta aaataatttt cctagtgtag tctaaacttt tttaaaaaga     240
catgtaatcc gcggagttag taactcaaaa cgagtgcatc tnggaagtat cgcagccgtt     300
nctggatnaa attcccagct tgctngcttg ctnagccggg gggcggtnaa aaaaacatct     360
gcagcccngg ggnaaaaacc ttcgcattgt tcttacgtgt ttacgttatt ttatttccct     420
nnagcaaggc ngggganttgg ggactcgaaa tggtacagtt gggctgggga tcgcccttgt     480
tacataaaag ncgtccagaa gagggacggt tacaggcngg ganctccaaa ggtcagtccc     540
```

tgccatt 547

<210> 670
<211> 232
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(232)
<223> n = A,T,C or G

<400> 670
cgaactattt agactaccta ggaaaattat tttagtatca gaagaatatc aggggtgtag 60
tactcatcag agctaaatga gagcgcttta aaaatgttag tttgtcttcc gccatttcta 120
cagaaagctg caatttcagg ttttcaacct aataggtgat atttaanaaa aaaaaaaagc 180
aatcgcaaat agccccactg cttttacaaa tcatttttc cccaacacaa tg 232

<210> 671
<211> 214
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(214)
<223> n = A,T,C or G

<400> 671
ctcccttcc ntccttcgct actncncatt ttcnnaaatt tntttcgcnt atgnggaaaa 60
acacccacat tnttcanctc gcacagaaca ngnnggggtg tgtaaaatga agggcttccn 120
cnctttctct tattnaanaa cactnaaana ggganggct aaaacccgcg ngatntctac 180
nctatcgcgg gcgcttttgg ngttggctag aaga 214

<210> 672
<211> 328
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(328)
<223> n = A,T,C or G

<400> 672
ngancagcgg ngtttaaacg ggcctctaga ctcgaggaga cncctgttgg atggtggatc 60
acanntcgnt actactatac aggacagagt atcggganct cttggntgtt ggngcctgcc 120
aaccactgct nctgttaact gcgtatctga agggactcgg actggcttca gaagaactac 180
cggctcgaat gnaccatgga tgattcncnc tagttgaaaa aaaactcagg cacatgtatt 240
gccactgatg actagcgcca gactnctctc ggctctntaa cgagcccaca tgncngtgtg 300
ncncccgtgc tgnctccaga agaggttc 328

<210> 673
<211> 223
<212> DNA
<213> Homo sapien

<220>

<221> misc_feature
<222> (1)...(223)
<223> n = A,T,C or G

<400> 673
gggggcaaag ctggctagcg tttaaactta agcttggtac cgagctcgga tcccnnagac 60
attgtgcatg aaaatgcaaa ttgagtgtgg tctatantgc catcntcacc tnctgncngc 120
tcaaaacaac ngctttctgc tgcaatgggt agggctcctn acncacggtc gcnnacggag 180
gccnncttat cctcntcggt nnggatccct ngaagcatnt tct 223

<210> 674
<211> 256
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(256)
<223> n = A,T,C or G

<400> 674
gnggggtcnt ngatgagcgc gcgtaatacn atcactntcn ggcgngntgg gtaccgggcc 60
ccccctcnaa gcggccgccc tttttttntt ttttttcatn acatgataan ntctttnttc 120
taaacagacc acaccactan agttcctttn ctttngtacg gaattgagtt aaagtagagn 180
atacaatgca gggcttcnnc tctatttcac attccaggnt ggttcngnat ggatcggccc 240
tgcctctccg atgggt 256

<210> 675
<211> 439
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(439)
<223> n = A,T,C or G

<400> 675
nnactagtcc agtgtggtgg aattccattg tgttgggctt gtatgggttt ttttgtctag 60
ttntttggga aatgttngtg ttactatntt ttggatatna tatatgatat gtatggccct 120
tctatgggct cctcanacng aactcaacca ttttccacaa aaccnattcc tcctttccct 180
tcatgactga gtggtgttgg tactatccng gaaactggga cattgtcctt cacatctntc 240
ccttanctgc ctngtccnat tgatgtcttt gagctntgan atgtctttgt taactntctc 300
ctncntctgt actgccggca naattaagca ccatntgtca caaaaagtat tgcgttacct 360
tcacgnatct gttngttncc atncttgctg cttctccngn ggaaaatagg ctnttctggc 420
aaccgaacng aanaaatac 439

<210> 676
<211> 587
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(587)
<223> n = A,T,C or G

<400> 676

```
nggnggcctn attaagcgcg cgtaatacna ctcactntgg ggcgaattgg gtaccgggnc      60
cccctcaagt tnatntgccn aacctctctt ttggaataac aaaaggttta acacatatgt     120
cctcataggg acgcgctttc acacnttcct gacngcttca tanacntcat tnctatttct     180
cctcagnaca agttnaggcn gaaggtgagg canacnttat aatttccatt tcacaaatnc     240
ggaaagtgag gctcaaaggg nttaaaaaat aacctgatac aantcataga gccggtntct     300
ggaanaagca ggagcaaagt ccaggcatcc tgatccaagc tnggtccact gccttccact     360
ctggagaggc ttcatctccg acaaaggaag ggacntgagt ggctgganaa tctcatggga     420
taaagacctc agnatttcat gctcctggaa atcccatggg ttgaacaaca ggtntttggc     480
ccgtggttct ntccctttgn ccatctttta accttggggt aaatgatggc ntctntnagc     540
nttttttttn aaagagatng aaattgaatg attattngct cattggg                   587
```

<210> 677
<211> 444
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(444)
<223> n = A,T,C or G

<400> 677

```
gtggggcatn attaagcgcg cgtaatacga ctcactatag ggcgaantg ggtaccgggc       60
ccccctcgaa gcggccgccc tttttttttt tttttactgt ccaaactntc tatngatnta     120
gttgaactgt ncaacgattt catgaaattc tatacacana gccttcaggt ccagagagta     180
aaacaaattt aaatttnttc accanattgn agcagncana agcatccnat natatccgac     240
tacaatgaat natatgctna nggtanctna tttacccact ntggggtctt tanggtctgt     300
cacaaactat tttcgtaaac atcnntttaa anttnggtga atggacctaa tnccagataa     360
ntctatttna tntaccctag catncctgtg gctnactttn cgggctgtgt tggcntactt     420
ttaggagaaa attggtataa atnn                                            444
```

<210> 678
<211> 670
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(670)
<223> n = A,T,C or G

<400> 678

```
actagtccag tgtggtggaa ttccattgtg ttgggagcag tttaaaaaaa aaaaagacna      60
aatatacnac tcttgatnaa acataaaggt acagtggtct atgaggaana gaaaaggtac     120
ctnaggatgc aaaantacct accacatggg aaccgttngt ccacactcat tccnnanaaa     180
accgagtcct ctcanttnca cacgtgtacg tttcagttgg gaagtgcttg ccattactcc     240
naagcctaga accttcacgt cctgaaggtt ctggaaggtt tttcagattg cttaaganac     300
gcngcccttc catattcntc tccactaccc nggggaacgg aacaaatgga gctgcgacng     360
ggaagcgtcc cttccontcc gaacgctttc tttcaaacct gcctgccttc cnggcgaatg     420
gaccggaagg tttnctngct tcctttcanc ccnaattact tcctgngttg aaaattggcc     480
tgttggtttg caaatgcngg aatttgttta ctttcntcat gtcctgtgtt gnncnaaccg     540
gctcncttgt tgcctccctt tngaaaggtt ttcatcaggc cccgcccttt ctcttntaan     600
ngtcctaatc cggncnggac cactcgggga aaatttttc ttttcgaaaa gccgccccnt      660
ccgtccggct                                                            670
```

<210> 679
<211> 449
<212> DNA

<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(449)
<223> n = A,T,C or G

<400> 679
actagtccag tgtggtggaa ttccattgtg ttgggagtag gtctactaca ncctacttcc 60
cctatcatan aaganctan caacnttcat gatccccccc tcntannccct tttcctcanc 120
tgcntcctag tcctgtttgt cctnttccta acantcntaa ganagatnac taatnctact 180
atctctnacc tccggaanct acaanacgtc tggaactatt cngaccccat gcanccncat 240
nctccatcgt cctcccagcc cctnccccttc ctttacntta ctnaacgaag gtcgacgatc 300
cctcccntac ctcccnnncc attgggnccc aanggnactg gacctcacga ntacaccnac 360
tacggggnga ctaagnctgn aactccttac atatntcccc gttacccccn gaacncagcg 420
aacngcnaca ccttggacnt caagaanta 449

<210> 680
<211> 670
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(670)
<223> n = A,T,C or G

<400> 680
tttcngtgtg gtggaattcg cggccgcgtc gacgagaaga nggaggagga naaggagaag 60
gagaagaagg agaanaagga ggagaaggag aagaaggaga agaaatcatc atcatcatca 120
tccactgtct ngcaactatt taagtttgcn antcccttga aaacaggtac ttttgtttca 180
atgtttggga ccactnctga cnatgannag aanaccaata aatgcttgat naatgaaaaa 240
nccacttttt acctgttaga accctgaggc taagagaant gatgtgactc gacttagtta 300
ccacaaacta tgatcctagc atnaattggg gcatctcaac acctcaactc cctgtgcaag 360
aacagatttt caatgtctac tgatgatttt aaatggatta nttcctctct ttacttctta 420
agggcatgaa gntttatgaa acaaaactat ncagttccag acgcttaacc cacatagtgt 480
taatagtcac cttcaacaca cnactaaacc cccaaaaaan gnttttacg gngtttcgac 540
agtttcttt tctttttgac ttgnttaaca cccnngacaa ctttgtnctn tttccntgaa 600
tcacanctt cnaanancca atggtncggt tttttctcnt tcngggccct tcccttnttn 660
aaaaccanat 670

<210> 681
<211> 494
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(494)
<223> n = A,T,C or G

<400> 681
tcatggtgtc cacagtctga tgtgagcgca ttaaatttaa ggatctccgc ccttctcctt 60
aaaactcagg acttggcaat gancctagga agcgcccctc ccctccccan ccanatccaa 120
gcccggacc gctgcgnctc cagctgcgcc tagtgaaacc gccgaattcg aattcacact 180
cggngggccg gcgaaggtgt gcgcgcccgc gggagcgccg gggcnagccc gagggactgc 240
aagccaanaa nggaggcatg ggtggcgggg ggcgccgtct gatccaggaa ggagcggagg 300
cgccgatcac acactcttna gacgccctgc ccgcgcctgg ccagcgcgca gnctgcagga 360

cgcgcggagc aggaactcgc tggagtttgc caagccccan gnctctggaa agtntgtagc 420
tcccttttcgg ancgnctctt ctggcccttt gggacgggtg tgtcattggg cgggggtctg 480
tataaggggg ggac 494

<210> 682
<211> 263
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(263)
<223> n = A,T,C or G

<400> 682
tgatcattca agcgntgngc gnataacgat tgctnagccc aacctttcat agggtcgttc 60
ctttgggaat nggatgtcta ttgaatggca gggatagggg cactcggcat tcgcctctgg 120
tacagttttg catatatatc ctcatcgcga gcgagcgtag ggganccgtta agtttgggga 180
aatgccnccg catgncccctn ccggagctta aaccccccaac aatncccatt ttnaaaaaag 240
ntttnttant taaaaaaaaa aac 263

<210> 683
<211> 255
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(255)
<223> n = A,T,C or G

<400> 683
cttgcccggc atgcacagac ntntttacgg acacnctact ccaagngagc ctgnanctgt 60
ctacggtcaa nctctaaggt tngncantgc cacanatggc atagtcccga gggcggtnan 120
tctggantgc tctctgcact tgaacntaaa gcgcntttca aganaggnct aatngcctgc 180
ctcttgacaa cnaacaancc cacaccnacc tangaccctn tangcaagga ctggattctg 240
naaatgcaat acaca 255

<210> 684
<211> 922
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(922)
<223> n = A,T,C or G

<400> 684
acccttcatt tcatgtgctt ctattttcct acatctttta catgactaag ggattaatga 60
aatcacctct tcataatcat gaccataatt tcatccaaca agtactcaag tttggtgtta 120
gcactttatt aatgcttacg aattctctct ctctccctct ttctcttttc cttagtcctt 180
gcacaataag gatttttgaa tgtataatat catcttaggt aagctttcat atggttttgg 240
catatgaagc ttatgactgt cataagccat accaagcctg tggagtatgg catgattttc 300
attacataat ccaatgaaaa tagacttatt ttaaatccct aactttgtag ttttaatttg 360
tatttcacta tcttgaaatt aacagctagt acttatccat cacagcagtc tcctactgac 420
atgaagcaag ttgttgaatg cagtaganca tgaatgaaag catttaatgt tanacaaaaa 480
tgggtgatac ccaagcattc tgaattattt gcatcaagga atgggacatg tacattagtg 540

gcatcatttc taccaatatg tgacttgaat tgttttttta aaaaaaggan aatgantttc 600
tcaatttgct ttaaaaaatt ttnaaaaagt tcaatggcat gctgctttgt ctggacttaa 660
tttattaaca attnttaanc cttccttaag gacanaattt tggtgttcag gatcnccctg 720
aagggtctta tttttnatan nattccaaac ccaaaaggtg gtttaaaatg ggngggttcc 780
ccccncnaaa atttggaccg gctttttttat atttaaaaaa nttnccnttt gngtttgaaa 840
nctnaatacc aattaagggg gaattttacc tnccagtggg aaaaaaaaac nctngccntt 900
naaaaaattc ccnggagnca at 922

<210> 685
<211> 531
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(531)
<223> n = A,T,C or G

<400> 685
tgaggctctg taaaactgtt cctctgctag gcatacttca tattctctat attaaactca 60
tctttaattg gcatggaaga ttcattgttc caaatctcag atgaagatcc tatattggat 120
gcaattaagc ctggcagcgc cctcaaaaga cagtcttgtc actgctagcc acagccagga 180
cacagtaaca gttccttcta gtgacccnag accataanaa atananatct aaagaattct 240
gactccaaag gcattagccc attcctggta ttgccaatta tgatagaaaa aattgccaag 300
ctcctgggac atggaaatac actcagtaca tttgagaact ggagaactan tttccaaaat 360
agtatgaaga catganggtg attgtagata tntgagtttg gagaanttga gggaaatcng 420
attacacatg tttactacaa gagatgttna taagtaaaga aggcctgata tacaatctaa 480
cagacnantg agataaatct taantcacaa ctgacntccc ttttggggcg g 531

<210> 686
<211> 336
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(336)
<223> n = A,T,C or G

<400> 686
ggngncctna tgagcgcgcg taatacgatc atatagggcg aattgggtac cgggcccccc 60
tcaagaacac tacaagctat gtcctcttct canagagccc tgaantttta acatattgaa 120
agctctnatc ttgccaaana actccactta acttcaaaac acaccctcca cacacatcat 180
gatcaactna gatcttactg aaccagaatc ctnaatggca tacttcagga acaggggtcc 240
anagaagcag ttctcaaant gcagctnaaa aagaaactga aaacccaatt catgcaanac 300
ctagggctta tttgagagca ttttccagtg cagatt 336

<210> 687
<211> 271
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(271)
<223> n = A,T,C or G

<400> 687

```
aatctgcact ggaaaatgct ctaaaataag ccctaggtct tgcatgaatt gggttttcag     60
tttcttttta agctgcactt tgagaactgc ttctctggac ccctgttcct gaagtatgcc    120
atttaggatt ctggttcagt aagatctcag ttaatcatga tgtgtgtgga gggtgtgttt    180
tgaagttnag tggagttctt tggcaagatc agagctttca atatgttnaa acttcagggc    240
tctctgagaa gaggacatag cttgtagtgt t                                   271
```

<210> 688
<211> 740
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(740)
<223> n = A,T,C or G

<400> 688

```
tgatgaagcg cgcgtnntac nactcactat nggggcgaan tatgggtacc gggncccccct     60
cgaagcggcc gccctttttt tntttttttg tgagagttta aataaaatat ttgagtttaa    120
tttaaagttt gagtttaatt aaaatatatg gcatatccca agttgggctt tgcanaaaga    180
acacttctca ggaactgtta gttggtgtac caggaactca gaagggtcct gttattaaat    240
atatttggaa aatgcatgga ttctctgaan atcnctctgc atgtgagcaa cacttacatc    300
ncaaaccaaa attggcattg catacatnaa ccaatatttc ccaaacattt ctggttatgg    360
cccaccccct ttgtgtanta cttattgctg ttttttggaa ccctggggaa attacttaaa    420
atattcagct ggaaattaca ggcgttactt ttaagggaanc aagaattaca gtgactccca    480
aaattgcaag tgttgattac tatttaagaa cccaagaatt tgaaagaaat tttgaaaagt    540
gaaaacngga aatnttaaat gacttctcaa attttgaaaa ctcnggnaaa catctccact    600
ttggtnccct tcctttaaaa attggctaaa aattntttnt tatncccacc ccattggaan    660
tnccccccccc ctggaacaat tggattcccc tatttcctaa aaaacggccn ccccccccgg    720
ggngaacncc nacnttttgn                                                740
```

<210> 689
<211> 635
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(635)
<223> n = A,T,C or G

<400> 689

```
actagtccag tgtggtggaa ttccattgtg ttgggattac atatactttt agcaattttt     60
aaagaagtgt acaaagttga gatgtttcct gagctctcat atatctgana atgtcatttt    120
acatctccgt cttcacctct caaaacttct ttcaattctt tggctcttaa tagtaatcaa    180
cacttgcact ctggagtcac tgtaattctt gctcctttac agctacncct gttatttcca    240
gctgaatatt tttagttatt tcccagggtt ccaaaaaaca gcaataagta ctacacaaag    300
ggggtgggcc ataaccagaa atgtttggga aatactggct catgtatgca atgccaaatc    360
tggtttgcna ttgtantgtt gctcacatgc agagtgaatc ttcaaanaat ccatgcattt    420
tccaaatata tttaataaca gggaaccttc tganttcctg gntacaccaa ctaacagttc    480
ctgaaaaatg ttctttctgc aaaacccaac ttggggatat gccatatatt ttaattaaac    540
tcaaacttta aattaaactn caattatttt attttaaact cctcaaaaaa aaaaaaaaaa    600
aggggggggcc cttccaangg ggggnccggt tcccc                              635
```

<210> 690
<211> 3923
<212> DNA
<213> Homo sapien

<400> 690

```
acagaagaaa tagcaagtgc cgagaagctg gcatcagaaa aacagagggg agatttgtgt     60
ggctgcagcc gagggagacc aggaagatct gcatggtggg aaggacctga tgatacagag    120
gaattacaac acatatactt agtgtttcaa tgaacaccaa gataaataag tgaagagcta    180
gtccgctgtg agtctcctca gtgacacagg gctggatcac catcgacggc actttctgag    240
tactcagtgc agcaaagaaa gactacagac atctcaatgg caggggtgag aaataagaaa    300
ggctgctgac tttaccatct gaggccacac atctgctgaa atggagataa ttaacatcac    360
tagaaacagc aagatgacaa tataatgtct aagtagtgac atgtttttgc acatttccag    420
cccctttaaa tatccacaca cacaggaagc acaaaaggaa gcacagagat ccctgggaga    480
aatgcccggc cgccatcttg ggtcatcgat gagcctcgcc ctgtgcctgg tcccgcttgt    540
gagggaagga cattagaaaa tgaattgatg tgttccttaa aggatgggca ggaaaacaga    600
tcctgttgtg gatatttatt tgaacgggat tacagatttg aaatgaagtc acaaagtgag    660
cattaccaat gagaggaaaa cagacgagaa aatcttgatg gcttcacaag acatgcaaca    720
aacaaaatgg aatactgtga tgacatgagg cagccaagct ggggaggaga taaccacggg    780
gcagagggtc aggattctgg ccctgctgcc taaactgtgc gttcataacc aaatcatttc    840
atatttctaa ccctcaaaac aaagctgttg taatatctga tctctacggt tccttctggg    900
cccaacattc tccatatatc cagccacact catttttaat atttagttcc cagatctgta    960
ctgtgacctt tctacactgt agaataacat tactcatttt gttcaaagac ccttcgtgtt   1020
gctgcctaat atgtagctga ctgtttttcc taaggagtgt tctggcccag gggatctgtg   1080
aacaggctgg gaagcatctc aagatctttc cagggttata cttactagca cacagcatga   1140
tcattacgga gtgaattatc taatcaacat catcctcagt gtctttgccc atactgaaat   1200
tcatttccca cttttgtgcc cattctcaag acctcaaaat gtcattccat taatatcaca   1260
ggattaactt tttttttaa cctggaagaa ttcaatgtta catgcagcta tgggaattta   1320
attacatatt ttgttttcca gtgcaaagat gactaagtcc tttatccctc ccctttgttt   1380
gatttttttt ccagtataaa gttaaaatgc ttagccttgt actgaggctg tatacagcac   1440
agcctctccc catccctcca gccttatctg tcatcaccat caacccctcc cataccacct   1500
aaacaaaatc taacttgtaa ttccttgaac atgtcaggac atacattatt ccttctgcct   1560
gagaagctct tccttgtctc ttaaatctag aatgatgtaa agttttgaat aagttgacta   1620
tcttacttca tgcaaagaag ggacacatat gagattcatc atcacatgag acagcaaata   1680
ctaaaagtgt aatttgatta taagagttta gataaatata tgaaatgcaa gagccacaga   1740
gggaatgttt atggggcacg tttgtaagcc tgggatgtga agcaaaggca gggaacctca   1800
tagtatctta tataatatac ttcatttctc tatctctatc acaatatcca acaagctttt   1860
cacagaattc atgcagtgca aatccccaaa ggtaaccttt atccatttca tggtgagtgc   1920
gctttagaat tttggcaaat catactggtc acttatctca actttgagat gtgtttgtcc   1980
ttgtagttaa ttgaaagaaa tagggcactc ttgtgagcca ctttagggtt cactcctggc   2040
aataaagaat ttacaaagag ctactcagga ccagttgtta agagctctgt gtgtgtgtgt   2100
gtgtgtgtgt gagtgtacat gccaaagtgt gcctctctct cttgacccat tatttcagac   2160
ttaaaacaag catgttttca aatggcacta tgagctgcca atgatgtatc accaccatat   2220
ctcattattc tccagtaaat gtgataataa tgtcatctgt taacataaaa aaagtttgac   2280
ttcacaaaag cagctggaaa tggacaacca caatatgcat aaatctaact cctaccatca   2340
gctacacact gcttgacata tattgttaga agcacctcgc atttgtgggt tctcttaagc   2400
aaaatacttg cattaggtct cagctggggc tgtgcatcag gcggtttgag aaatattcaa   2460
ttctcagcag aagccagaat ttgaattccc tcatctttta ggaatcattt accaggtttg   2520
gagaggattc agacagctca ggtgctttca ctaatgtctc tgaacttctg tccctctttg   2580
tgttcatgga tagtccaata aataatgtta tctttgaact gatgctcata ggagagaata   2640
taagaactct gagtgatatc aacattaggg attcaaagaa atattagatt taagctcaca   2700
ctggtcaaaa ggaaccaaga tacaaagaac tctgagctgt catcgtcccc atctctgtga   2760
gccacaacca acagcaggac ccaacgcatg tctgagatcc ttaaatcaag gaaaccagtg   2820
tcatgagttg aattctccta ttatggatgc tagcttctgg ccatctctgg ctctcctctt   2880
gacacatatt agcttctagc ctttgcttcc acgactttta tcttttctcc aacacatcgc   2940
ttaccaatcc tctctctgct ctgttgcttt ggacttcccc acaagaattt caacgactct   3000
caagtctttt cttccatccc caccactaac ctgaatgcct agacccttat ttttattaat   3060
ttccaataga tgctgcctat gggctatatt gctttagatg aacattagat atttaaagct   3120
caagaggttc aaaatccaac tcattatctt ctctttcttt cacctccctg ctcctctccc   3180
tatattactg attgcactga acagcatggt ccccaatgta gccatgcaaa tgagaaaccc   3240
agtggctcct tgtggtacat gcatgcaaga ctgctgaagc cagaaggatg actgattacg   3300
cctcatgggt ggaggggacc actcctgggc cttcgtgatt gtcaggagca agacctgaga   3360
```

```
tgctccctgc cttcagtgtc ctctgcatct cccctttcta atgaagatcc atagaatttg    3420
ctacatttga gaattccaat taggaactca catgttttat ctgccctatc aattttttaa    3480
acttgctgaa aattaagttt tttcaaaatc tgtccttgta aattactttt tcttacagtg    3540
tcttggcata ctatatcaac tttgattctt tgttacaact tttcttactc ttttatcacc    3600
aaagtggctt ttattctctt tattattatt atttcttttt actactatat tacgttgtta    3660
ttattttgtt ctctatagta tcaatttatt tgatttagtt tcaatttatt tttattgctg    3720
acttttaaaa taagtgattc ggggggtggg agaacagggg agggagagca ttaggacaaa    3780
tacctaatgc atgtgggact taaaacctag atgatgggtt gataggtgca gcaaaccact    3840
atggcacacg tatacctgtg taacaaacct acacattctg cacatgtatc ccagaacgta    3900
aagtaaaatt taaaaaaaag tga                                            3923
```

<210> 691
<211> 882
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(882)
<223> n = A,T,C or G

<400> 691

```
ttactcacta tagggctcga gcggccgctg aattctgctg cagtgagctg tgattatgtc      60
cctgcactcc agcctggatg acagaacacg atcatttctc taaagacaaa caaaaaacat     120
aaaataaaac tagtataagg atagaagccc agggttgatt taagtctgcg gaaatcataa     180
accataggtc agacttctca ttgatgaggt acttgtgggt tagaatacaa ttaggtatat     240
ttggtctaga aaccaggatg gaattagaga ataaaagact gagcaatagc atgttatagt     300
attagaaata ctatagaaat aggaaaagcc ctgattatga ctttggagtt ctgatccaac     360
atctgggatt atttagatat tttaaaggaa aacgatgact tttagctctc aggatgttag     420
tttcctcaac cataaaatga agagcctcga aaagatttcg tttaccagat tatttctgaa     480
gtcaattcca gttctaaaat tccatcactg ngcactaagg caaattgaat tgaataaagt     540
attgggnatg cataaaatac tctattttta aaaangaata gtaattatcc attggnaaca     600
gacgcantca tccagncatc tcctaccctg ncccatgncn tatgtagana tgtanctcta     660
atcccttaac aaaccgattt tgcaaaggag cttanccttg gggtacttgg tcanggcaac     720
tggtctactt tnaagactca tcttcactta ctgggcacca aatncctacc attgcatcaa     780
actggggttc ccatncaagg caaaccctgn gaaatcttta atcccgaaat tggcgcccaa     840
ttttgngggg tttccnaaaa gaatcntccc ccccgagggg cc                        882
```

<210> 692
<211> 235
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(235)
<223> n = A,T,C or G

<400> 692

```
ccgcactngt aangnccgcc agngngctgn aantccgctn agcncggatc cactagtcca      60
ttgatggtaa aagggtagct tactggnatg tccgnctgct ccanganata atacncagga     120
cttctcanag cacttaatat gttaatataa aactncgnga aaaaagatnt tcnatgaanc     180
nttcctctta ggaggtcagg ngagaatagt gttaatgnca ttaagganag aacga          235
```

<210> 693
<211> 383
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(383)
<223> n = A,T,C or G

<400> 693
nttatgtaag aaatgtcata tatcttttat tttctttaaa tcaaaataaa tatgactttg 60
agcatcccat cccatgcccc atcctatcag aatggtagga acatcaacac aaataattag 120
taatgcaccg catctacatt cccatgctct ctttacttct tcagcattgc ctaaaggcat 180
aatacacctt taattaatta attcagcctc ctaatgcaca ttaacaaagc ccctgctaga 240
ctctgtccat aatggnaaac ctgnatgatc cttgatatta acantttaag gaatgctcat 300
ggattggttn cagacttaaa aaattgaggg ggctgaanaa aatctaangg anaaatcatg 360
gaagcatttg cacatattac ata 383

<210> 694
<211> 204
<212> DNA
<213> Homo sapien

<400> 694
tctcttggct ggtcagcctg aagggtggta atgactcacc aacgctacta atccttcttc 60
actgtccctt attttttttcc ctcccaggct cataactcga ggttaaactc tcttttatac 120
aagaaccctg tctgatgaag catcatttca gaattttaag tcaacttaca aatgtggtat 180
tattcacatc tgagtacaaa ttta 204

<210> 695
<211> 670
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(670)
<223> n = A,T,C or G

<400> 695
gcaccagccc aggtgctgtt tcttcacttg agctccatga ccctccctgt gtggtgggtt 60
gaacggtgac ctccaaaaga tatgtccacc tggaacctca gaataagatc ttatttggaa 120
tagtctttgt agatgtcagt aaggtaaaga tttggagatg agaccctcct ggattagggt 180
aggccctagg tccactggca ggtgtgcttc tcagggtctg aaaggggaag acagggccac 240
ccagaggagg agacggaggc agagacaggg ccacccagag gaggagacgg aggcagagac 300
agggccaccc agaggaggag acggaggcag agacaggggc cacccanagg aggagacgga 360
ggcagagaca gggccaccca gaggaggaga cggaggcaga gacagggcca cccaaaggag 420
gagacggagg cagaanacag gccccccaa agaaganacc ggaggcanaa aacagggcca 480
cccanaggag gagacggagg canaaacagg gccaccccaa aggaggagac ggaggcaaaa 540
cagggccacc caaaaggagg aagccggaag gaaaaaacag ggccccccca aaggaggaag 600
ncggagggcn aaaaanaggg cccccccaa agngagaaaa ccnggnaggc nanaaaaccn 660
ggggcccnnc 670

<210> 696
<211> 317
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(317)

<223> n = A,T,C or G

<400> 696
tgacccgttn tttctgcaaa ggagagtggg gaaggagggn tgggaagaca aaagttacat 60
gttagcaggg aagagaacag aattttatcc acccttatct ctttagtgag tgaacaaaca 120
gcccactgtc atcgtggata catttcactt ttttcacatg actaaggagc tctccggagt 180
gaagagtgag taaatatgtt tattacgcat tcatttgcta agaatcatca agaacccaaa 240
gttagagacg tttcgtggtt gaactttctc cctactgtct agtagaatta tatggggatt 300
ctggatctgc tggtgcc 317

<210> 697
<211> 246
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(246)
<223> n = A,T,C or G

<400> 697
ctncagctct aatcgactnc tatnaggnat gatggcncgt gcngcgcgta cgtantgctt 60
ggatcctcnn anagcggacg cctactacta ctaaattcgc ggncgcgttg acttttttttg 120
ttttttttcct tnacagagnt ntttttgtgc ccttggttct tatgctcana ctcngcaaaa 180
aanatcaaaa gntacnnatg aaaaacntat nccatctnca naaaggaggt gnagntatta 240
ctttct 246

<210> 698
<211> 3674
<212> DNA
<213> Homo sapien

<400> 698
agaaagtttc cttttttttt tttaatggtg aaaagatata cacatattta gaattagcca 60
gctgggctca gtttagatta ttccaatttt gttggcaaca tccagagcat cgtaatcagg 120
agccagtgaa acatattcct tcttctctcc atcaggccaa atcacggtgt tgaccttggc 180
cacatcaatg tcttagaact tcttcacagc ctgtttgatc tggtgcttgt tggctttaac 240
atccacaatg aacacaagtg tgttgttgtc ttctatcttc ttcgtggtga ctcagtggtc 300
agcggaaact tgatgatagc gtagtggtca agcttgtatc tcctgggagc gctcttccaa 360
agatatttgg gctgcctcgg gagttgcagc gtcttgggcc gccggaaggt gggtgacgta 420
cggatcttct ttttttgtgt ggctgtggac acctttcaac actgtcttct tggcctttaa 480
atccttcgct ttggtttcgg ctataggagg ggcaggagct tccttcttca ctttcggcgc 540
catcttgtga aaagggaaag tttcctttct aataccattt tcacttctcc cgaattttgt 600
ggatcgtttc ttggtatcta ccccagattt caggagtgtt ggctggatct tagggattgt 660
gaagtcttca tttccctgtg gtgagatctg aggcatgatt ttaaacagtg tgagggaagg 720
agatctccag gcactttaat agaatggaga agcaggatgg gatttgagag gaaatctgat 780
tttgaaaaaa ggagaactag agttgagttc gtaattaact agcaccttaa aggtcattca 840
gcatgcccat ctgcacagtg ggtgtaatca ccctacagaa caaaaacaaa aaggcaatgg 900
agaggaagct gtaaagcact gtacatgttt aactcattgt tatgtaagct agccgaaggc 960
ttcacagact tgaattcatc tcccaagttc tcttcctgta ctggaaactc tgccttaggt 1020
tgcttaaaac ttgagaaaca gaatattgct tcccctgcct gccttcttga gtacacttgc 1080
ctacacaaag atgcacatcc ttgtttgtgt gtgtgtgtcc atttgctgtg acattcttgt 1140
gaaagtcaaa gtttcccagc tgttgacata cacaagtttg tttggtgcaa cctgtcagat 1200
gcatccctta gacaggccct ttgatactct gggaaagaca ttggacttac agtcggaacg 1260
aaaagaaaga aatgtgatat gtatagcgtg cagtgagttg gagttttacc tgtattgttt 1320
taatttcaac aagcctgagg actagccaca aatgtaccca gtttacaaat gaggaaacag 1380
gtgcaaaaag gttgttacct gtcaaaggtc gtatgtggca gagccaagat ttgagcccag 1440
ttatgtctga tgaacttagc ctatgctctt taaacttctg aatgctgacc attgaggata 1500

```
tctaaactta gatcaattgc attttccctc caagactatt tacttatcaa tacaataata   1560
ccacctttac caatctattg ttttgatacg agactcaaat atgccagata tatgtaaaag   1620
caacctacaa gctctctaat catgctcacc taaaagattc ccgggatcta ataggctcaa   1680
agaaacttct tctagaaata taaaagagaa aattggatta tgcaaaaatt cattattaat   1740
tttttcatc catcctttaa ttcagcaaac atttatctgt tgttgacttt atgcagtatg   1800
gcctttaag gattggggga caggtgaaga acggggtgcc agaatgcatc ctcctactaa   1860
tgaggtcagt acacatttgc attttaaaat gccctgtcca gctgggcatg gtggatcatg   1920
cctgtaatct caacattgga aggccaaggc aggaggattg cttcagccca ggagttcaag   1980
accagcctgg gcaacataga aagaccccat ctctcaatca atcaatcaat gccctgtctt   2040
tgaaaataaa actctttaag aaaggtttaa tgggcagggt gtggtagctc atgcctataa   2100
tacagcactt tgggaggctg aggcaggagg atcactttag cccagaagtt caagaccagc   2160
ctgggcaaca agtgacacct catctcaatt ttttaataaa atgaatacat acataaggaa   2220
agataaaaag aaaagtttaa tgaaagaata cagtataaaa caaatctctt ggacctaaaa   2280
gtatttttgt tcaagccaaa tattgtgaat cacctctctg tgttgaggat acagaatatc   2340
taagcccagg aaactgagca gaaagttcat gtactaacta atcaacccga ggcaaggcaa   2400
aaatgagact aactaatcaa tccgaggcaa ggggcaaatt agacggaacc tgactctggt   2460
ctattaagcg acaactttcc ctctgttgta tttttctttt attcaatgta aaaggataaa   2520
aactctctaa aactaaaaac aatgtttgtc aggagttaca aaccatgacc aactaattat   2580
ggggaatcat aaaatatgac tgtatgagat cttgatggtt tacaaagtgt acccactgtt   2640
aatcacttta aacattaatg aacttaaaaa tgaatttacg gagattggaa tgtttctttc   2700
ctgttgtatt agttggctca ggctgccata acaaaatacc acagactggg aggcttaagt   2760
aacagaaatt catttctcac agttctgggg gctggaagtc cacgatcaag gtgcaggaaa   2820
ggcaggcttc attctgaggc ccctctcttg gctcacatgt ggccaccctc ccactgcgtg   2880
ctcacatgac ctctttgtgc tcctggaaag agggtgtggg ggacagaggg aaagagaagg   2940
agagggaact ctctggtgtc tcgtctttca aggaccctaa cctgggccac tttggcccag   3000
gcactgtggg gtggggggtt gtggctgctc tgctctgagt ggccaagata aagcaacaga   3060
aaaatgtcca aagctgtgca gcaaagacaa gccaccgaac agggatctgc tcatcagtgt   3120
ggggacctcc aagtcggcca ccctggaggc aagcccccam agagcccatg caaggtggca   3180
gcagcagaag aagggaattg tccctgtcct tggcacattc ctcaccgacc tggtgatgct   3240
ggacactgcg atgaatggta atgtggatga gaatatgatg gactcccaga aaaggagacc   3300
cagctgctca ggtggctgca aatcattaca gccttcatcc tggggaggaa ctggggggcct   3360
ggttctgggt cagagagcag cccagtgagg gtgagagcta cagcctgtcc tgccagctgg   3420
atccccagtc ccggtcaacc agtaatcaag gctgagcaga tcaggcttcc cggagctggt   3480
cttgggaagc cagccctggg gtgagttggc tcctgctgtg gtactgagac aatattgtca   3540
taaattcaat gcgccccttgt atcccttttt ctttttttatc tgtctacatc tataatcact   3600
atgcatacta gtctttgtta gtgtttctat tcmacttaat agagatatgt tatacttaaa   3660
aaaaaaaaaa aaaa                                                      3674
```

<210> 699
<211> 2051
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(2051)
<223> n = A,T,C or G

<400> 699

```
ggaccagggg ctgaagtgaa cccccagcac agcacagctg ctctataaaa acgtggccag     60
actttttttt ttgaagcaag tccctgttct tgttcgtcct gactagtccc atcagggccc    120
tggatcccaa gactcagcat ccaaggtccc ctccaggaat cctggcagct cagcatactt    180
tatcctgttt catctgagag caaaaatgta aaattggatg cacagaaaag tgactcaaag    240
tgcttaatga ctagaagaaa tctaggagca gcaagaagag caggacaaac aggccaggcg    300
gtgtcaggag cccaggtctc cagctggang gaacgtcaac cctgcagtgg gagcaggggc    360
cctttgcaca tcctaggcac agatggtaat gtagacacca caggtaagct gggcttggta    420
cctacccctc cccggattca gaaagaaacc aaacaaggag ctttgtgtgg aatgaaacct    480
cctttcctcc cagaagcact gctgactgtt tggtggttgc catttgtggc agtgagccct    540
```

```
tgtttgttct gaggttgggc tggtttctcc tcttggccct gccctacaga tcataaagga     600
gaacagcaag acgtccccag caaacatcca cagatggcct tggaaataag tcaccttcct     660
caccctgcag gaatgccagt gaacatattg ctgacatctt ggagctcagt acctcatagt     720
gtaacggcgt cagtagatct gcctgtgctg ggacttcctg tactacccat tcctgagggg     780
cgatgcttct gcagggcctg tgacttggtg cacaacttca gacaccatca tcttgcagca     840
gcaccgcacc ctcactagcc agggtgttga tgacttcctc aaggccaagg ccacattcaa     900
ggcttcggac ttcattgatg cgcttgtgct gagcaaggtg gcttctccgg gatcttaatt     960
caggaggtag aatggagctt gagatcaagt gtctgatcaa gcctcagtgt atgggcgctg    1020
ttcatcctct ggtgctgaag cagccaagag acccaagtct gcctggctgc ctcttaggat    1080
atgacagcag agccagtggc ctctactaga tcctgtacaa cctcacaaaa cacccagaca    1140
tcgggagtgc tgccagcctg tgatgcaaga gtcctaatcc tgaagacatt gaatgacctg    1200
tcgttgtgct gtttttacca aaaaggatca tgaggatcag agaggaaaag tcacttgccc    1260
aaagtcacac agctgaacag tggtggagtt caactttgac cgtgggctgt ctggccccca    1320
aggtgtatgc ttgcttctct cccaagagac tcctttctta tcaggctcaa atgaatgaaa    1380
ggaggatgtt aaagacaacg ccattattga cgagatcact cccaagcgga ttggagattg    1440
tcccaatatt tagacctata gcaaggcctt gggagaaatg gtggtgcagc aggagagcag    1500
gaacctaacc attgccatcc taaggccctc cattgtgtgg agcaacgtgg caccagcttt    1560
tcctgggttg ggttgataat ctaaatggat gtagccgact cattattgcg gtatgtatag    1620
ggatgaagaa gtaactgtaa tgtagtggag gaatagtaag aaaattctta gtgctggctt    1680
agcttaattg atccaaaaac ataaatgcta ctttactatc aattgaagca tattatttca    1740
attattctgg ttataatatg gaggcaggat gaaattgttt ttattctttt agaatttttt    1800
tttatcagga aaacagaggt aaagtgctat caattactat ttaagagttc tattttgaaa    1860
agtgagaatt aaggattttt cttttctttt taaaaaaaac tttttaaaa attaaaaata    1920
aaagaagcaa aagtcttagg aaaatgaagc aagtagccct gccactctat gtacagtaat    1980
aacaatatct gtcccagtta ttatgtacaa tattataaaa aatgtcgcag acagtaaaaa    2040
aaaaaaaaa a                                                          2051
```

<210> 700
<211> 2841
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(2841)
<223> n = A,T,C or G

<400> 700

```
gcagagcaca gcatagctgc tttaccaaat catggccaga ctgcttctgt aagcaggccc      60
ctgatcctgt tccacctcac tggacaggac ctcccaactg ggcctccag ctacccccac      120
cagcatccct tggccaatgg aaatttgaaa tgttcctggg acagagctcc tggagagagg     180
ggcaggccac cacctttgct gtttgggtga ctagccgttc tggcctgcag gctttggaga     240
gcccaagctg acaaggggta gaagaggtgc ctcagcacag cacagccacg ctacgaaaac     300
atggccagac tcttgtttaa gtcagtcccc gaacacattt ctagtcagtg ggtgaagtct     360
ttcaaccagg gtctctggct accttgactg ctgttctctg gccgacagag gtctcaggcc     420
tccctgagtc agagctcccg gggggaggac cagattgtca tctttgctgt ttgggtgacc     480
cagccatttc agccttaggg cttcagagtg tctgaggtag ccaggggctg aagtgaaccc     540
ccagcacagc acagctgctg tataaaaacg tggccagact ttttctttaa gcaagtccct     600
gttcttattc ctcctgacta ggtaagactt ctcaacttgc ctccagccac atcttattgg     660
tgtgttcaga ttggcaacag gtttgtacct cagtggtaca gagctcccag aggaaggggt     720
aggctatcat cttccctgga aaatacgagt caattaggga cttgagggga cccccagcat     780
tccacagcag cccttcagaa aagtggccag actctgtact tgatgggcag atcctcctgg     840
cctgtgtctc tagccagccc accactggag ctatcaagcc agtagcaact cagcagttcc     900
ttggacagag cttccaggag caaatgaaat cctttctgcc actgcctttg cagtgaactg     960
cccttgctat cctcagaaga tatatcacgg gagcaaagac cctaagtgcc atatcaacac    1020
ctccaataag ctgcagttga cccaaagaac aagccaatcc atctcccaca ggttccacac    1080
acactccact actcatcacc agacagggaa ccctggcttg ggcccacagc acagaccctc    1140
catcctgggc cgattacact gagtgattgc taactcacat gtctctggga tggagcaccc    1200
```

```
aggagacaag caaagtggtg gagcagcaag tcaggtgatg tggagcccag agggcaggga    1260
gagctatctc tctgggctcc acttgccctt gtgagacact ttgtcccagc actccttagt    1320
ctgcttgcct ctcccagggc cccagcctgg ccacacctgc ttacagggca ctctcagatg    1380
cccataccat agtttctgtg ctagtggacc gtaccatatc agtggagagc tgcagcaagg    1440
tggcccntac ggccacgcac cagcctgcac attacctctc catactgcag ccctttatat    1500
ggaaacttcc tacatcactt tgctgtgtgt gtttacacag gtggattttg ctttacttgc    1560
actgacagca cacaggaggg cagcacacac cccaacccac atcaactgcc attaaagaaa    1620
agaaatttca gcccataatt tcatgtccag caaaattagg catcataagt gaaggagaaa    1680
taagatcctt ttcagacaag caaatgctga gggaattcaa tatcaccaga tctaccttac    1740
aagagctcct gaaggaagca ctaaatatgg aaagaaaaaa ccatcaccag ccactacaaa    1800
aatgcagtga agaacgcagt gaattacgca gtccagtgat gctaaaaacc aaccacatac    1860
gttaagtctg caaaataacc agctgacagc atgacgacag gataaatcca cacataccat    1920
tactaacctt aaatgaaaat gggctaaatg ctcccattga aagacatggg gcaagctgga    1980
taaagaacca agacccactg gagtatgctg tcttcaagaa acccatctca catgcggtgg    2040
catacatagg ctcaaaataa aggaatggag aaaaatattt caagcaaatg gaaaacagaa    2100
aaaagcaggt gttgcactcc tactttctga caaaacagac tatgcgaata aagataaaaa    2160
agagaaggac attacaaagg tggtcctgac ctttgatata tctcattgct tgataccaac    2220
ctgggctgtt ttaattgccc aaanccaata ggataatttg ctgaggttgt ggagcttctc    2280
ccctgcagag agtccctgat ctcccaaaat ttggttgaga tgtaaggttg attttgctgt    2340
acaactcctt ttctgaagtt ttactcattt ccaaaaagga aggcaagttt tcctgcttcc    2400
atgacgatgg agagcaggca tctcctttcc tgagtttcag cttgcttctg acagggaagg    2460
tgagtgtaag ttttttccag cttctaagat ggcagagaac gatcaccagc ctgagcctta    2520
tttccaggta agtagctgaa ttagagtttt gtcttaaaat ttttccttaa tgattaaaat    2580
gtaagattac ccaccagctg cttttaattt ctcccttagc attagaacac tcagtaatca    2640
tatgaattgt gcatttgttt gttttgctta actctttctg tttgtttatg tttggggttt    2700
tattgttgtt gtttcacttt tctcccatct cttcctgact tggtcaaatc caaaggaatg    2760
ttcgaaattg tggggagcaa ggcatctgaa atggctaaaa ctcctgtggc tgcaaaaaat    2820
agaaataaaa aaaaaaaaaa a                                              2841
```

<210> 701
<211> 3228
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(3228)
<223> n = A,T,C or G

<400> 701

```
tccgccccat tgacgcaaat ggcggtaggc gtgtacggtg ggaggtctat ataagcagag      60
ctctcnggct aactagagaa cccactgctt actggcttat cgaaattaat acgactcact     120
atagggagac ccaagctggc tagcgtttaa acttaagctt ggtaccgagc tcggatccac     180
tagtccagtg tggtggaatt ccattgtgtt gggcaggaaa caagcaaagt ggtggagcag     240
caagtcaggt gatgtggagc ccagaggtca gggatggctg tctctctagg gtccacttgc     300
ccttgtgaga cactttatcc cagcacttta ggaatactga ggtcatacca gccacatctt     360
atatgcaaga ttgcccagca gagatcaggt ccgagagttc ccttttttaaa aaaaggagac    420
ttgcttaata aaagaagtct agccacgttt gtgtagagcg gctgtgctgt gctgggggtt     480
cacttttgag agagttctcc tctgagacct gatctctgga ggctgggcaa tcttgcactt     540
gagatggggc tggtctgatc tcagcactcc ttagtctgct cgcctctccc atggccccag     600
cctggccaca cctgcttacg ggcactcttt agatgcccac accataactt ccatgctagt     660
ggactgtacc atatcagtgg agagctgcag caaggtggcc cctagagcca cgcaccagcc     720
tgcacattgc ctctccatac ggcagccctt tatttggaaa cttcctaaat cactttgctg     780
tgtgtgttta cacgggtgtg ttttgcttta cttgccctga gagcacacgg gagtgcagca     840
cacaccccaa cccacatcaa ctgccattaa agaaaagaaa tttcagccca gaatttcatg     900
tccagcaaaa ttaagcatca taagtgaagg agaaataaga tcctttttcag acaagcaagt    960
gctgagggaa tttggtatca ccagatctac cttacgagag ctcctgaagg aagcactaaa    1020
tatggaaaga aaagatcatc acctgctact acaaaaacac actgaagtac acagtccaat    1080
```

```
gatgctaaaa agcaagcaca tatgtaagtc tgcaaaataa ccagctgaca gcatgacgac 1140
aggataaaat ccacacatac cattactaac cttaaatgta aatgggctaa atgctcccat 1200
tgaaagacac ggggcaagct gggtaaagaa ccaagaccca ctggagtatg ccgtcttcaa 1260
gcaacccatc tcacgtgcag tgccatacat aggctcaaaa taaaggaatg gagaaaaata 1320
tttcaagcaa atggaaaaca gaaaaaaggt gttgcactcc cagtttctga caaaacagac 1380
tctaccaata aagataaaaa aagagaagga cattacaaag gtggtcctga cctttgataa 1440
atctcattat tgcttgatac caacctgggc tatttgtatt gcccaaacga ataggataat 1500
ttgctgaggt tgtggagctt ctccccttca cagagtccct gatctccgaa aatttggttg 1560
agatgtaagg ttgattttgc tgtacaactc ctttttgaa gttttactca tttccaacaa 1620
ggaaggcaag ttttcctgct tccattgaca aaggagagca ggcacctcct ttcctgagtt 1680
tcagcttgct tctgacaggg aaggagcttt gagatttgaa tactggcctg ctgggttttg 1740
gacgtgcatt gggcctgtgg tcccatttgt gttatttttc tgggaaattt cttccctttg 1800
gagtgagaaa gcttacccaa tgcctgtacc atcatcgtac cttaaaagaa ctccatttta 1860
agttcaggga ctccttggca gaagagaccg tagccttgta tcagatcata aaggagaaga 1920
gcaagaggtc cccggcaaac atccacagat ggccttggaa ataagtcacc ttgctcaccc 1980
tgcaggaatg ccagtgaact tattgctgac atcttggagc tcagtaccct catagtgtaa 2040
cggcgtcagc agatctgcct gtgctgggac ttcctgtact acccattcct gaggggcgat 2100
gcttctgcag ggcctgtgac ttggtgcaca acttcagaca ccatcatctt gcagcagcac 2160
cgcaccctca ctagccaggg tgttgatgac ttcctcaagg ccaaggccac attcaaggct 2220
tcggacttca ttgatgcgct tgtgctgagc aaggtggctt ctccgggatc ttaattcagg 2280
aggtagaatg gagcttgaga tcaagtgtct gatcaagcct cagtgtatgg gcgctgttca 2340
tcntctggtg ctgaagcagc caagagaccc aagtctgcct ggctgcntct taggatatga 2400
cagcagagcc agtggcctct actagatcct gtacaacctc acaaaacacc cagacatcgg 2460
gagtgctgcc agcctgtgat gcaagagtcc taatcctgaa gacattgaat gacctgtcat 2520
tctgctgttt ttaccaaaaa ggatcatgag gatcagagag gaaaagtcac ttgcccaaag 2580
tcacacagct gaacagtggt ggagttcaac tttgaccgtg ggctgtctga ccccaaggtg 2640
tatgcttgct tctctcccaa gagacaactt tcttatcagg ctcaaatgaa tgaaaggagg 2700
atgttaaagg taggatctct gaagcctgtg ccagtggaac cgcagctcat ggctggcacc 2760
tgtgttctca ttcttacctc attaagagta aagtttattg agtttattga atttaagtat 2820
ctttagtgag atcatatatt attagtaaga actgggacca aacagatttt ctgactctaa 2880
aagagagatt ttcacagaaa cagatatata cctgtaagta tacagacacg catacacaca 2940
tttctttact gctcataaaa attagtcctt attagaatgt gggatgtata aatgtaagag 3000
aattttcatg ttaaaattga cagatacatt tttaaattgt cctaaaataa atttaattat 3060
ttttntttta gaattttcca ttattaatgt tattttttatg agaaactata taactttatt 3120
gataatacat acaataaccc tttgttttc aaattgaaaa tacagtgtat tttgcaaata 3180
actaagtcct aattttgtat taaaatttta aattttcaaa aaaaaaa 3228
```

<210> 702
<211> 4894
<212> DNA
<213> Homo sapiens

<400> 702

```
ctgcacgcgc tggctccggg tgacagccgc gcgcctcggc caggatctga gtgatgagac 60
gtgtccccac tgaggtgccc cacagcagca ggtgttgagc atgggctgag aagctggacc 120
ggcaccaaag ggctggcaga aatgggcgcc tggctgattc ctaggcagtt ggcggcagca 180
aggaggagag gccgcagctt ctggagcaga gccgagacga agcagttctg gagtgcctga 240
acggccccct gagccctacc cgcctggccc actatggtcc agaggctgtg ggtgagccgc 300
ctgctgcggc accggaaagc ccagctcttg ctggtcaacc tgctaacctt tggcctggag 360
gtgtgtttgg ccgcaggcat cacctatgtg ccgcctctgc tgctggaagt gggggtagag 420
gagaagttca tgaccatggt gctgggtgag tcactacatc ctccttcctt cctgttccag 480
atacatgcca cctggcatgt gggacaggag tacctctgcc ctgggagctg cttggaggga 540
gaggtggtct gctgggaagg cattgctggg caggaggtg accctgggct gagggggcac 600
accaagagaa agaagagaat accaaggaca taccccagtc acctctggat ccctggtcct 660
gcacagagcc tggctcatag gagacactgg agaaatgctc ctaacctttg gctagccctt 720
ttataattta tagcgattat ctcatttaat gcttacaacc accatttgag gtgatccatt 780
ttacagagaa ggaagcagag gcttttaaga ggttaggtaa gtcttagcca aagccaaata 840
```

gcagctgaac agtagagctg ggactccatc aaggtctccc agccggagct tgctcctacc 900
cctaggacaa ggggtggact cctgactctg cagataaatt ctacaaaagc cacagaaggc 960
aagtagtaac cattgtgtga caacccctca cccccaggaa gaggggcccc tgtgaggatt 1020
gcaggctctg gagtcacact gcttgttgaa acgctgcctc ttaccctccc taggtctgcg 1080
cctttgaata agtatcactt cttagttgct ccatgcctca gtttgtccat ctgaaaatgg 1140
gggcatctgt aatgcctgtg ttatgaggag taaattacag catccctgtg aagacgtagc 1200
acagtgtcga gtacggaatg ttatttccat ccttctcacg gagcttggtt ccccttcccc 1260
ttgcccttta cttgtcccag ccattgactc atactacttc ccttcttgca ggcattggtc 1320
cagtgctggg cctggtctgt gtcccgctcc taggctcagc cagtgaccac tggcgtggac 1380
gctatggccg ccgccggccc ttcatctggg cactgtcctt gggcatcctg ctgagcctct 1440
ttctcatccc aagggccggc tggctagcag ggctgctgtg cccggatccc aggcccctgg 1500
agctggcact gctcatcctg ggcgtggggc tgctggactt ctgtggccag gtgtgcttca 1560
ctccactgga ggccctgctc tctgacctct tccgggaccc ggaccactgt cgccaggcct 1620
actctgtcta tgccttcatg atcagtcttg gggggctgcct gggctacctc ctgcctgcca 1680
ttgactggga caccagtgcc ctggcccccct acctgggcac ccaggaggag tgcctctttg 1740
gcctgctcac cctcatcttc ctcacctgcg tagcagccac actgctggtg gctgaggagg 1800
cagcgctggg ccccaccgag ccagcagaag ggctgtcggc cccctccttg tcgcccccact 1860
gctgtccatg ccgggcccgc ttggctttcc ggaacctggg cgccctgctt ccccggctgc 1920
accagctgtg ctgccgcatg ccccgcaccc tgcgccggct cttcgtggct gagctgtgca 1980
gctggatggc actcatgacc ttcacgctgt tttacacgga tttcgtgggc gaggggctgt 2040
accagggcgt gcccagagct gagccgggca ccgaggcccg gagacactat gatgaaggta 2100
aggccttggc agccagcaga ggctggtgtg ggagccgccc accagagacg acactcgggg 2160
ctgtgtctgg gctggtgcct ctccatcctg gccccgactt ctctgtcagg aaagtgggga 2220
tggaccccat ctgcatacac ggcttctcat gggtgtggaa catctctgct tgcggtttca 2280
ggaaggcctc tggctgctct aggagtctga tcagagtcgt tgccccagtt tgacagaagg 2340
aaaggcggag cttattcaaa gtctagaggg agtggaggag ttaaggctgg atttcagatc 2400
tgcctggttc cagccgcagt gtgccctctg ctcccccaac gactttccaa ataatctcac 2460
cagcgccttc cagctcaggc gtcctagaag cgtcttgaag cctatggcca gctgtctttg 2520
tgttccctct cacccgcctg tcctcacagc tgagactccc aggaaacctt cagactacct 2580
tcctctgcct tcagcaaggg gcgttgccca cattctctga gggtcagtgg aagaacctag 2640
actcccattg ctagaggtag aaaggggaag ggtgctgggg agcagggctg gtccacagca 2700
ggtctcgtgc agcaggtacc tgtggttccg ccttctcatc tccctgagac tgctccgacc 2760
cttccctccc aggctctgtc tgatggcccc tctccctctg caggcgttcg gatgggcagc 2820
ctggggctgt tcctgcagtg cgccatctcc ctggtcttct ctctggtcat ggaccggctg 2880
gtgcagcgat tcggcactcg agcagtctat ttggccagtg tggcagcttt ccctgtggct 2940
gccggtgcca catgcctgtc ccacagtgtg gccgtggtga cagcttcagc cgccctcacc 3000
gggttcacct tctcagccct gcagatcctg ccctacacac tggcctccct ctaccaccgg 3060
gagaagcagg tgttcctgcc caaataccga ggggacactg gaggtgctag cagtgaggac 3120
agcctgatga ccagcttcct gccaggccct aagcctggag ctccccttccc taatggacac 3180
gtgggtgytg gaggcagtgg cctgctccca cctccacccg cgctctgcgg ggcctctgcc 3240
tgtgatgtct ccgtacgtgt ggtggtgggt gagcccaccg aggccagggt ggttccgggc 3300
cggggcatct gcctggacct cgccatcctg gatagtgcct tcctgctgtc ccaggtggcc 3360
ccatccctgt ttatgggctc cattgtccag ctcagccagt ctgtcactgc ctatatggtg 3420
tctgccgcag gcctgggtct ggtcgccatt tactttgcta cacaggtagt atttgacaag 3480
agcgacttgg ccaaatactc agcgtagaaa acttccagca cattggggtg gagggcctgc 3540
ctcactgggt cccagctccc tgctcctgtt agccccatgg ggctgccggg ctggccgcca 3600
gtttctgttg ctgccaaagt aatgtggctc tctgctgcca ccctgtgctg ctgaggtgcg 3660
tagctgcaca gctgggggct ggggcgtccc tctcctctct ccccagtctc tagggctgcc 3720
tgactggagg ccttccaagg gggtttcagt ctggacttat acagggaggc cagaagggct 3780
ccatgcactg gaatgcgggg actctgcagg tggattaccc aggctcaggg ttaacagcta 3840
gcctcctagt tgagacacac ctagagaagg gtttttggga gctgaataaa ctcagtcacc 3900
tggtttccca tctctaagcc ccttaacctg cagcttcgtt taatgtagct cttgcatggg 3960
agtttctagg atgaaacact ccaccatggg atttgaacat atgaaagtta tttgtagggg 4020
aagagtcctg aggggcaaca cacaagaacc aggtcccctc agcccacagc actgtctttt 4080
tgctgatcca ccccctcttt accttttatc aggatgtggc ctgttggtcc ttctgttgcc 4140
atcacagaga cacaggcatt taaatattta acttatttat ttaacaaagt agaagggaat 4200
ccattgctag cttttctgtg ttggtgtcta atatttgggt agggtggggg atccccaaca 4260
atcaggtccc ctgagatagc tggtcattgg gctgatcatt gccagaatct tcttctcctg 4320

gggtctggcc ccccaaaatg cctaacccag gaccttggaa attctactca tcccaaatga 4380
taattccaaa tgctgttacc caaggttagg gtgttgaagg aaggtagagg gtggggcttc 4440
aggtctcaac ggcttcccta accacccctc ttctcttggc ccagcctggt tccccccact 4500
tccactcccc tctactctct ctaggactgg gctgatgaag gcactgccca aaatttcccc 4560
tacccccaac tttcccctac cccaacttt ccccaccagc tccacaaccc tgtttggagc 4620
tactgcagga ccagaagcac aaagtgcggt ttcccaagcc tttgtccatc tcagccccca 4680
gagtatatct gtgcttgggg aatctcacac agaaactcag gagcaccccc tgcctgagct 4740
aagggaggtc ttatctctca ggggggggttt aagtgccgtt tgcaataatg tcgtcttatt 4800
tatttagcgg ggtgaatatt ttatactgta agtgagcaat cagagtataa tgtttatggt 4860
gacaaaatta aaggctttct tatatgttta aaaa 4894

<210> 703
<211> 2904
<212> DNA
<213> Homo sapiens

<400> 703
gtctatgcct tcatgatcag tcttgggggc tgcctgggct acctcctgcc tgccattgac 60
tgggacacca gtgccctggc cccctacctg ggcacccagg aggagtgcct ctttggcctg 120
ctcaccctca tcttcctcac ctgcgtagca gccacactgc tggtggctga ggaggcagcg 180
ctgggcccca ccgagccagc agaagggctg tcggcccccct ccttgtcgcc ccactgctgt 240
ccatgccggg cccgcttggc tttccggaac ctgggcgccc tgcttccccg gctgcaccag 300
ctgtgctgcc gcatgccccg caccctgcgc cggctcttcg tggctgagct gtgcagctgg 360
atggcactca tgaccttcac gctgttttac acggatttcg tgggcgaggg gctgtaccag 420
ggcgtgccca gagctgagcc gggcaccgag gcccggagac actatgatga aggaaggcct 480
ctggctgctc taggagtctg atcagagtcg ttgccccagt ttgacagaag gaaaggcgga 540
gcttattcaa agtctagagg gagtggagga gttaaggctg gatttcagat ctgcctggtt 600
ccagccgcag tgtgccctct gctcccccaa cgactttcca aataatctca ccagcgcctt 660
ccagctcagg cgtcctagaa gcgtcttgaa gcctatggcc agctgtcttt gtgttccctc 720
tcacccgcct gtcctcacag ctgagactcc caggaaacct tcagactacc ttcctctgcc 780
ttcagcaagg ggcgttgccc acattctctg agggcgttcg gatgggcagc ctggggctgt 840
tcctgcagtg cgccatctcc ctggtcttct ctctggtcat ggaccggctg gtgcagcgat 900
tcggcactcg agcagtctat ttggccagtg tggcagcttt ccctgtggct gccggtgcca 960
catgcctgtc ccacagtgtg gccgtggtga cagcttcagc cgccctcacc gggttcacct 1020
tctcagccct gcagatcctg ccctacacac tggcctccct ctaccaccgg gagaagcagg 1080
tgttcctgcc caaataccga ggggacactg gaggtgctag cagtgaggac agcctgatga 1140
ccagcttcct gccaggccct aagcctggag ctcccttccc taatggacac gtgggtgctg 1200
gaggcagtgg cctgctccca cctccacccg cgctctgcgg ggcctctgcc tgtgatgtct 1260
ccgtacgtgt ggtggtgggt gagcccaccg aggccagggt ggttccgggc cggggcatct 1320
gcctggacct cgccatcctg gatagtgcct tcctgctgtc ccaggtggcc ccatccctgt 1380
ttatgggctc cattgtccag ctcagccagt ctgtcactgc ctatatggtg tctgccgcag 1440
gcctgggtct ggtcgccatt tactttgcta cacaggtagt atttgacaag agcgacttgg 1500
ccaaatactc agcgtagaaa acttccagca cattggggtg gagggcctgc ctcactgggt 1560
cccagctccc cgctcctgtt agccccatgg ggctgccggg ctggccgcca gtttctgttg 1620
ctgccaaagt aatgtggctc tctgctgcca ccctgtgctg ctgaggtgcg tagctgcaca 1680
gctgggggct ggggcgtccc tctcctctct ccccagtctc tagggctgcc tgactggagg 1740
ccttccaagg gggtttcagt ctggacttat acagggaggc cagaagggct ccatgcactg 1800
gaatgcgggg actctgcagg tggattaccc aggctcaggg ttaacagcta gcctcctagt 1860
tgagacacac ctagagaagg gtttttggga gctgaataaa ctcagtcacc tggtttccca 1920
tctctaagcc ccttaacctg cagcttcgtt taatgtagct cttgcatggg agtttctagg 1980
atgaaacact cctccatggg atttgaacat atgaaagtta tttgtagggg aagagtcctg 2040
aggggcaaca cacaagaacc aggtcccctc agcccacagc actgtctttt tgctgatcca 2100
cccccctctt acctttttatc aggatgtggc ctgttggtcc ttctgttgcc atcacagaga 2160
cacaggcatt taaatattta acttatttat ttaacaaagt agaaggggaat ccattgctag 2220
cttttctgtg ttggtgtcta atatttgggt agggtggggg atccccaaca atcaggtccc 2280
ctgagatagc tggtcattgg gctgatcatt gccagaatct tcttctcctg ggtctggcc 2340
ccccaaaatg cctaacccag gaccttggaa attctactca tcccaaatga taattccaaa 2400

tgctgttacc caaggttagg gtgttgaagg aaggtagagg gtggggcttc aggtctcaac 2460
ggcttcccta accacccctc ttctcttggc ccagcctggt tcccccact tccactcccc 2520
tctactctct ctaggactgg gctgatgaag gcactgccca aaatttcccc tacccccaac 2580
tttcccctac ccccaacttt ccccaccagc tccacaaccc tgtttggagc tactgcagga 2640
ccagaagcac aaagtgcggt ttcccaagcc tttgtccatc tcagccccca gagtatatct 2700
gtgcttgggg aatctcacac agaaactcag gagcaccccc tgcctgagct aagggaggtc 2760
ttatctctca ggggggggttt aagtgccgtt tgcaataatg tcgtcttatt tatttagcgg 2820
ggtgaatatt ttatactgta agtgagcaat cagagtataa tgtttatggt gacaaaatta 2880
aaggctttct tatatgttta aaaa 2904

<210> 704
<211> 4034
<212> DNA
<213> Homo sapiens

<400> 704
aaccagcctg cacgcgctgg ctccgggtga cagccgcgcg cctcggccag gatctgagtg 60
atgagacgtg tccccactga ggtgccccac agcagcaggt gttgagcatg ggctgagaag 120
ctggaccggc accaaagggc tggcagaaat gggcgcctgg ctgattccta ggcagttggc 180
ggcagcaagg aggagaggcc gcagcttctg gagcagagcc gagacgaagc agttctggag 240
tgcctgaacg gccccctgag ccctacccgc ctggcccact atggtccaga ggctgtgggt 300
gagccgcctg ctgcggcacc ggaaagccca gctcttgctg gtcaacctgc taacctttgg 360
cctggaggtg tgtttggccg caggcatcac ctatgtgccg cctctgctgc tggaagtggg 420
ggtagaggag aagttcatga ccatggtgct gggcattggt ccagtgctgg gcctggtctg 480
tgtcccgctc ctaggctcag ccagtgacca ctggcgtgga cgctatggcc gccgccggcc 540
cttcatctgg gcactgtcct tgggcatcct gctgagcctc tttctcatcc caagggccgg 600
ctggctagca gggctgctgt gcccggatcc caggcccctg gagctggcac tgctcatcct 660
gggcgtgggg ctgctggact tctgtggcca ggtgtgcttc actccactgg aggccctgct 720
ctctgacctc ttccgggacc cggaccactg tcgccaggcc tactctgtct atgccttcat 780
gatcagtctt gggggctgcc tgggctacct cctgcctgcc attgactggg acaccagtgc 840
cctggccccc tacctgggca cccaggagga gtgcctcttt ggcctgctca ccctcatctt 900
cctcacctgc gtagcagcca cactgctggt ggctgaggag gcagcgctgg gccccaccga 960
gccagcagaa gggctgtcgg ccccctcctt gtcgccccac tgctgtccat gccgggcccg 1020
cttggctttc cggaacctgg gcgccctgct tccccggctg caccagctgt gctgccgcat 1080
gccccgcacc ctgcgccggc tcttcgtggc tgagctgtgc agctggatgg cactcatgac 1140
cttcacgctg ttttacacgg atttcgtggg cgaggggctg taccagggcg tgcccagagc 1200
tgagccgggc accgaggccc ggagacacta tgatgaaggt aaggccttgg cagccagcag 1260
aggctggtgt gggagccgcc caccagagac gacactcggg gctgtgtctg ggctggtgcc 1320
tctccatcct ggccccgact tctctgtcag gaaagtgggg atggacccca tctgcataca 1380
cggcttctca tgggtgtgga acatctctgc ttgcggtttc aggaaggcct ctggctgctc 1440
taggagtctg atcagagtcg ttgccccagt ttgacagaag gaaaggcgga gcttattcaa 1500
agtctagagg gagtggagga gttaaggctg gatttcagat ctgcctggtt ccagccgcag 1560
tgtgccctct gctcccccaa cgactttcca aataatctca ccagcgcctt ccagctcagg 1620
cgtcctagaa gcgtcttgaa gcctatggcc agctgtcttt gtgttccctc tcacccgcct 1680
gtcctcacag ctgagactcc caggaaacct tcagactacc ttcctctgcc ttcagcaagg 1740
ggcgttgccc acattctctg agggtcagtg gaagaaccta gactcccatt gctagaggta 1800
gaaaggggaa gggtgctggg gagcagggct ggtccacagc aggtctcgtg cagcaggtac 1860
ctgtggttcc gccttctcat ctccctgaga ctgctccgac ccttccctcc caggctctgt 1920
ctgatggccc ctctccctct gcaggcgttc ggatgggcag cctggggctg ttcctgcagt 1980
gcgccatctc cctggtcttc tctctggtca tggaccggct ggtgcagcga ttcggcactc 2040
gagcagtcta tttggccagt gtggcagctt tccctgtggc tgccggtgcc acatgcctgt 2100
cccacagtgt ggccgtggtg acagcttcag ccgccctcac cgggttcacc ttctcagccc 2160
tgcagatcct gccctacaca ctggcctccc tctaccaccg ggagaagcag gtgttcctgc 2220
ccaaataccg aggggacact ggaggtgcta gcagtgagga cagcctgatg accagcttcc 2280
tgccaggccc taagcctgga gctcccttcc ctaatggaca cgtgggtgct ggaggcagtg 2340
gcctgctccc acctccaccc gcgctctgcg ggcctctgc ctgtgatgtc tccgtacgtg 2400
tggtggtggg tgagcccacc gaggccaggg tggttccggg ccggggcatc tgcctggacc 2460

```
tcgccatcct ggatagtgcc ttcctgctgt cccaggtggc cccatccctg tttatgggct 2520
ccattgtcca gctcagccag tctgtcactg cctatatggt gtctgccgca ggcctgggtc 2580
tggtcgccat ttactttgct acacaggtag tatttgacaa gagcgacttg gccaaatact 2640
cagcgtagaa aacttccagc acattggggt ggagggcctg cctcactggg tcccagctcc 2700
ccgctcctgt tagccccatg gggctgccgg gctggccgcc agtttctgtt gctgccaaag 2760
taatgtggct ctctgctgcc accctgtgct gctgaggtgc gtagctgcac agctgggggc 2820
tggggcgtcc ctctcctctc tccccagtct ctagggctgc ctgactggag gccttccaag 2880
ggggtttcag tctggactta tacagggagg ccagaagggc tccatgcact ggaatgcggg 2940
gactctgcag gtggattacc caggctcagg gttaacagct agcctcctag ttgagacaca 3000
cctagagaag ggtttttggg agctgaataa actcagtcac ctggtttccc atctctaagc 3060
cccttaacct gcagcttcgt ttaatgtagc tcttgcatgg gagtttctag gatgaaacac 3120
tcctccatgg gatttgaaca tatgaaagtt atttgtaggg gaagagtcct gaggggcaac 3180
acacaagaac caggtcccct cagcccacag cactgtcttt ttgctgatcc accccctct 3240
tacctttat caggatgtgc ctgttggtcc ttctgttgcc atcacagaga cacaggcatt 3300
taaatattta acttatttat ttaacaaagt agaagggaat ccattgctag cttttctgtg 3360
ttggtgtcta atatttgggt agggtggggg atccccaaca atcaggtccc ctgagatagc 3420
tggtcattgg gctgatcatt gccagaatct tcttctcctg ggtctggcc ccccaaaatg 3480
cctaacccag gaccttggaa attctactca tcccaaatga taattccaaa tgctgttacc 3540
caaggttagg gtgttgaagg aaggtagagg gtggggcttc aggtctcaac ggcttcccta 3600
accacccctc ttctcttggc ccagcctggt tccccccact tccactcccc tctactctct 3660
ctaggactgg gctgatgaag gcactgccca aaatttcccc tacccccaac tttcccctac 3720
ccccaacttt ccccaccagc tccacaaccc tgtttggagc tactgcagga ccagaagcac 3780
aaagtgcggt ttcccaagcc tttgtccatc tcagccccca gagtatatct gtgcttgggg 3840
aatctcacac agaaactcag gagcaccccc tgcctgagct aagggaggtc ttatctctca 3900
ggggggggttt aagtgccgtt tgcaataatg tcgtcttatt tatttagcgg ggtgaatatt 3960
ttatactgta agtgagcaat cagagtataa tgtttatggt gacaaaatta aaggctttct 4020
tatatgttta aaaa 4034
```

<210> 705
<211> 6976
<212> DNA
<213> Homo sapiens

<400> 705

```
gaagctggac cggcaccaaa gggctggcag aaatgggcgc ctggctgatt cctaggcagt 60
tggcggcagc aaggaggaga ggccgcagct tctggagcag agccgagacg aagcagttct 120
ggagtgcctg aacggccccc tgagccctac ccgcctggcc cactatggtc cagaggctgt 180
gggtgagccg cctgctgcgg caccggaaag cccagctctt gctggtcaac ctgctaacct 240
ttggcctgga ggtgtgtttg gccgcaggca tcacctatgt gccgcctctg ctgctggaag 300
tgggggtaga ggagaagttc atgaccatgg tgctgggtga gtcactacat cctccttcct 360
tcctgttcca gatacatgcc acctggcatg tgggacagga gtacctctgc cctgggagct 420
gcttggaggg agaggtggtc tgctgggaag gcattgctgg gcaggagggt gaccctgggc 480
tgaggggca caccaagaga aagaagagaa taccaaggac ataccccagt cacctctgga 540
tccctggtcc tgcacagagc ctggctcata ggagacactg gagaaatgct cctaaccttt 600
ggctagccct tttataattt atagcgatta tctcatttaa tgcttacaac caccatttga 660
ggtgatccat tttacagaga aggaagcaga ggcttttaag aggttaggta agtcttagcc 720
aaagccaaat agcagctgaa cagtagagct gggactccat caaggtctcc cagccggagc 780
ttgctcctac ccctaggaca aggggtggac tcctgactct gcagataaat tctacaaaag 840
ccacagaagg caagtagtaa ccattgtgtg acaacccctc acccccagga agaggggccc 900
ctgtgaggat tgcaggctct ggagtcacac tgcttgttga aacgctgcct cttaccctcc 960
ctaggtctgc gcctttgaat aagtatcact tmttagttgc tccatgcctc agtttgtcca 1020
tctgaaaatg gggcatctg taatgcctgt gttatgagga gtaaattaca gcatccctgt 1080
gaagacgtag cacagtgtcg agtacggaat gttatttcca tccttctcac ggagcttggt 1140
tccccttccc cttgcccttt acttgtccca gccattgact catactactt cccttcttgc 1200
aggcattggt ccagtgctgg gcctggtctg tgtcccgctc ctaggctcag ccagtgacca 1260
ctggcgtgga cgctatggcc gccgccggcc cttcatctgg gcactgtcct tgggcatcct 1320
gctgagcctc tttctcatcc caaggccgg ctggctagca gggctgctgt gcccggatcc 1380
```

caggcccctg gagctggcac tgctcatcct gggcgtgggg ctgctggact tctgtggcca 1440
ggtgtgcttc actccactgg aggccctgct ctctgacctc ttccgggacc cggaccactg 1500
tcgccaggcc tactctgtct atgccttcat gatcagtctt gggggctgcc tgggctacct 1560
cctgcctgcc attgactggg acaccagtgc cctggccccc tacctgggca cccaggagga 1620
gtgcctcttt ggcctgctca ccctcatctt cctcacctgc gtagcagcca cactgctggt 1680
ggctgaggag gcagcgctgg gccccaccga gccagcagaa gggctgtcgg ccccctcctt 1740
gtcgccccac tgctgtccat gccgggcccg cttggctttc cggaacctgg gcgccctgct 1800
tccccggctg caccagctgt gctgccgcat gccccgcacc ctgcgccggc tcttcgtggc 1860
tgagctgtgc agctggatgg cactcatgac cttcacgctg ttttacacgg atttcgtggg 1920
cgagggggctg taccagggcg tgcccagagc tgagccgggc accgaggccc ggagacacta 1980
tgatgaaggt aaggccttgg cagccagcag aggctggtgt gggagccgcc caccagagac 2040
gacactcggg gctgtgtctg ggctggtgcc tctccatcct ggccccgact tctctgtcag 2100
gaaagtgggg atggacccca tctgcataca cggcttctca tgggtgtgga acatctctgc 2160
ttgcggtttc aggaaggcct ctggctgctc taggagtctg atcagagtcg ttgccccagt 2220
ttgacagaag gaaaggcgga gcttattcaa agtctagagg gagtggagga gttaaggctg 2280
gatttcagat ctgcctggtt ccagccgcag tgtgccctct gctcccccaa cgactttcca 2340
aataatctca ccagcgcctt ccagctcagg cgtcctagaa gcgtcttgaa gcctatggcc 2400
agctgtcttt gtgttccctc tcacccgcct gtcctcacag ctgagactcc caggaaacct 2460
tcagactacc ttcctctgcc ttcagcaagg ggcgttgccc acattctctg agggtcagtg 2520
gaagaaccta gactcccatt gctagaggta gaaaggggaa gggtgctggg gagcagggct 2580
ggtccacagc aggtctcgtg cagcaggtac ctgtggttcc gccttctcat ctccctgaga 2640
ctgctccgac ccttccctcc caggctctgt ctgatggccc ctctccctct gcaggcgttc 2700
ggatgggcag cctggggctg ttcctgcagt gcgccatctc cctggtcttc tctctggtca 2760
tggaccggct ggtgcagcga ttcggcactc gagcagtcta tttggccagt gtggcagctt 2820
tccctgtggc tgccggtgcc acatgcctgt cccacagtgt ggccgtggtg acagcttcag 2880
ccgccctcac cgggttcacc ttctcagccc tgcagatcct gccctacaca ctggcctccc 2940
tctaccaccg ggagaagcag gtactcattg gccagtgggt ggagtcaggg tgggaggggt 3000
ggtctgggtt tttgggaggc caactagctc agaacctggt atctggcaag caactttgga 3060
gaatgcttct ttgaatcaga gaagaagctt atcctagccc caggccaga ggcttgggct 3120
gcagaacagt gtagattaga ttctgggaat gacttcctgg ggtcaggact gtgtagcact 3180
tgaatggatg attgcaggaa atgcaaaata cgatagtggg aatcccgaag ggtcaggcca 3240
gcaggagccc taggcttcta ggctggttgt tctatggaga ggcagggcgc tgaatcagat 3300
gacccctggg ccattcagcc tcagcagacg ggagtgggaa tggtccagcc ttagcaacac 3360
ctttcttcag ggagcagcaa cctgacttag cctgtatcct actctggtct ctgagatggg 3420
gcaggctcct tcctaccccc tttctttctg gcttattttt cttttctgtc taattccctt 3480
ttcttttcct gcatccctcc tttgcctcct tccctttctc cttccccttc cccttcccct 3540
gtggcagata tctgagcttg acacctgacc cactcacttg ggcactgtgt aagttgtggg 3600
gacctccttc ttggttggcc ctacactaac cagcccctcc aggggcccct ttccttggga 3660
agccacctaa cccaggtagt gtggtcatcc ttgtcccctc cactgacctc actgagctac 3720
aaacctgggt gctggactct gccttgaggg gcatgaagtt ggggtgtccc aagggaggag 3780
gagatgcagg actgctctca tagagctctc agactgtagg gaagacctgc ccctgcgtct 3840
cgtagcactt gaggagagga gtaggtaagt tcgtagctga gaggctggtt aactgagtag 3900
gtagctgcag gggtgagagg tatggagggg aggggctaag gttttggttg ggggagcctg 3960
gtccctgaga cccctgttag cccactgata accttcttca gccttcactc ttctgcttgc 4020
ctgggctggg ggcagggggc tggcatcagc ggccaggcct gagtatgtgc tgtcgtgcca 4080
gggaacgttc tggggctagc catcttctcc agatggagga gcatgtctgt cctcggacca 4140
ctccagactc caacctcagc ggacattcct ggggtggcag gcagggagga gaagtcctgg 4200
gaggcccctt cctaacagca gctgatggca gacttggcac tgcacgctgt ctgcctgttc 4260
ctttgcccac ttgttgagct gcatggtgag ccgtgggctt ccctggtgtc aggtttgagc 4320
tctgccatgg ctcccacctc gcaaatgcag ccaactcaac tcttctggca tggggacaat 4380
gttggataag acctggcctt gtccttaaat aggaggctct gggccatcaa gggcaggggt 4440
tggggggatg gtggtcgacc agtcactctg atctaagtca gacagcagga aggaagtgag 4500
aagccttcaa cattagcaca gctggggctg ggggaggtgg gaagagggac attcctcctg 4560
cttggggtct actggattct ccctgcccca aggctgggga caagggagct catggcaggg 4620
cagctaccct agtggcatct gggaccccag agaggcagag cttctctgca ccgggcaatg 4680
aggatttcca gatgtcggag tggagggcag gcaggaagga aggttaggag agcctgcgtg 4740
gggtttgggc catcaggggc cctgccttgg cttttgttcc tctgttctgt gcatctctta 4800
ccaccgtctt cattccccct gtgtcttttc cttaccttgg agctctgttc tctctgatct 4860

```
gtgatattga gtttgtctgc ctcttacctg ttctaagagg ctagaggaga cctagacttc 4920
tgggttcaca tttgtccccg ccctaccccg ttacccttct cccactcctg aggaagggtc 4980
ctggttagac ttggaccaag tagggtctcc atcttctctc ctgctcctga ttctcatgaa 5040
gtcccattgc ccctgggatg gaggcaaggg tctgttctca cagctggggt ggtgccagtg 5100
ctgggtacac acctgtcctc ttcccctttt cttcacccct ctgccttagg tgttcctgcc 5160
caaataccga ggggacactg gaggtgctag cagtgaggac agcctgatga ccagcttcct 5220
gccaggccct aagcctggag ctcccttccc taatggacac gtgggtgctg gaggcagtgg 5280
cctgctccca cctccacccg cgctctgcgg ggcctctgcc tgtgatgtct ccgtacgtgt 5340
ggtggtgggt gagcccaccg aggccagggt ggttccgggc cggggcatct gcctggacct 5400
cgccatcctg gatagtgcct tcctgctgtc ccaggtggcc ccatccctgt ttatgggctc 5460
cattgtccag ctcagccagt ctgtcactgc ctatatggtg tctgccgcag gcctgggtct 5520
ggtcgccatt tactttgcta cacaggtagt atttgacaag agcgacttgg ccaaatactc 5580
agcgtagaaa acttccagca cattggggtg gagggcctgc ctcactgggt cccagctccc 5640
cgctcctgtt agccccatgg ggctgccggg ctggccgcca gtttctgttg ctgccaaagt 5700
aatgtggctc tctgctgcca ccctgtgctg ctgaggtgcg tagctgcaca gctgggggct 5760
ggggcgtccc tctcctctct ccccagtctc tagggctgcc tgactggagg ccttccaagg 5820
gggtttcagt ctggacttat acagggaggc cagaagggct ccatgcactg gaatgcgggg 5880
actctgcagg tggattaccc aggctcaggg ttaacagcta gcctcctagt tgagacacac 5940
ctagagaagg gtttttggga gctgaataaa ctcagtcacc tggtttccca tctctaagcc 6000
ccttaacctg cagcttcgtt taatgtagct cttgcatggg agtttctagg atgaaacact 6060
cctccatggg atttgaacat atgaaagtta tttgtagggg aagagtcctg aggggcaaca 6120
cacaagaacc aggtcccctc agcccacagc actgtctttt tgctgatcca cccccctctt 6180
accttttatc aggatgtggc ctgttggtcc ttctgttgcc atcacagaga cacaggcatt 6240
taaatattta acttatttat ttaacaaagt agaagggaat ccattgctag ctttctgtg 6300
ttggtgtcta atatttgggt agggtggggg atccccaaca atcaggtccc ctgagatagc 6360
tggtcattgg gctgatcatt gccagaatct tcttctcctg ggtctggcc ccccaaaatg 6420
cctaacccag gaccttggaa attctactca tcccaaatga taattccaaa tgctgttacc 6480
caaggttagg gtgttgaagg aaggtagagg gtggggcttc aggtctcaac ggcttcccta 6540
accacccctc ttctcttggc ccagcctggt tccccccact tccactcccc tctactctct 6600
ctaggactgg gctgatgaag gcactgccca aaatttcccc tacccccaac tttcccctac 6660
ccccaacttt ccccaccagc tccacaaccc tgtttggagc tactgcagga ccagaagcac 6720
aaagtgcggt ttcccaagcc tttgtccatc tcagccccca gagtatatct gtgcttgggg 6780
aatctcacac agaaactcag gagcaccccc tgcctgagct aagggaggtc ttatctctca 6840
gggggggttt aagtgccgtt tgcaataatg tcgtcttatt tatttagcgg ggtgaatatt 6900
ttatactgta agtgagcaat cagagtataa tgtttatggt gacaaaatta aaggctttct 6960
tatatgttta aaaaaa 6976
```

<210> 706
<211> 123
<212> PRT
<213> Homo sapiens

<400> 706

```
Met Gly Ser Leu Gly Leu Phe Leu Gln Cys Ala Ile Ser Leu Val Phe
                5                   10                  15
Ser Leu Val Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg Ala Val
            20                  25                  30
Tyr Leu Ala Ser Val Ala Ala Phe Pro Val Ala Ala Gly Ala Thr Cys
        35                  40                  45
Leu Ser His Ser Val Ala Val Val Thr Ala Ser Ala Ala Leu Thr Gly
    50                  55                  60
Phe Thr Phe Ser Ala Leu Gln Ile Leu Pro Tyr Thr Leu Ala Ser Leu
65                  70                  75                  80
Tyr His Arg Glu Lys Gln Val Leu Ile Gly Gln Trp Val Glu Ser Gly
                85                  90                  95
Trp Glu Gly Trp Ser Gly Phe Leu Gly Gly Gln Leu Ala Gln Asn Leu
            100                 105                 110
```

Val Ser Gly Lys Gln Leu Trp Arg Met Leu Leu
115 120

<210> 707
<211> 150
<212> PRT
<213> Homo sapiens

<400> 707
Met Val Gln Arg Leu Trp Val Ser Arg Leu Leu Arg His Arg Lys Ala
5 10 15
Gln Leu Leu Leu Val Asn Leu Leu Thr Phe Gly Leu Glu Val Cys Leu
20 25 30
Ala Ala Gly Ile Thr Tyr Val Pro Pro Leu Leu Leu Glu Val Gly Val
35 40 45
Glu Glu Lys Phe Met Thr Met Val Leu Gly Glu Ser Leu His Pro Pro
50 55 60
Ser Phe Leu Phe Gln Ile His Ala Thr Trp His Val Gly Gln Glu Tyr
65 70 75 80
Leu Cys Pro Gly Ser Cys Leu Glu Gly Glu Val Val Cys Trp Glu Gly
85 90 95
Ile Ala Gly Gln Glu Gly Asp Pro Gly Leu Arg Gly His Thr Lys Arg
100 105 110
Lys Lys Arg Ile Pro Arg Thr Tyr Pro Ser His Leu Trp Ile Pro Gly
115 120 125
Pro Ala Gln Ser Leu Ala His Arg Arg His Trp Arg Asn Ala Pro Asn
130 135 140
Leu Trp Leu Ala Leu Leu
145 150

<210> 708
<211> 371
<212> PRT
<213> Homo sapiens

<400> 708
Met Leu Phe Pro Ser Phe Ser Arg Ser Leu Val Pro Leu Pro Leu Ala
5 10 15
Leu Tyr Leu Ser Gln Pro Leu Thr His Thr Thr Ser Leu Leu Ala Gly
20 25 30
Ile Gly Pro Val Leu Gly Leu Val Cys Val Pro Leu Leu Gly Ser Ala
35 40 45
Ser Asp His Trp Arg Gly Arg Tyr Gly Arg Arg Arg Pro Phe Ile Trp
50 55 60
Ala Leu Ser Leu Gly Ile Leu Leu Ser Leu Phe Leu Ile Pro Arg Ala
65 70 75 80
Gly Trp Leu Ala Gly Leu Leu Cys Pro Asp Pro Arg Pro Leu Glu Leu
85 90 95
Ala Leu Leu Ile Leu Gly Val Gly Leu Leu Asp Phe Cys Gly Gln Val
100 105 110
Cys Phe Thr Pro Leu Glu Ala Leu Leu Ser Asp Leu Phe Arg Asp Pro
115 120 125
Asp His Cys Arg Gln Ala Tyr Ser Val Tyr Ala Phe Met Ile Ser Leu
130 135 140
Gly Gly Cys Leu Gly Tyr Leu Leu Pro Ala Ile Asp Trp Asp Thr Ser
145 150 155 160
Ala Leu Ala Pro Tyr Leu Gly Thr Gln Glu Glu Cys Leu Phe Gly Leu
165 170 175

```
Leu Thr Leu Ile Phe Leu Thr Cys Val Ala Ala Thr Leu Leu Val Ala
            180                 185                 190
Glu Glu Ala Ala Leu Gly Pro Thr Glu Pro Ala Glu Gly Leu Ser Ala
        195                 200                 205
Pro Ser Leu Ser Pro His Cys Cys Pro Cys Arg Ala Arg Leu Ala Phe
    210                 215                 220
Arg Asn Leu Gly Ala Leu Leu Pro Arg Leu His Gln Leu Cys Cys Arg
225                 230                 235                 240
Met Pro Arg Thr Leu Arg Arg Leu Phe Val Ala Glu Leu Cys Ser Trp
                245                 250                 255
Met Ala Leu Met Thr Phe Thr Leu Phe Tyr Thr Asp Phe Val Gly Glu
            260                 265                 270
Gly Leu Tyr Gln Gly Val Pro Arg Ala Glu Pro Gly Thr Glu Ala Arg
        275                 280                 285
Arg His Tyr Asp Glu Gly Lys Ala Leu Ala Ala Ser Arg Gly Trp Cys
    290                 295                 300
Gly Ser Arg Pro Pro Glu Thr Thr Leu Gly Ala Val Ser Gly Leu Val
305                 310                 315                 320
Pro Leu His Pro Gly Pro Asp Phe Ser Val Arg Lys Val Gly Met Asp
                325                 330                 335
Pro Ile Cys Ile His Gly Phe Ser Trp Val Trp Asn Ile Ser Ala Cys
            340                 345                 350
Gly Phe Arg Lys Ala Ser Gly Cys Ser Arg Ser Leu Ile Arg Val Val
        355                 360                 365
Ala Pro Val
    370
```

<210> 709
<211> 141
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(141)
<223> n=A,T,C or G

<400> 709
tacggcgtgg tgcggagggc ggtaccccac aaataacacn nacaccccat cctatctgtg 60
tccacanata aantgactca ttcctctcct cgcatanccc actntcccct ngcgataccg 120
taacnaancc cttccccctt t 141

<210> 710
<211> 196
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(196)
<223> n=A,T,C or G

<400> 710
cnatccttcn cntacaccca tgangtccat gtcgcacgtc cacctcccct caaaacttgg 60
gtccncatcc acccgtcact ctccccntaa ncnataaccc cttttngcga atagacccca 120
ccttancaat nggtttttcn ttttttgtcc ctnggnccgn gcgattcaan aaattgaagg 180
cccanaaaaa cccccct 196

<210> 711
<211> 177
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(177)
<223> n=A,T,C or G

<400> 711
ntacntcnct ccnaatgaaa ttcgaanctc ggttacccgg gggnattccg attaggngcg 60
tantctcgga tgtgcagtca caagtctttt gctaatnctt ataattntcn ctaccctttc 120
ttcnacaata ctgctatcct anttnttctn tcncctctct cccannttac taaccac 177

<210> 712
<211> 185
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(185)
<223> n=A,T,C or G

<400> 712
aaacgnacca nngccaacga tangtgttgg ngttggttgc ggttgttcct cttatntgca 60
ctggttgtcc gtgtcgcacg ganggccacg tccctctgnc ntgagtanca catagcatcc 120
acgtttagtc gactntnccg ggcggccgct ctacccntnt atngattctt attaaaantc 180
ggatc 185

<210> 713
<211> 172
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(172)
<223> n=A,T,C or G

<400> 713
nntggtcgcc tgngcgtnta ctctaaagga tntactatnc atatggantc naanacgact 60
cactacacgg cnctctncgg agccnnggtc agtgcctnct nggagacctt ctctggggca 120
ggangagcac tnggtatgtt cacgtatcnc ttcntaaana tacnnccctc cg 172

<210> 714
<211> 112
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(714)
<223> n=A,T,C or G

<400> 714
nttgcgtgcc tggacgtnta ctctgcanga tctactactc atgngaattc taantacgga 60

ctcactatnc ggcancgcag gcgcagcagg gaangggtca cctcccagtc tc 112

<210> 715
<211> 326
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(326)
<223> n=A,T,C or G

<400> 715
tactctanag gatctncgng tcatntggat tctatntcga ctcactctag ggctcnagcn 60
gtcngccggg caagttattc ggatcgtcgg gntccgagct tcgcaattaa ntgtgccatc 120
gttctncaac gttcctgact nggaancccc ngcngttcng atccncnggt acctagctcc 180
anntcccccg tnctccttct ggngtntcat naangaggac cnccctcgat cnccccttcct 240
taatctgcnc acnctgaacg nccaatggac atngtgcgtt taatntanna ggcccgnttc 300
gngtgccctt cccgtnannt cagctc 326

<210> 716
<211> 122
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(122)
<223> n=A,T,C or G

<400> 716
nntgcgtcgc ctgngcgtnt actctagatg atctgantag tcatatggat tctaatacga 60
ctcannatag ggctctagcg nggatncnga ttcgtcntcc ngattcantg acnccggtan 120
ca 122

<210> 717
<211> 203
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(203)
<223> n=A,T,C or G

<400> 717
cntgcatgcc tgcaggtcga ctctagagga tctactagtc atatggatcg agcggccgcc 60
cgggcaggtg tnaatgataa anatgcatca tactanccta cagaanggag agataatgtt 120
ngntggacca ngttggtttt cttgcgtgtg tgtggcagta gtaagttatt agtttttana 180
atcantaccg ccctccgcac cac 203

<210> 718
<211> 168
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature

<222> (1)...(168)
<223> n=A,T,C or G

<400> 718
ggcagganga tcncttgagc cccngaggtc gaggctacag tgagccanga gtgcactact 60
gtnncgccct ccgcatncac gngtggtccg atccccgggt accganctng anttcactgg 120
anttcttttt aancgtnttg antggtacna ccctcgantc cctggctg 168

<210> 719
<211> 210
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(210)
<223> n=A,T,C or G

<400> 719
cancgtcgnc ataacacgta ttttntgatn aagattctna ctgacccatn aantctacnt 60
ctcaagctct tncanngtcc agtnaangga atgtgtatnn gtngggatnc cacanaaaaa 120
aganatntcg gncgcttcat tantcatcct tcttacccan ntctctngat ncncagtntg 180
ancntgaacg cacactacng gatntctcca 210

<210> 720
<211> 131
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(131)
<223> n=A,T,C or G

<400> 720
tccatcctaa tacgactcac tatagggctg ccaacctgcc atccactact gaggaagacc 60
cgnanactta ggggctcact gcgagccacc ggccacaggt cgtatagggc aaagcacgng 120
gaagcacccc t 131

<210> 721
<211> 121
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(121)
<223> n=A,T,C or G

<400> 721
tccatcctaa tacgactcac tatagggccg ntgantnctg gcgaaaggct tacaattaag 60
naggaaaaan ganccaacaa ctaaaaaaaa nncggncgtg ncagcttnga tgactngtcc 120
a 121

<210> 722
<211> 246
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(246)
<223> n=A,T,C or G

<400> 722
anctggagtc gcgcgctgca gtcacattgt ggatccanaa aatcggcaca agctctcntg 60
gnttcntcga tatgaanaac actaatccca tgtngtntgn gtctccgtga ttcatccctc 120
gcacnggtcc ccntccnaac cnttgcatag gtgttatgtt gtantctccc cagtgcacaa 180
agattnacac tctctcantg tctganatat gcacgagttc attgtcctgt cnccgtnaac 240
atcaag 246

<210> 723
<211> 160
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(160)
<223> n=A,T,C or G

<400> 723
cctccggaaa atccaantag agtaantncn ctctaatccg gggnaattgg nggggtnnat 60
acgtcctcct ccccccagnt aggattnana aaaggnctcc cagancaaaa nctccaaagt 120
gnatcnanta gccgtncccg anatncaacg cccctacgtc 160

<210> 724
<211> 156
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(156)
<223> n=A,T,C or G

<400> 724
tnanccnata tacaccaaat tctgattcta aantcccacc caagggaaaa aagttgagaa 60
gagcctttcc acttttctac taataaaaaa atgcaccagc ccctaccann agtgnggaaa 120
acctccttag gcccttgnnt ggaacaancg aaaatc 156

<210> 725
<211> 347
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(347)
<223> n=A,T,C or G

<400> 725
aganggttnt atncatgctg tactcgcgcg cctgcagtcg acactagtgg atccaaagaa 60
ttcggcacga gagacggtgc gcgatggacc gagggcccca gccggngagg cgccgccgcc 120
gagcccgcgg ncagacgccc catcagtagc gtccgcaccg ggnagccgcg gntctcgccc 180
gagccgtggg cgcgcccgag gggcgggctc gcctcccgcc gtccctcgca gctctgccgg 240

gcccgagccc gcgccgtcgc cgccgccgnc ttgccgctcg gnccgcgcgg nccggnaaac 300
gcggtcgagg tctggatgng gcanngcccg cncctntcgc tgagcct 347

<210> 726
<211> 162
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(162)
<223> n=A,T,C or G

<400> 726
ttgggtgggt tgggtggggg naaatttncc catttgggtg ggtttggggg ggnaaatact 60
tcccgccttt tnggtnccca aaganacnaa gggggagtcc cttnatagag gnagngcgat 120
ncntcncaac nacntngact ttgnccatgg ggagnaaggt gg 162

<210> 727
<211> 120
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(120)
<223> n=A,T,C or G

<400> 727
gtgtgggtgg ggaattccat tgtggttggg ggnaaatctc cgcttgtcca aagnacaggg 60
ggggtcnctt anagngnagg gggttcctcc ccaccacttg ncttgnccat tgngagnaag 120

<210> 728
<211> 130
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(130)
<223> n=A,T,C or G

<400> 728
gacccactgc agcgttnaac ttagcttgga ccgagctcgg atccctagtc cgtgtggtgg 60
aattccatgt gtcgagagag gggcaaatac nctccaanac ancnccctca tgctcnacac 120
atattcgcat 130

<210> 729
<211> 182
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(182)
<223> n=A,T,C or G

<400> 729

cngactgctn gcgtttaaac ttaagcnagg taccgaacgg ggatnnacga ctantgatcg 60
gctggctgct tccagtcgat tanatttgtg aaaaagctga accncngccn gttaaggggg 120
annatgcaaa anatncatcc nnctgccccn taaactgntc tntccnaggg aaaaaangga 180
ag 182

<210> 730
<211> 678
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(678)
<223> n=A,T,C or G

<400> 730
cactcncact ccggacctag gcncttcacc actgctctct tcctcctcct cctcctcntc 60
ctcggggctg ggggaccttc cccagtgacc atctcacttt ggctgaancc cactcggggc 120
agcctgagtt tggggctctt ggccttctca ccctcctcgg ccccctcctt ggcccgcacc 180
aggccaaacc ggggcagccg taccttgagc ttgtgtccgg cctctccctc cccctctgcc 240
acctggtact cggcatggtt gcccccggga tggcgagagc tccacgtcgg gcagtgagaa 300
gcagaaagta cgctcggccc ctgggggctg ctcctcagca ccctcgcccc ccaccctagc 360
tctggccccc agtgtgggca acttcagcct cagcccaccc tcgcctgtgg ccgcctcgcc 420
cgcctgtgcc tctcggctta gccccacgtc caactcaagc tggggcactg tcacggtggg 480
catcttaaag acaccctcac ccaccagcag ctcaccacct gcaacctggg ctccaggcaa 540
aaaaagggtc acctggggca nctgaaccct gtacctgctg tgccctctgc tgaanggaat 600
gttatctgaa cctgctgccc tgggggtact gccttcccaa aaccgggtca antccacctg 660
ttggaaggna aatncccc 678

<210> 731
<211> 135
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(135)
<223> n=A,T,C or G

<400> 731
gagatccgac gtcacccccct tccggcggcc caagacgctg caactcccga ggcngcccaa 60
atatctttgg aagagcgctc ccagcccaac acaatggaat tccaccacac tggnntagtg 120
gatccgagct aagcc 135

<210> 732
<211> 660
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(660)
<223> n=A,T,C or G

<400> 732
gcttggtacc gagctnggat ccctagtaac ggccgccagt gtgctggaat tcggctttct 60
tcaatcagnt nacgagctgc atggtctgct aacattgtca taattgctgg catagattac 120
tgaaaataaa gaaaaaaaat tgaagctgcc tatcaagttt tggtattatc aaaaacttcc 180

tacaagttat tttacttcaa ccatgttatt acaaatattt taatgaatac tttagagact 240
ttaattacaa aaaactgaga tagtaaaagc aagtaataaa agctgaaatt acttagctat 300
ttgataatta cataaattat tatggtccat tcaacttttc tagtgtttag tttatacacc 360
aggaagactt tcctattcta ctaacattta taaagtatgc taacctatta tttaaacgca 420
tccactatta ggattttatg gcctaaaacg tgatacagtt cagtatcttg atgtcaaaac 480
tttttaagca agtagggatt aagttcaagt gaatgtgatt ttctttcttc ccagtagggt 540
cttctgaata actcagnaaa gctcacttcc attatcttac tttataaaaa aatgctataa 600
gacagaatgg gccgacgtgg nggctccacc tgtatccacc tttggaggcg agnggcgaat 660

<210> 733
<211> 836
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(836)
<223> n=A,T,C or G

<400> 733
aattaatgac ttttttcccg ccctgccaag ctagtttgtc taaatataat gtaaagaaat 60
tagctactca ttttctggtc cacgaaggtt cctaaaatgg gaagaagtgg agatctgacc 120
ttgttagttc taaatacact aaactgggag tgccatggat ggctttcagg atgtcctgaa 180
tcctctataa ttgtatacaa aatcgtgagt tttaaaaac tgggttagag ctattggttc 240
ctcagagtct caggcatctt agaccccaa aaaggttaag gactactgac ttaaccaatt 300
aggtttgagt ggcattggct ttgaagaaaa gcagaggaaa gatatatttt ataattctgg 360
gcaacaaaaa agtggatgtg tgccagcatc ttagagtaga atcctcttaa aaggatagca 420
ctgcatatga actagtaggt tttaaccagt gcatatttag gcgaagtagc tcatttttct 480
gttagaattc ttttttattt gggaatgggc aagcttttac agcttttacc ttgccaatga 540
atacctggaa tttaaaaaat cttgttaggc atattgccca taaagttttt tttcctagat 600
catatattca gtaaatatgt ttgtagcttt atttcaatcc cccaattcat tgagggttga 660
aacaatttga atggtttgag tgtagaagct aagttatttc tgtagaggct aagggcattt 720
ataccaanat atgttagact tgnggntcct gttaaccatg ctgtanacaa taggaattac 780
tgtatatcca cattttaatt ttaacatctt ctgctttgnt gntggtttga gangga 836

<210> 734
<211> 694
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(694)
<223> n=A,T,C or G

<400> 734
nagtnctatt tncactaaac tgngagtgcc ttggatggct ttcaggatgt cctgaatcct 60
ctataattgt atacaaaatc gtgagttttt aaaaactggg ttagagctat tggttcctca 120
gagtctcagg catcttagac cccaaaaag gttaaggact actgacttaa ccaattaggt 180
ttgagtggca ttggctttga agaaaagcag aggaaagata tattttataa ttctgggcaa 240
caaaaaagtg gatgtgtgcc agcatcttag agtagaatcc tcttaaaagg atagcactgc 300
atatgaacta gtaggtttta accagtgcat atttaggcga agtagctcat ttttctgtta 360
gaattctttt ttatttggga atgggcaagc ttttacagct tttaccttgc caatgaatac 420
ctggaattta aaaaatcttg ttaggcatat tgcccataaa gttttttttc ctagatcata 480
tattcagtaa atatgtttgt agctttattt caatccccca attcattgag ggttgaaaca 540
atttgaatgg tttgagtgta gaagctaagt tatttctgta gaggctaagg gcatttatac 600
caagatatgt tagacttgtg gttcctgtta accattgctg tagacaatag gaattactgt 660
atatccacat tttaattttt aacatcattc tgtc 694

<210> 735
<211> 126
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(126)
<223> n=A,T,C or G

<400> 735
ncnttgaaac nggttgacca gacttcaggc ctgtgcgctc aatcgtggag aatctcgtgc 60
cgaattcggc acgagtctct ctctctctct ctctctctct ctctctctct ntctctctct 120
ctctct 126

<210> 736
<211> 165
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(165)
<223> n=A,T,C or G

<400> 736
cagaagcctt taaaccggtt ngaccagact tcaggcctgt gcgctcaatc gtggagaatc 60
tcgtgccgaa ttcggcacga gtctctctct ctctctctct ctctctctct ctctctctct 120
ctctctctct ctctctctct ctctctctct ctctctctct ctctc 165

<210> 737
<211> 125
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(125)
<223> n=A,T,C or G

<400> 737
ggnagcccct ttaaccgttt gtccagactt caggcctgtg cgctcaatcg tggagaatct 60
cgtgccgaat tcggcacgag tctctctctc tctctctctc tctctctctc tctctntctc 120
tctct 125

<210> 738
<211> 137
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(137)
<223> n=A,T,C or G

<400> 738

ggagncnctt gancaggatg accgacttca ggcctgtgcg ctcaatcgtg gagaatctcg 60
tgccgaattc ggcacgagtc tctctctctc tctctctctc tctctctctc tctctctctc 120
tctctctctc tctctct 137

<210> 739
<211> 970
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(970)
<223> n=A,T,C or G

<400> 739
aggcctattt aggtgacact atagaacaag tttgtacaaa aaagcaggct ggtaccggtc 60
cggaattcgc ggccgcgtcg acggcccttn gtgccactag ntctttcatt cttccccccc 120
atcaatcagt gaacttttta gcctactcaa agctttgctc caatgcatag gatttatgat 180
tgtggggatt tccagataat ataaatattc aacatgaata ttttaaatta aggcatgaga 240
catttttcct aactgagcat agccatgaac ctctcacgtc tgttcctctg tgtcagtttg 300
tancactgaa tacagcagcc ctcctaaaag tccaggcagt gcacaggtct tgacatgatg 360
aagtgacgtg ttgctatggt gattttgcag ctggccaaat agtcactggt tgattttacc 420
cagcaggaga tttttgcaaa aatttcctgg gtgagagtga aatcaaactc ctattttgnt 480
tctcctctgc aagctgnagt taagatggat taatgagtac ttttagatta attaactctg 540
aagagaaaat gggagaaaag tgaggaaggt tgttggcaga agtcattgct ggaatccttc 600
tgaagggagt actgacttca cttgcaaaga cnagagacta naagacaatg aagttaaact 660
tggcctgtct ctcatatgat agatgctgag agtcaggntc agggaaattt aattctgtca 720
tacgcatatn ggattatgtg gtcatggatt tgttggcact aaccngcctn taatcagnat 780
aagaaaagtg ttttggtaga naaagaaaat tatggcccag aaaaacctgg aanacttgga 840
aaaaatgntn gggggccttg ggtggtggtc tnaaaanacc ccctggggat ntttaaacca 900
aaantgaaga agggaaaaat ntttccccnt ntttttnttt tttgcccccct tgggattggn 960
ttttntttcc 970

<210> 740
<211> 739
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(739)
<223> n=A,T,C or G

<400> 740
gntgtcnaaa aagcaggctg gtaccggtcc ggaattcgcg gccgcgtcga cggcccttgg 60
tgccactagt tctttcattc ttccccncca tcaatcagtg aacttttttag cctactcaaa 120
gctttgctcc aatgcatagg atttatgatt gtggggattt ccagataata taaatattca 180
acatgaatat tttaaattaa ggcatgagac atttttccta actgagcata gccatgaacc 240
tctcacgtct gttcctctgt gncagtttgt agcactgaat acagcagccc tcctaaaagt 300
ccaggcagtg cacaggtctt gacatgatga agtgacgtgt tgctatggtg attttgcagc 360
tggccaaata gtcactggtt gattttaccc agcaggagat ttttgcaaaa atttcctggg 420
tgagagtgaa atcaaactcc tattttgttt ctcctctgca agctgnagtt aanatggatt 480
aatgagtact tttagattaa ttaactctga agagaaaatg ggagaaaagn gaggaaggtt 540
gttggcagaa gtcattgctg gaatccttct gaagggagta ctgacttcac ttgcaaagac 600
aagagactan aagacaatga agttaaactt ggcctgtctn tcatatgata gatgcttgag 660
agtacaggnt cagggaaatt ttaattctgn catacgcata ttggattatg tgggtcatgg 720
ctttgtttgg cncctaacc 739

<210> 741
<211> 1171
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(1171)
<223> n=A,T,C or G

<400> 741
gccttgnggt gacactatag aacatgtttg tacaaaaaag caggctggta ccggtccgga 60
attcgcggcc gcgtcgacgg cccttnntgc cactagttct ttcattcttc ccccccatca 120
atcagtgaac tttttagcct actcaaagct ttgctccaat gcataggatt tatgattgtg 180
gggatttcca gataatataa atattcaaca tgaatatttt aaattaaggc atgagacatt 240
tttcctaact gagcatagcc atgaacctct cacgtctgtt cctctgtgtc agtttgtagc 300
actgaataca gcagccctcc taaaagtcca ggcagtgcac aggtcttgac atgatgaagt 360
gacgtgttgc tatggtgatt ttgcagctgg ccaaatagtc actggttgat tttacccagc 420
aggagatttt tgcaaaaatt tcctgggtga gagtgaaatc aaactcctat tttgtttctc 480
ctctgcaagc tgtagttaag aagggattaa tggagtactt tttaagaatt aaattaacct 540
cttgaaagaa gaaaaaatgg gggaagaaaa aaagtggaag ggaaaagggn ttggttttgg 600
gccnaaaaaa aagttccaan tttnggcntt ggggaaaaat tccccntttt ccttggnaaa 660
aggggggnaa ggttaancct tgggaacctt tttccnncct tttnggccca aaaggggaac 720
ccanggggaa agaaccttta ggnaaaggaa acccatttgg gaanggtttt naaaaccntt 780
ngggcccccg ggccctcctc caanaaggga aaaaaaaagg cctggaaaan gtaccagggt 840
ttcangggna aaanttaaaa ttcttggcca atancnccat aattgggaat tatggggggg 900
ccatgggctt ttggtttggg cncttaaccc cgcnttttaa attcaaanna aaaaaaagng 960
gtttggaaaa nnaaanaaaa aaaattnaan ggncccnaaa aaaaaccctg gaaaaccttt 1020
ggaaaaaaat tngnnggggg gccntttggt tgggggggtt tnaaaaaacc ccctnggggg 1080
ttttttaagc ccaaaagggg gggaggggna aaanggtncc cttnttttt ttttnngccc 1140
cccttgggga atggnttant tcanggggcc c 1171

<210> 742
<211> 739
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(739)
<223> n=A,T,C or G

<400> 742
gntgtcnaaa aagcaggctg gtaccggtcc ggaattcgcg gccgcgtcga cggcccttgg 60
tgccactagt tctttcattc ttccccncca tcaatcagtg aactttttag cctactcaaa 120
gctttgctcc aatgcatagg atttatgatt gtggggattt ccagataata taaatattca 180
acatgaatat tttaaattaa ggcatgagac atttttccta actgagcata gccatgaacc 240
tctcacgtct gttcctctgt gncagtttgt agcactgaat acagcagccc tcctaaaagt 300
ccaggcagtg cacaggtctt gacatgatga agtgacgtgt tgctatggtg attttgcagc 360
tggccaaata gtcactggtt gattttaccc agcaggagat ttttgcaaaa atttcctggg 420
tgagagtgaa atcaaactcc tattttgttt ctcctctgca agctgnagtt aanatggatt 480
aatgagtact tttagattaa ttaactctga agagaaaatg ggagaaaagn gaggaaggtt 540
gttggcagaa gtcattgctg gaatccttct gaagggagta ctgacttcac ttgcaaagac 600
aagagactan aagacaatga agttaaactt ggcctgtctn tcatatgata gatgcttgag 660
agtacaggnt cagggaaatt ttaattctgn catacgcata ttggattatg tgggtcatgg 720
ctttgtttgg cncctaacc 739

<210> 743
<211> 610
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(610)
<223> n=A,T,C or G

<400> 743
ctgtccttat ttctttagca aaaatttccc aagagaagaa ttgctgggat aatgcacatt 60
taaatttttg atagacattc ccaaatatta tacctgtttt tgagaccttt aattcctgtt 120
gtcaaattgc cctatatatg gagtaataaa cacgatttaa agaaatgagg actaaaaaaa 180
gattatatat aacccaacat aaaggcaacc tcttaggcgt tgacagaaac tgacaacttt 240
ttatctgtgg gtgcgatcca ttataagtaa cctgagcacc ttattttttc tttttaaact 300
ctaggtagga tacccgaggt ccacaaattt ttcataagaa atatttttttc tctgccctat 360
gagattttaa aaaatattat actgcttcaa ttgcatcaaa agaaatggac cctaatatct 420
atgatgaagg atttggagtt agaagacctg agtttcaatt ttggcatggc tgtttgtcta 480
gctctgngat cttggacagg tcaattgact tggcttaatc ttctcatcca tttagnggag 540
acagcaccac tattcacagg actattgncn gaattaccag acaatagcat aggngaaaat 600
ataangcctt 610

<210> 744
<211> 127
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(127)
<223> n=A,T,C or G

<400> 744
ttnacctccc tggaccgggc ccccttccc cgggcggntc ccccgggctg caggaattct 60
gcacgaggga gagagagttn gagagagaga gagagagaga gagagagaga gagananaga 120
gagagag 127

<210> 745
<211> 458
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(458)
<223> n=A,T,C or G

<400> 745
gatatcccgg gattcgcggc cgcgtcgacg tggcctctag tttgtcctgg tccaaagcag 60
ggaagctggg ctacgtcctg cccaggtcag ccttaggtta agggctgcct gggggaggga 120
acttcctggg ccttcgggtc tctgtgcact ggggtggctc ctgtggccca gaatgccctg 180
gagaagggtc ctactggaag cgaaggtgca gggcagcagg gcctgaggcg caggagctgg 240
tggaggctcc cagcacaggt cgccgcccca gtcacatcac tgctgatggt gggggactt 300
ggggagtttc ccccgagaat gggaggtctc acagtccccg tgctgcaatg ctgtcggtgc 360
actgngncng caatgtgctc atggncactt gctttttctc tgtggccccg gccgatttat 420
ccagcanngc acccctcttc tnctctccgg anaaagcc 458

<210> 746
<211> 893
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(893)
<223> n=A,T,C or G

<400> 746
aagcaggctg gtaccggtcc ggaattcgcg gccgcgtcga cgtggggagt tagctctctg 60
gaccccgtca tagagtaagt catcgataga gcatttgctt gatggggact tccagaaggc 120
canngaaagt cctgccgact tcctggggaa gcccatccgc acgtggggtg agggtcccca 180
natggaagca gctgtgtatg caggggagggg gcagaggctg ctgccaatgg gcatgtccct 240
tacctgaaag ggccacctct ccaggtgaca tgtcctgggg gagccggggc cgtctgctcc 300
ggccagaggc gctcagctca ggccacacca ggcagggcac ctcccaacct ggacaggtgg 360
ggaccaaggt ggccttggac aaaactctct gtgtttgcca agcacccaat cggacacaga 420
gagtcaacca caccccagtc acatggtgtc cacacngcag ggtcaagga ggcccggccc 480
ctccccctca gacgtccctg ggcctctggg agtcagcaag gacgaggacg gcattgccct 540
tcgagacagg aagggagtga cctcctcccg gcggcatcca ggctcngctt ctccggagag 600
gagaggggc tacttgctgg ataaancggc cggggccaca gagaaaaagc aaggtgacca 660
tgagcacctt gcaaacacag tgcacccacc agcatttnag caccngggac tgtgaagacc 720
tcccatttct tcgggggaa acncgcccaa ngttcccccc accntcacta gtgnattgtg 780
acctggggn cgggccgacc cctgtngctt gggnnagccc tccncccagg tttctnnggc 840
ngcccnttaa nggnccctng nttggcccct tggccncctt tncgcttttc cca 893

<210> 747
<211> 738
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(738)
<223> n=A,T,C or G

<400> 747
gatatcccgg gaattcgcgg ccgcgtcnac gaagcacaga cctgngccct gctctcatgg 60
ggcagactgc catttgtcat tnattactga aggaaaggga tcctcagttt gcttgtggac 120
atttcaaatt tgaggtgaga gttggataag taagaataaa gctgctcttc aaagagatga 180
atatagaaaa agaaacaaga tacagncttg gcagtaaggc tgggaggaag gggaaaaggt 240
aataaagaat gaaagagtga gaaatgtgag caggagctga acacagaaaa gttcagngac 300
agaagcanaa ggagggaaga agggaggagg gtccctttca cagaggctca cgaggatgct 360
ttatgngtgc catgcagtcc atgttcagga tgtctgcttc ttanctctct acttttctaa 420
tanaaatttg gatacttact gatcctacat atgtaacagg gagagaaggt gaatttcaaa 480
gcantaaatt gaaaaattgt tcacaatttc atttttttaaa aaaagggagc taacagaaga 540
agaggttaat gtggtaatta taggatgnct cttgcgacac atgaatgnat ctggtatcat 600
ctgagtggga ggggagctgt cttcctgacc caaaaggatc ctttcgttan ccngnactta 660
ngtcccaaaa cctcaccacc ttggagaaat natttccttt tgggggtntc attaaanccт 720
tttggncccc gcaaaagc 738

<210> 748
<211> 647
<212> DNA
<213> Homo sapiens

<220>

<221> misc_feature
<222> (1)...(647)
<223> n=A,T,C or G

<400> 748
ctntgtggcg gtggctgtct catttgggtg gactttttgg gtcgtaggaa cctggtatng 60
aggtcgagag taagacgggc tattagtagt cgcatcggag ttatttgtga aaacctggtt 120
agggcctctg tctccgctgc gctcgcctaa attggtatgg ctcgacttgg aaacacggtt 180
ctaacacgcg ttgttagcgc ccttgctagc atgtgaagga cactggccct accaagaaag 240
attcgagtcg ctccttccgg tatcgttcac ggaggcgata tttactcttc ttactacggt 300
tacttcgaga ttgtctgtga agtttaagac tactaaaaag agtattaagc ctatcgggaa 360
ttagctagat cgacacgcta aaaccaaggg caatcggcgg aaatatagag gcaccaataa 420
tagggcctac agaaggcccg agggttagac tcacgtttaa taccggccac gggagaaata 480
aaaagataaa gtatacatcg tttagcggtc ctcggaagcc ttcggcttta atgccaagga 540
gtcggaagca tcgtcggcga gtaataaact ccatcgcgcc gagactatct acgacgccct 600
ccttaanatc cgtaaattac tcccggaaag agtatttagg cggctct 647

<210> 749
<211> 642
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(642)
<223> n=A,T,C or G

<400> 749
ctntgtggcg gtggntgtct catttgggtg gactttttgg gtcgtaggaa cctggtatgc 60
aggtccgcgg agcgtgggct ctcgtcgtgg atgttggggg ttggtgtggt gccggttgtt 120
tttggttctg ttgagcgtag tgtgtttgaa ggttagcgtt cgtgtcttgc ttgtggtttg 180
gtgtttaggg cgggtgggga ggttgttgtg tagctgttgt atgtcatatt gttggtgttg 240
ctgccctgtg ctgtttgtcc ttggttattg tggttgttac cccgcctgtg tggaagtgtt 300
gtggcagggc gggaatttaa gtgggagagt tgtgggaccc gtggttgttg ttacgttgct 360
gcttttgtcg tgggcggtgg cggcgcgtct gataattaga attggatacg gagtgtataa 420
tacttctagt aaatggggac ctagtgcttg acttcccgga atagggatct atgcgaagtc 480
cttaggatag tctttgataa gtttaacgcc cacgacccta aaattataca cgattagacg 540
cataacgact cctccaggaa agataaagaa tctcacatat agaacgggac cccatacacg 600
tcggatagga aacaagagaa ctaattttng ttaaaaagac tt 642

<210> 750
<211> 639
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(639)
<223> n=A,T,C or G

<400> 750
tttgtggcgg tggtgtctca tttgggtgga tttttgggtc gtaggtaacc tggtatngag 60
gtatagatgc cgattggtcc cgacgagcgt cacgataaat tcggtagttt cgcccttttt 120
agaaggcgct agtactcgga acttcacttc atctcggtag tttactttgg cgtatatagc 180
cttctccctc gaagactagc cgtcacattc gttccctagg aatcgtttct gcccctaaga 240
atccgagagc gagatcccga aactagagga accttagaag agtcgtattt ccacaaggac 300
cccacagtca ttccgggaaa atccctagga ccatacggtt aggattcccc cggaacccgg 360
agcaaagctc atgatttccc acaccgcgag agcgcctata accctatccc atttcttcgg 420

gttatcgagg atattacgat caagccgaga gaaccgctag aaccgctttc ttcgctttct 480
cacggaacct ataagtagaa agagaaactc aggtcttaag ggggcgcttc ggctaacgaa 540
acttctactt acgaagagag tatctagaca ttaagtcata aaaatccact acgcacctcg 600
tgtacgatat catcgggagc ggttcataga cggtgtccg 639

<210> 751
<211> 637
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(637)
<223> n=A,T,C or G

<400> 751
cttttgtggc ggnggtgtct catttgggtg gatttttggg tcgtaggnaa cctggtatng 60
aggcagctct gagccccccc cccccccccc cccccncccc cccccccccta ggnggttggg 120
aanacggtgg atacctaaat cgagtgngtt cattaaaagt agttgattac nccctaaaat 180
aanaanaggg cttcgtcggg anaaatcggt aagganaagt ctttntggca tcataanaat 240
actggctcgg gtcctaanat ntttaaggng gtcnccgagg gtnttcatac cgataanaaa 300
cgttttccta tcggcaacgg gcttacctga gggnggactt ctcncggngc ggngattnan 360
acgaanacgt agaggattnc cgntacttnt tganatcacn cgtatcatac ttgtaagcat 420
aattntcctg aaaagtgtta taanaatacg cncgcatatt cgctttttcg tcctagggat 480
gcttaaatgg cgatactgct atagcgggtg agcgttggtt ctcgagnaan aaagcgtgtc 540
ctaatgcgtc taaggnttta aggncgttgg tttaaaaata nccttagaaa cctcgaggcg 600
gatactggtt tntttttaac gaaacaaagc accccnn 637

<210> 752
<211> 644
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(644)
<223> n=A,T,C or G

<400> 752
tntgtggcgg tggtgctcat ttgggtggat ttttgggtcg taggaacctg gtatgaggtc 60
ttgcgagttg ttggtgtgtc ctgtcgttcg gtggttccct tttgagttga gtttgtcctt 120
tgaggttgtt agctgctgtt cgtttgtgtt cgtgtagtgc tttgggttga gagggttatg 180
gtggtggtta cggtgtattg tcgcccgtgg tcgcggggtt ggggtggtcg tcggttttgt 240
ggttcatagt agtcttctgc gttcggtggt gcgggtttgg gtgagtagtt tcgttcttgg 300
atgtcccatt gacccgccat aatctaagta agggttagta gaaacctctc cccgatagac 360
acaaccgtcg tccactaaag acctcgcctc tgatttttaa aaggacccga aaaacatccc 420
ttcaacggaa aaaacggaaa aaaagtcagc gaattcaaag aagccacggg agagaaaaaa 480
gaactaaagt tagtccgtca ttatatgtct cctcggagga ggaagcggcg gtggcggaaa 540
atgaggcggt aagaaagacg acctctatcg gcggcttang ccctaaaagg gcgatacctt 600
acgggatgat aaggacccta ggacgcctcc ttctcggatc gtcc 644

<210> 753
<211> 635
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature

<222> (1)...(635)
<223> n=A,T,C or G

<400> 753
ctttgtggcg gtggtgctca tttgggtgga tttttgggtc gtaggaacct ggtatgaggg 60
aatcagctcg accccccccc cccccccct ccgaagcaga gcccaaccca aagtccaccg 120
actacccgag taaactctcg gagggtagaa taagaaggag taggtcctag ccaatagaag 180
tagttccgag ccgttaggac agcggacgga acattnaaga aagagcctat attagggagg 240
aagtaacgtt cctctttcgg agctctttaa ggggtagtcc cagaacaagg gaagaggacc 300
cgtcggctat tgcccgtcga tacgggctct cacggngagc ctaggttcga ggatagggcc 360
gctcgtaaaa ttatacggtt tccgagaaac gcttccgtag accgggtcct aaatcgtccg 420
gagtattngg agagggatcc ttcggaccct agggacagag agaggagaac ggaggttaca 480
ggaggagaac gtntcctcnc tagttttctt tangtcgaaa aatttcttac cgatagggtt 540
cctagggtcg gngaatttac ggttcgaaaa acggtagtnc ctaanggntg ntattngggg 600
tagtatcggg tcgtttacaa ntcgtccgtc ttntg 635

<210> 754
<211> 721
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(721)
<223> n=A,T,C or G

<400> 754
accggattng ttnctgagcg cgtgactgct aataaaaaag atggantgcc atcttttttt 60
ttnccttgct ttatatatcc agcagcaaaa caaaattgtt ctgcngggct ataaaatttg 120
gcttgtgagt cntgtacaca actcaggagt gtgacacagc taccagcttt cctcctaact 180
ctcaagggaa gaaaattcaa gttctgtcta ggctcactct gtaaagtggg aaacttgctg 240
gttttgtagg ctttttttcc ccttctttcc ctctctcagc ttctccctgc ttctcagaan 300
atggagttgt gatgcctgca acttaccaaa tttatctatg aatcagattc cagtgggaga 360
cccctaaagc agagggagaa taaggagttc tccccatgat ggaaaatatc caaagacaag 420
gtttcatgga gcaaagaatt ctggctagat ttggtttgta agtggatccc tccccactgc 480
gtgtacactt tatctgtctc tttgcttctt ccccaccctc tttcccagct ctctctctgt 540
ctctctcttg ntcccctgac cctttttttct tcccantgca tacttttttn tttccctttt 600
ttaatcttct atantcttaa ncctaccaan gggccctcnt gannaatttn tcacccctga 660
ataggggatt ctntangccc tgagaatttc nttatcanaa aaatattttt ttaaagcatt 720
a 721

<210> 755
<211> 721
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(721)
<223> n=A,T,C or G

<400> 755
accggattng ttnctgagcg cgtgactgct aataaaaaag atggantgcc atcttttttt 60
ttnccttgct ttatatatcc agcagcaaaa caaaattgtt ctgcngggct ataaaatttg 120
gcttgtgagt cntgtacaca actcaggagt gtgacacagc taccagcttt cctcctaact 180
ctcaagggaa gaaaattcaa gttctgtcta ggctcactct gtaaagtggg aaacttgctg 240
gttttgtagg ctttttttcc ccttctttcc ctctctcagc ttctccctgc ttctcagaan 300
atggagttgt gatgcctgca acttaccaaa tttatctatg aatcagattc cagtgggaga 360

cccctaaagc agagggagaa taaggagttc tccccatgat ggaaaatatc caaagacaag 420
gtttcatgga gcaaagaatt ctggctagat ttggtttgta agtggatccc tccccactgc 480
gtgtacactt tatctgtctc tttgcttctt ccccaccctc tttcccagct ctctctctgt 540
ctctctcttg ntcccctgac ccttttttct tcccantgca tactttttn tttccctttt 600
ttaatcttct atantcttaa ncctaccaan gggccctcnt gannaatttn tcacccctga 660
ataggggatt ctntangccc tgagaatttc nttatcanaa aaatattttt ttaaagcatt 720
a 721

<210> 756
<211> 873
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(873)
<223> n=A,T,C or G

<400> 756
ggaagaatac agtaagtttg caaattaaaa tttctctatt tttctgttat ttattcattt 60
ggaaactgtc agcctgtctc tttcactttg ggcaagtgaa agcaaagacg tccagtccta 120
tcagcaatta ggctgaaagt caacgccaag ctggcgggca agggctggtc tgagtagagg 180
ttccctaggc aggcaagaga gagactccca ctcgatactc ccagctcggc aactgcctga 240
atgccaatga gcactcatta taacccgccc tattttatag gatttaattt tacacttcag 300
gcttaatcag tctgaaagtt aaactgacag tgttaagtta cggaatcaat gacatttagg 360
ctttatgact ttgtagctga atatctatgg gctatatttc cattctaaca gtgatatcct 420
gttccagaat ctcattcttt ggtgatggca ctttctagtg gagcagtcat ggtaacagtc 480
cacacccatt accatgtggg tgctttacag catactgacg gaaggactga ggagccaccg 540
gagcaggagt tcctctcagg gaggacgctg acacttccac agctgcctan gtatgggcac 600
ctgatgccaa cgaanaaccc aaagcgctct cccttccaga tggaagctgc cccacactgg 660
gctgacagca tctggagctg ctctggctca aatcccggaa tcgcacanct cctancgggg 720
gcgtttanag atcctcnggg ccagctaccg accacttttg acaagggnct taggagcgat 780
aactagnctg gcgcgttaca cncggatgga acgtcttgga cttgagacct cttgggggan 840
atggcncccc caaataantt gggaaaantn ggg 873

<210> 757
<211> 782
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(782)
<223> n=A,T,C or G

<400> 757
ggcccctcga gggatactct agagcggccg ccgactagtg agctcgtcga cgatatcccg 60
ggatttgaga ccaggagaca gctccagatg ctgtcagccc agtgctgggg gcaggcttcc 120
atctgtgaag tggagaggcg ctttgggctt cttcgttggc atcaggtgcc catacctagg 180
gcagctgtgg aagtgtcagc gtcctccctg agaggaactc ctgctccggt ggctcctcag 240
tccttccgtc agtatgctgt aaagcaccca catggtaatg ggtgnggact ggtaccatga 300
ctgntccctt aaaaggtggc cttccccnaag aaaggagaat tcttggacna gggatttcac 360
ttgnttagaa atgggaaaaa ttacccatta gaattttcgn ttccaaggcn tnaagnccta 420
aaaggccttt gattcccgaa ccttaaccct gggcagttaa cctttcaaac gggataaacc 480
ctganggga aaatnaaatc ctttaaaaaa gggggggttt naaggagggc tctttggctt 540
tcaggcantt gccaacctgg gaaattcana ggggaagtnt tttttttgc ctgcctaggg 600
aacctttact taaacnaacc cttgnccccc catttggggt tgactttcan cctaattgct 660
gaaaggaccg ggccgntttt gntttccttt gncccaaagg naaanaaacg ggtgccantt 720

```
cccangggat tanttcccga aaatttggnn aatttttntt tgnaactttt tgggtttttt 780
cc                                                                782

<210> 758
<211> 647
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(647)
<223> n=A,T,C or G

<400> 758
ntttgtggcg gtggtgtctc atttgggtgg actttttggg tcgtaggaac ctggtatnga 60
gggaagagcg ccgtcggtcc gagtacagta tggagtagta tagtcttcgc gccttctcgg 120
gcggcggggc tattctctcc aaaggcagag gtccctagtc gacctcgctc ccctaggtta 180
ggaacagccg tcgaatattt taggttcgtc gaggctttct tccgagctct acgcctaagt 240
agctccgcga gcaaagtatc ggtcattttc ccctatccat cactccccta agtacgcctc 300
attattccgg aaggcaagag gccagcattc ctccttagag tagagggtag gtacctccgt 360
cgcgtgccgc gaaagggcag agcttcgtgt cttccctccg cagcagctta acggtctacg 420
taggcgttct cgatcttttc acgggaatcg ggtccgggga gggcggcgga aaacgtcgac 480
gtctcggtca ccgtcaccgc cccgaacaac tagcggcttt ccgctttcaa ctgaggaacc 540
ccgcacccct cattagcgct tacgaaatcg gggangtgat tgcgccaatt cgttagcctt 600
cgataattat tctctattag cggtcctatc tcgcgctttc gatttat               647

<210> 759
<211> 657
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(657)
<223> n=A,T,C or G

<400> 759
ctttgtggcg gtggtgtctc atttgggtgg actttttggg tcgtaggaac ctggtatnga 60
gggctctata gaaagcctct tgtctttaga tacgggcttt ctggtccttc gttctggaag 120
tgtagtagta ggtactgcgg gaaggcgaag agtcctttca aggacgattt acttaagttg 180
gcttattcta tagttccttc gggacataag gtcggtacga tctatactgc gtgggaagct 240
gataggttgg gacttaaggc gaataagaag gaggcggcgg aggtcgcgat taccgcagag 300
atattattta cggcggccgc gggtaccgcg ggtcatgcgg aaattttctg aggttcttgg 360
attcctaaga tcgctcccgt cgagtatact agcgacgaac gtaagagtgc cctcacaaga 420
accggtacaa actcaagaag aagttcccat taagcatcgt aagaaacggt aggacgagga 480
cggtaagaag taatcggaga aaggatccta gtngttacga agaagcatcg ttnagctact 540
ttgcgctacc gtttatattt agacgtgttc cgtccttctc cgtgtttana aaaaaggttt 600
attccgacgg gagacttagg cgaatggagg gttccgcggt tganaatcgg ancgggg    657

<210> 760
<211> 644
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(644)
<223> n=A,T,C or G
```

<400> 760
ctttgtggcg gtggtgtctc atttgggtgg actttttggg tcgtaggaac ctggtatgna 60
ggaaaagaag taagcctcga agcctatctc cgaccgtatt tatttcgcag aagacggaac 120
tacggacgtc gttaaccccg agtagccccc gtaagaaagg actaaagcga atggaaaagt 180
cgggaattcc ggcggagggg cggcgattac tgaaaggagt aagagtaaga ctattgcgat 240
acttgaggcg ttccctctta aaaggcaccc gaaacactct attaaaaaac acccgaagaa 300
gaacaactca tgcgatcggc cgtgtgcagc cgtcaatagt aaagagagcc atgaaccatg 360
ccatccttag accaattagg atgaagaaga ggaggaagat gaggaccaaa ccctacccac 420
tcggaaaacc ccgcacgagc ctccgaacaa aatccgggaa ttaaaacggc ggcccacttc 480
cgcactctcg tagcgcggac cgaatagaaa accggaaact acagctaaag ggtcctttcc 540
ggcctgttat ctacccaccc gcaatccgat cctccccccc cctcgtccaa aaaccctaac 600
ctctgcggca acattagagc agaaggagag ggcgatccct tgan 644

<210> 761
<211> 647
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(647)
<223> n=A,T,C or G

<400> 761
ctttgtggcg gtggtgtctc atttgggtgg actttttggg tcgtaggaac ctggtatnga 60
ggcgggtact ctctgggata atcggtataa gtgttgtaaa attgggggta agagaaagtt 120
tcattataag aagtggaagc acgagccggg gtgtttagtc gttaatatta agaccggttt 180
ttgttgtact tatatagctt gcgcgtgggg aggcaataag aaacattgcg tttcgaggcc 240
ggatgcgggg aaccctcttc ggggtctaga gcgccgcatc tgcaaaataa ggactactga 300
cgccgctcat aacgtactca acaatgagtc ggcctgcatt aagatttcgg cgaagaaccg 360
tactgcgtct actgatagta tattgcattg atagcggcat gagctttatc acgtgtcgtt 420
ttcgggttgt aagaagggag ttaagtcgat cttcgaggaa gaagagaccc caaataaaaa 480
atgactcaaa aaaacctaga agaaacacga cgaaaggaaa aagaacgtta aaactagtag 540
ctcttcggan gagtagcctt agtagggtaa gtcctccgtg cgtactgtcc taaggtttgg 600
atagcgcggt tgaatagacg gtcacgcgtc agaaggtaaa aanccgg 647

<210> 762
<211> 628
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(628)
<223> n=A,T,C or G

<400> 762
cattgtgttg gggtcactga gcccactttt ttccagattt tttgtaaaat tgtttcgcat 60
tgtgttccct ttattcgctt gtattaatat ttgcgtagtg gattaaacaa atacttggtg 120
ttgactgtca gtcttagagg actgactaga agtagttttc atttggggct caggaaatac 180
ctactttata tttctagcta attaggaaag tcatttttca gttaggttgg tgttttggtt 240
caggcactcg ctagctagat gacctaacat gctacttaat ttctgagtgt ttgtgtccat 300
ccctgtagga ttgttgcggg gttaaatgaa attgtgtata tttgtaaagc atttacctca 360
gtgcccagac tgtgacagag tagattatta ggcttgctct tatttctgtg attaaattta 420
gtgtcagatt agcaacctat agctacttct aaagctgctg ctgctttctt tgtttagggt 480
taggaagaaa catgctggac agtttgccaa atgagagtta catgatgtgg cttgtgggaa 540
cattctaact tggaacttgc ccatttccag gactttgngg ttcanagatt tttggggata 600

gatgtaaggg ttaaaaaaaa cngaaaac 628

<210> 763
<211> 147
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(147)
<223> n=A,T,C or G

<400> 763
cattgtgttg gggcagagat aaataattcc tctgaaaagt gttttattgg aatttcaaat 60
gaaaagctaa ctggataact tacagcatgt ttctgccaat aatctcttan aacaggcctc 120
tttttttat gcacaccacc ttcnggc 147

<210> 764
<211> 146
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(146)
<223> n=A,T,C or G

<400> 764
cattgtgttg ggtatgtttt ttgaaggcag gtggacagga tttgctgatg ggtaaatggc 60
agagttaggg ggactgttag aacagagaaa ganatcatgg ggttgggttt gagtctgatg 120
nnnaactggt gccgnntgct cagtat 146

<210> 765
<211> 129
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(129)
<223> n=A,T,C or G

<400> 765
tncncgattc gntnctagcg tntacactna tgtcttggta ccgagctcgg atccactagt 60
ccagtgtggg nggaattcca ttgtgttggg gcaggaggng ctttgngtac ngtgcggctg 120
nagaggcgg 129

<210> 766
<211> 175
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(175)
<223> n=A,T,C or G

<400> 766

cattgtgttg ggcctagtcc gaatactttt agtaacttca gacagatctc ctcatctctt 60
tctggggctt ggnttttctc ctttgtanaa tgatgccttt ctgtggtttt gtcatttcta 120
acattctgtg ngtgatgagg tgtatattcg anganctcta tcnccanagt actct 175

<210> 767
<211> 602
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(602)
<223> n=A,T,C or G

<400> 767
nnntttaaaa nctgtnctcc ccgcggtggc ggccgctcta gaactagtgg atcctttcca 60
cctggtttgt tttcagtgtt taatcctatt agtatcagca ggatataggt caggatatca 120
ggtgcagaac ctgtggaatc agccaatttg gcttgctcat ttactttaat aaggtcccat 180
aatgagtgag agtacaaagt tcaagccctg ttgagggtct gcattaaact ctcagaagta 240
tttagagtgt gccaggagcc gcgaaggtct ggttcgggtg gtggcgggaa ctgtattaga 300
gtgctaggca cggcgcgaca aagtctgtcc aacccaaaac ggtgctgagg cgttgggtgt 360
gagctccagt actcagaaaa gcatctcagc aggtactcaa cagatcctca ggggcttggg 420
ggcccagcac tggcagtgag ggcatgaaag acataaaagg gcactacctg tgggtatttt 480
ctgttctcca aggaggaagt agcaaaaatt aggacgctgg aatatcctat gttgtagcaa 540
tcccagaaca actgatgctc aacaaatacc acacaaaaca aattttttaa aatttaatct 600
ta 602

<210> 768
<211> 671
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(671)
<223> n=A,T,C or G

<400> 768
tccaccgcgg tggcggccgc tctagactag tggatccact agtccagtgt gggtgggaat 60
tcgcggcncg cgtcgacaaa aatactgcta aagtaatatt tttatagatg actatttgcc 120
ttggggccag gaaaagcagc tggagttatt cacttagtac catttttaca tactaacttt 180
gccttttcca tgcttgcttg atgcggcttg cagcactgaa gaacagtttc aattgctagc 240
caaccagaga gcatgatcaa accaaacaag ttccctgttt caggaaaaac aggttttagg 300
taactgaagg gttaccagtt actgattcca caatcttctc tgtaaaanat ttctgcctat 360
tatgcagact gggcggcttt aaanntggta aaactatnaa atacccatac aatattttaa 420
nggggccccn ttatnaagct tttcaggcct tccccttccc atagcattgg tgggatacaa 480
gaaaccttta aacagcaacn agctatcnag gcccaaaagg aaagtaattn tgatttttta 540
nagattccgn aacgaaaaaa tggctgggtt caaatacnac cttcttttta aaatggnttc 600
cttattaaac nttttttttt tttaatttta ccccatggtc ntgatnttng ngcttccgcc 660
canaaaatng n 671

<210> 769
<211> 877
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature

<222> (1)...(877)
<223> n=A,T,C or G

<400> 769
aaagctggag ctccccgcgg tggcggccgc tctagaacta gtggatccac tagtccanng 60
ngggggaatt cgcggccgcg tcgacctcta tacctttgnt catgcagctt cctctgactg 120
ggtttgttct tcacttggct aacccctctt ttacttaagc acaccttgaa cattccctcc 180
ttccccattt ccccgcagng cccctaatgg acatacttct gaataacaca ggtggtattc 240
cttccttgtt ggaacctcct ggaggaagag acagatgatt aacaaatcct tccatcaacc 300
cctttgacca tgacatcaac agtgctccaa attatggggt accgtattag cctatgtcta 360
tcttgatcag aatccttacc tcggtgtatt gaaattatct atttcgtgcc tgcctcttta 420
aagtcagggt ttgccttatc tattgtctaa caccatgcag taggtaacat gcagtaggaa 480
acatggcatt aaattatttg ggttcaaatc ccagttatgg tgtgtaaatg cctaccaggc 540
cgtgaggcac ctgctaagca ggttgcacgc atcatttgaa ttcacaccac cctttgcaa 600
tagaacagat aggcaacaga ggctcatttg ggctaaagga tttgatggag gggaagtgcc 660
aggattccca ccaaggcctc anggcccagg tccanggacc atgtctgttg tgacaactgg 720
agtgcatttc atatcccctn ctctgngggg naaggtccct cncgnggaga acnnttaaaa 780
caatcatntc tngggggntt aatgcttctt nccccagtgt ggtncactgc ngccacgagt 840
cccanccact agtcccangt ctgtcatgaa ccanccc 877

<210> 770
<211> 874
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(874)
<223> n=A,T,C or G

<400> 770
ctggnctccc cgcggtggcg gccgctctag aactagtgga tccactagtc cagtgtggtg 60
gaattcgcgg ccgcgtcgac cttttcaaag gttaacttat ttaattatca cannngcaac 120
ccgatgagta ggtaacagta ttttactgat aggtaatcta aagaaggagg ctaaataaat 180
tgcccaattt cgaacagtga gaggaagaat taggattgaa acacatatag tggcttcaga 240
atctgtaacc ctcacgatgc cactactact tctttcagaa taccctttgc ctatctattc 300
tgttcctatg tcatcaaatt atacttactt taaaaagtat ttgtctttat tatttttaaa 360
aaaacacagg gaagtatttc tgatcagggg cagtattggt tctgaaagac aagccagtgt 420
ttttgagggt ttctcccttg ccagtttttc tatgctgggt tattcaagtc ctaagaattg 480
tgtagctatt acagaaccgc tttagcaaat gtgttccatt aatcaaggtg atttataaca 540
aaatttcatc caagtttgga gtgctctgaa aacatagcca aaatgttcgc agggtctacc 600
cctctcgtgt gtcccttttt tttagctatt tcagaagcac actggtgcaa tattttacga 660
aatgagtttc ttccccttac ctctgcatcc tctaagaaaa aatcattgnt gttttatgaa 720
natgaanatc ctgctatttc atatcttgat tggagctgct taattaaatg accattttna 780
aatttgtttt gattccnngc aaaaaaagtt tnttnttgga tgtagggggc tcnnaaagnc 840
caaaaccccc caaaattttt nnttgggaac ccna 874

<210> 771
<211> 156
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(156)
<223> n=A,T,C or G

<400> 771

ttaaaaanct ggnctccccg cggtggcggc cgctctagaa ctagtggatc cactagtcca 60
gtgtggtgga attcgcggcc gcgtcgaccg cgagcggtcg cccttttttt tttttttttn 120
ngtttttttg aanaattcat tgggtattta ttattc 156

<210> 772
<211> 586
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(586)
<223> n=A,T,C or G

<400> 772
ncaanctggn ctccaccgcg gtggcggccg ctctagacta gtggatccac tagtccagtg 60
tggtggaatt cgcggccgcg tcgatcacaa agtgctcaca agtccngnat ttattttatc 120
tccagatatg aaacttaccc ccagctatgg tcttctattt gttatttaat ttctaggcca 180
attttttcca cttgaatgtc agtattttaa ttcaaagtca ccttgtccaa ataccaagtc 240
atcaacttac cctcaaatta tatcctcatt cagaaaatct acatctatta atggtagcta 300
ttttatccct gccccctgct ttttcttttt atatttaatt aatttgntca tccagcaaat 360
gcttattgag caggtattgt aggctaaaca attctanact ttaaggggac acagnttgca 420
aaacaaaatc ctgccttgna tggatactta tgnnatggng ggatacagac aatcaacata 480
atgangngca tcatatataa tggttagnan aatgataagg gnttttggga aaaaaatgca 540
cccanccaan anggattggg aagtggangg ganggtcang ggangg 586

<210> 773
<211> 2983
<212> DNA
<213> Homo sapiens

<400> 773
agagatagag tcttccctgg cattgcagga gagaatctga agggatgatg gatgcatcaa 60
aagagctgca agttctccac attgacttct tgaatcagga caacgccgtt tctcaccaca 120
catgggagtt ccaaacgagc agtcctgtgt tccggcgagg acaggtgttt cacctgcggc 180
tggtgctgaa ccagcccta caatcctacc accaactgaa actggaattc agcacagggc 240
cgaatcctag catcgccaaa cacaccctgg tggtgctcga cccgaggacg ccctcagacc 300
actacaactg gcaggcaacc cttcaaaatg agtctggcaa agaggtcaca gtggctgtca 360
ccagttcccc caatgccatc ctgggcaagt accaactaaa cgtgaaaact ggaaaccaca 420
tccttaagtc tgaagaaaac atcctatacc ttctcttcaa cccatggtgt aaagaggaca 480
tggttttcat gcctgatgag gacgagcgca aagagtacat cctcaatgac acgggctgcc 540
attacgtggg ggctgccaga agtatcaaat gcaaaccctg gaactttggt cagtttgaga 600
aaaatgtcct ggactgctgc atttccctgc tgactgagag ctccctcaag cccacagata 660
ggagggaccc cgtgctggtg tgcagggcca tgtgtgctat gatgagcttt gagaaaggcc 720
agggcgtgct cattgggaat tggactgggg actatgaagg tggcacagcc ccatacaagt 780
ggacaggcag tgccccgatc ctgcagcagt actacaacac gaagcaggct gtgtgctttg 840
gccagtgctg ggtgtttgct gggatcctga ctacagtgct gagagcgttg ggcatcccag 900
cacgcagtgt gacaggcttc gattcagctc acgacacaga aaggaacctc acggtggaca 960
cctatgtgaa tgagaatggc aagaaaatca ccagtatgac ccacgactct gtctggaatt 1020
tccatgtgtg gacggatgcc tggatgaagc gaccggatct gcccaagggc tacgacggct 1080
ggcaggctgt ggacgcaacg ccgcaggagc gaagccaggg tgtcttctgc tgtgggccat 1140
caccactgac cgccatccgc aaaggtgaca tctttattgt ctatgacacc agattcgtct 1200
tctcagaagt gaatggtgac aggctcatct ggttggtgaa gatggtgaat gggcaggagg 1260
agttacacgt aatttcaatg gagaccacaa gcatcgggaa aaacatcagc accaaggcag 1320
tgggccaaga caggcggaga gatatcacct atgagtacaa gtatccagaa ggctcctctg 1380
aggagaggca ggtcatggat catgccttcc tccttctcag ttctgagagg gagcacagac 1440
gacctgtaaa agagaacttt cttcacatgt cggtacaatc agatgatgtg ctgctgggaa 1500

actctgttaa tttcaccgtg attcttaaaa ggaagaccgc tgccctacag aatgtcaaca 1560
tcttgggctc ctttgaacta cagttgtaca ctggcaagaa gatggcaaaa ctgtgtgacc 1620
tcaataagac ctcgcagatc caaggtcaag tatcagaagt gactctgacc ttggactcca 1680
agacctacat caacagcctg gctatattag atgatgagcc agttatcaga ggtttcatca 1740
ttgcggaaat tgtggagtct aaggaaatca tggcctctga agtattcacg tctttccagt 1800
accctgagtt ctctatagag ttgcctaaca caggcagaat tggccagcta cttgtctgca 1860
attgtatctt caagaatacc ctggccatcc ctttgactga cgtcaagttc tctttggaaa 1920
gcctgggcat ctcctcacta cagacctctg accatgggac ggtgcagcct ggtgagacca 1980
tccaatccca aataaaatgc accccaataa aaactggacc caagaaattt atcgtcaagt 2040
taagttccaa acaagtgaaa gagattaatg ctcagaagat tgttctcatc accaagtagc 2100
cttgtctgat gctgtggagc cttagttgag atttcagcat ttcctacctt gtgcttagct 2160
ttcagattat ggatgattaa atttgatgac ttatatgagg gcagattcaa gagccagcag 2220
gtcaaaaagg ccaacacaac cataagcagc cagacccaca aggccaggtc ctgtgctatc 2280
acagggtcac ctcttttaca gttagaaaca ccagccgagg ccacagaatc ccatcccttt 2340
cctgagtcat ggcctcaaaa atcagggcca ccattgtctc aattcaaatc catagatttc 2400
gaagccacag agtctctccc tggagcagca gactatgggc agcccagtgc tgccacctgc 2460
tgacgaccct tgagaagctg ccatatcttc aggccatggg ttcaccagcc ctgaaggcac 2520
ctgtcaactg gagtgctctc tcagcactgg gatgggcctg atagaagtgc attctcctcc 2580
tattgcctcc attctcctct ctctatccct gaaatccagg aagtccctct cctggtgctc 2640
caagcagttt gaagcccaat ctgcaaggac atttctcaag ggccatgtgg ttttgcagac 2700
aaccctgtcc tcaggcctga actcaccata gagacccatg tcagcaaacg gtgaccagca 2760
aatcctcttc ccttattcta aagctgcccc ttgggagact ccagggagaa ggcattgctt 2820
cctccctggt gtgaactctt tctttggtat tccatccact atcctggcaa ctcaaggctg 2880
cttctgttaa ctgaagcctg ctccttcttg ttctgccctc cagagatttg ctcaaatgat 2940
caataagctt taaattaaac tctacttcaa gaaaaaaaaa ccg 2983

<210> 774
<211> 3064
<212> DNA
<213> Homo sapiens

<400> 774
aattctaaaa atgcttttgc aagcttgcat gcctgcaggt gcagcggccg ccagtgtgat 60
ggatatctgc agaattcggc ttgcgctcag ctggaattcc gcagagatag agtcttccct 120
ggcattgcag gagagaatct gaagggatga tggatgcatc aaaagagctg caagttctcc 180
acattgactt cttgaatcag gacaacgccg tttctcacca cacatgggag ttccaaacga 240
gcagtcctgt gttccggcga ggacaggtgt ttcacctgcg gctggtgctg aaccagcccc 300
tacaatccta ccaccaactg aaactggaat tcagcacagg gccgaatcct agcatcgcca 360
aacacaccct ggtggtgctc gaccccgagga cgccctcaga ccactacaac tggcaggcaa 420
cccttcaaaa tgagtctggc aaagaggtca cagtggctgt caccagttcc cccaatgcca 480
tcctgggcaa gtaccaacta aacgtgaaaa ctggaaacca catccttaag tctgaagaaa 540
acatcctata ccttctcttc aacccatggt gtaaagagga catggttttc atgcctgatg 600
aggacgagcg caaagagtac atcctcaatg acacgggctg ccattacgtg gggctgcca 660
gaagtatcaa atgcaaaccc tggaactttg gtcagtttga gaaaaatgtc ctggactgct 720
gcatttccct gctgactgag agctccctca agcccacaga taggagggac cccgtgctgg 780
tgtgcagggc catgtgtgct atgatgagct ttgagaaagg ccagggcgtg ctcattggga 840
attggactgg ggactacgaa ggtggcacag ccccatacaa gtggacaggc agtgccccga 900
tcctgcagca gtactacaac acgaagcagg ctgtgtgctt tggccagtgc tgggtgtttg 960
ctgggatcct gactacagtg ctgagagcgt tgggcatccc agcacgcagt gtgacaggct 1020
tcgattcagc tcacgacaca gaaaggaacc tcacggtgga cacctatgtg aatgagaatg 1080
gcgagaaaat caccagtatg acccacgact ctgtctggaa tttccatgtg tggacggatg 1140
cctggatgaa gcgaccctac gacggctggc aggctgtgga cgcaacgccg caggagcgaa 1200
gccagggtgt cttctgctgt gggccatcac cactgaccgc catccgcaaa ggtgacatct 1260
ttattgtcta tgacaccaga ttcgtcttct cagaagtgaa tggtgacagg ctcatctggt 1320
tggtgaagat ggtgaatggg caggaggagt tacacgtaat ttcaatggag accacaagca 1380
tcgggaaaaa catcagcacc aaggcagtgg gccaagacag gcggagagat atcacctatg 1440
agtacaagta tccagaaggc tcctctgagg agaggcaggt catggatcat gccttcctcc 1500
ttctcagttc tgagagggag cacagacagc ctgtaaaaga gaactttctt cacatgtcgg 1560

tacaatcaga tgatgtgctg ctgggaaact ctgttaattt caccgtgatt cttaaaagga 1620
agaccgctgc cctacagaat gtcaacatct tgggctcctt tgaactacag ttgtacactg 1680
gcaagaagat ggcaaaactg tgtgacctca ataagacctc gcagatccaa ggtcaagtat 1740
cagaagtgac tctgaccttg gactccaaga cctacatcaa cagcctggct atattagatg 1800
atgagccagt tatcagaggt ttcatcattg cggaaattgt ggagtctaag gaaatcatgg 1860
cctctgaagt attcacgtca aaccagtacc ctgagttctc tatagagttg cctaacacag 1920
gcagaattgg ccagctactt gtctgcaatt gtatcttcaa gaataccctg gccatccctt 1980
tgactgacgt caagttctct ttggaaagcc tgggcatctc ctcactacag acctctgacc 2040
atgggacggt gcagcctggt gagaccatcc aatcccaaat aaaatgcacc ccaataaaaa 2100
ctggacccaa gaaatttatc gtcaagttaa gttccaaaca agtgaaagag attaatgctc 2160
agaagattgt tctcatcacc aagtagcctt gtctgatgct gtggagcctt agttgagatt 2220
tcagcatttc ctaccttgtg cttagctttc agattatgga tgattaaatt tgatgactta 2280
tatgagggca gattcaagag ccagcaggtc aaaaaggcca acacaaccat aagcagccag 2340
acccacaagg ccaggtcctg tgctatcaca gggtcacctc ttttacagtt agaaacacca 2400
gccgaggcca cagaatccca tccctttcct gagtcatggc ctcaaaaatc agggccacca 2460
ttgtctcaat tcaaatccat agatttcgaa gccacagagc tcttccctgg agcagcagac 2520
tatgggcagc ccagtgctgc cacctgctga cgaccccttga gaagctgcca tatcttcagg 2580
ccatgggttc accagccctg aaggcacctg tcaactggag tgctctctca gcactgggat 2640
gggcctgata gaagtgcatt ctcctcctat tgcctccatt ctcctctctc tatccctgaa 2700
atccaggaag tccctctcct ggtgctccaa gcagtttgaa gcccaatctg caaggacatt 2760
tctcaagggc catgtggttt tgcagacaac cctgtcctca ggcctgaact caccatagag 2820
acccatgtca gcaaacggtg accagcaaat cctcttccct tattctaaag ctgccccttg 2880
ggagactcca gggagaaggc attgcttcct ccctggtgtg aactcttttct ttggtattcc 2940
atccactatc ctggcaactc aaggctgctt ctgttaactg aagcctgctc cttcttgttc 3000
tgccctccag agatttgctc aaatgatcaa taagctttaa attaaaccgg aatccgcgga 3060
attc 3064

<210> 775
<211> 684
<212> PRT
<213> Homo sapiens

<400> 775
Met Met Asp Ala Ser Lys Glu Leu Gln Val Leu His Ile Asp Phe Leu
5 10 15
Asn Gln Asp Asn Ala Val Ser His His Thr Trp Glu Phe Gln Thr Ser
20 25 30
Ser Pro Val Phe Arg Arg Gly Gln Val Phe His Leu Arg Leu Val Leu
35 40 45
Asn Gln Pro Leu Gln Ser Tyr His Gln Leu Lys Leu Glu Phe Ser Thr
50 55 60
Gly Pro Asn Pro Ser Ile Ala Lys His Thr Leu Val Val Leu Asp Pro
65 70 75 80
Arg Thr Pro Ser Asp His Tyr Asn Trp Gln Ala Thr Leu Gln Asn Glu
85 90 95
Ser Gly Lys Glu Val Thr Val Ala Val Thr Ser Ser Pro Asn Ala Ile
100 105 110
Leu Gly Lys Tyr Gln Leu Asn Val Lys Thr Gly Asn His Ile Leu Lys
115 120 125
Ser Glu Glu Asn Ile Leu Tyr Leu Leu Phe Asn Pro Trp Cys Lys Glu
130 135 140
Asp Met Val Phe Met Pro Asp Glu Asp Glu Arg Lys Glu Tyr Ile Leu
145 150 155 160
Asn Asp Thr Gly Cys His Tyr Val Gly Ala Ala Arg Ser Ile Lys Cys
165 170 175
Lys Pro Trp Asn Phe Gly Gln Phe Glu Lys Asn Val Leu Asp Cys Cys
180 185 190
Ile Ser Leu Leu Thr Glu Ser Ser Leu Lys Pro Thr Asp Arg Arg Asp

195 200 205
Pro Val Leu Val Cys Arg Ala Met Cys Ala Met Met Ser Phe Glu Lys
210 215 220
Gly Gln Gly Val Leu Ile Gly Asn Trp Thr Gly Asp Tyr Glu Gly Gly
225 230 235 240
Thr Ala Pro Tyr Lys Trp Thr Gly Ser Ala Pro Ile Leu Gln Gln Tyr
245 250 255
Tyr Asn Thr Lys Gln Ala Val Cys Phe Gly Gln Cys Trp Val Phe Ala
260 265 270
Gly Ile Leu Thr Thr Val Leu Arg Ala Leu Gly Ile Pro Ala Arg Ser
275 280 285
Val Thr Gly Phe Asp Ser Ala His Asp Thr Glu Arg Asn Leu Thr Val
290 295 300
Asp Thr Tyr Val Asn Glu Asn Gly Lys Lys Ile Thr Ser Met Thr His
305 310 315 320
Asp Ser Val Trp Asn Phe His Val Trp Thr Asp Ala Trp Met Lys Arg
325 330 335
Pro Asp Leu Pro Lys Gly Tyr Asp Gly Trp Gln Ala Val Asp Ala Thr
340 345 350
Pro Gln Glu Arg Ser Gln Gly Val Phe Cys Cys Gly Pro Ser Pro Leu
355 360 365
Thr Ala Ile Arg Lys Gly Asp Ile Phe Ile Val Tyr Asp Thr Arg Phe
370 375 380
Val Phe Ser Glu Val Asn Gly Asp Arg Leu Ile Trp Leu Val Lys Met
385 390 395 400
Val Asn Gly Gln Glu Glu Leu His Val Ile Ser Met Glu Thr Thr Ser
405 410 415
Ile Gly Lys Asn Ile Ser Thr Lys Ala Val Gly Gln Asp Arg Arg Arg
420 425 430
Asp Ile Thr Tyr Glu Tyr Lys Tyr Pro Glu Gly Ser Ser Glu Glu Arg
435 440 445
Gln Val Met Asp His Ala Phe Leu Leu Leu Ser Ser Glu Arg Glu His
450 455 460
Arg Arg Pro Val Lys Glu Asn Phe Leu His Met Ser Val Gln Ser Asp
465 470 475 480
Asp Val Leu Leu Gly Asn Ser Val Asn Phe Thr Val Ile Leu Lys Arg
485 490 495
Lys Thr Ala Ala Leu Gln Asn Val Asn Ile Leu Gly Ser Phe Glu Leu
500 505 510
Gln Leu Tyr Thr Gly Lys Lys Met Ala Lys Leu Cys Asp Leu Asn Lys
515 520 525
Thr Ser Gln Ile Gln Gly Gln Val Ser Glu Val Thr Leu Thr Leu Asp
530 535 540
Ser Lys Thr Tyr Ile Asn Ser Leu Ala Ile Leu Asp Asp Glu Pro Val
545 550 555 560
Ile Arg Gly Phe Ile Ile Ala Glu Ile Val Glu Ser Lys Glu Ile Met
565 570 575
Ala Ser Glu Val Phe Thr Ser Phe Gln Tyr Pro Glu Phe Ser Ile Glu
580 585 590
Leu Pro Asn Thr Gly Arg Ile Gly Gln Leu Leu Val Cys Asn Cys Ile
595 600 605
Phe Lys Asn Thr Leu Ala Ile Pro Leu Thr Asp Val Lys Phe Ser Leu
610 615 620
Glu Ser Leu Gly Ile Ser Ser Leu Gln Thr Ser Asp His Gly Thr Val
625 630 635 640
Gln Pro Gly Glu Thr Ile Gln Ser Gln Ile Lys Cys Thr Pro Ile Lys
645 650 655
Thr Gly Pro Lys Lys Phe Ile Val Lys Leu Ser Ser Lys Gln Val Lys

```
            660                 665                 670
Glu Ile Asn Ala Gln Lys Ile Val Leu Ile Thr Lys
        675                 680
```

<210> 776
<211> 679
<212> PRT
<213> Homo sapiens

<400> 776

```
Met Met Asp Ala Ser Lys Glu Leu Gln Val Leu His Ile Asp Phe Leu
                5                   10                  15
Asn Gln Asp Asn Ala Val Ser His His Thr Trp Glu Phe Gln Thr Ser
            20                  25                  30
Ser Pro Val Phe Arg Arg Gly Gln Val Phe His Leu Arg Leu Val Leu
        35                  40                  45
Asn Gln Pro Leu Gln Ser Tyr His Gln Leu Lys Leu Glu Phe Ser Thr
    50                  55                  60
Gly Pro Asn Pro Ser Ile Ala Lys His Thr Leu Val Val Leu Asp Pro
65                  70                  75                  80
Arg Thr Pro Ser Asp His Tyr Asn Trp Gln Ala Thr Leu Gln Asn Glu
                85                  90                  95
Ser Gly Lys Glu Val Thr Val Ala Val Thr Ser Ser Pro Asn Ala Ile
            100                 105                 110
Leu Gly Lys Tyr Gln Leu Asn Val Lys Thr Gly Asn His Ile Leu Lys
        115                 120                 125
Ser Glu Glu Asn Ile Leu Tyr Leu Leu Phe Asn Pro Trp Cys Lys Glu
    130                 135                 140
Asp Met Val Phe Met Pro Asp Glu Asp Glu Arg Lys Glu Tyr Ile Leu
145                 150                 155                 160
Asn Asp Thr Gly Cys His Tyr Val Gly Ala Ala Arg Ser Ile Lys Cys
                165                 170                 175
Lys Pro Trp Asn Phe Gly Gln Phe Glu Lys Asn Val Leu Asp Cys Cys
            180                 185                 190
Ile Ser Leu Leu Thr Glu Ser Ser Leu Lys Pro Thr Asp Arg Arg Asp
        195                 200                 205
Pro Val Leu Val Cys Arg Ala Met Cys Ala Met Met Ser Phe Glu Lys
    210                 215                 220
Gly Gln Gly Val Leu Ile Gly Asn Trp Thr Gly Asp Tyr Glu Gly Gly
225                 230                 235                 240
Thr Ala Pro Tyr Lys Trp Thr Gly Ser Ala Pro Ile Leu Gln Gln Tyr
                245                 250                 255
Tyr Asn Thr Lys Gln Ala Val Cys Phe Gly Gln Cys Trp Val Phe Ala
            260                 265                 270
Gly Ile Leu Thr Thr Val Leu Arg Ala Leu Gly Ile Pro Ala Arg Ser
        275                 280                 285
Val Thr Gly Phe Asp Ser Ala His Asp Thr Glu Arg Asn Leu Thr Val
    290                 295                 300
Asp Thr Tyr Val Asn Glu Asn Gly Glu Lys Ile Thr Ser Met Thr His
305                 310                 315                 320
Asp Ser Val Trp Asn Phe His Val Trp Thr Asp Ala Trp Met Lys Arg
                325                 330                 335
Pro Tyr Asp Gly Trp Gln Ala Val Asp Ala Thr Pro Gln Glu Arg Ser
            340                 345                 350
Gln Gly Val Phe Cys Cys Gly Pro Ser Pro Leu Thr Ala Ile Arg Lys
        355                 360                 365
Gly Asp Ile Phe Ile Val Tyr Asp Thr Arg Phe Val Phe Ser Glu Val
    370                 375                 380
```

```
Asn Gly Asp Arg Leu Ile Trp Leu Val Lys Met Val Asn Gly Gln Glu
385                 390                 395                 400
Glu Leu His Val Ile Ser Met Glu Thr Thr Ser Ile Gly Lys Asn Ile
                405                 410                 415
Ser Thr Lys Ala Val Gly Gln Asp Arg Arg Arg Asp Ile Thr Tyr Glu
            420                 425                 430
Tyr Lys Tyr Pro Glu Gly Ser Ser Glu Glu Arg Gln Val Met Asp His
        435                 440                 445
Ala Phe Leu Leu Leu Ser Ser Glu Arg Glu His Arg Gln Pro Val Lys
    450                 455                 460
Glu Asn Phe Leu His Met Ser Val Gln Ser Asp Asp Val Leu Leu Gly
465                 470                 475                 480
Asn Ser Val Asn Phe Thr Val Ile Leu Lys Arg Lys Thr Ala Ala Leu
                485                 490                 495
Gln Asn Val Asn Ile Leu Gly Ser Phe Glu Leu Gln Leu Tyr Thr Gly
            500                 505                 510
Lys Lys Met Ala Lys Leu Cys Asp Leu Asn Lys Thr Ser Gln Ile Gln
        515                 520                 525
Gly Gln Val Ser Glu Val Thr Leu Thr Leu Asp Ser Lys Thr Tyr Ile
    530                 535                 540
Asn Ser Leu Ala Ile Leu Asp Asp Glu Pro Val Ile Arg Gly Phe Ile
545                 550                 555                 560
Ile Ala Glu Ile Val Glu Ser Lys Glu Ile Met Ala Ser Glu Val Phe
                565                 570                 575
Thr Ser Asn Gln Tyr Pro Glu Phe Ser Ile Glu Leu Pro Asn Thr Gly
            580                 585                 590
Arg Ile Gly Gln Leu Leu Val Cys Asn Cys Ile Phe Lys Asn Thr Leu
        595                 600                 605
Ala Ile Pro Leu Thr Asp Val Lys Phe Ser Leu Glu Ser Leu Gly Ile
    610                 615                 620
Ser Ser Leu Gln Thr Ser Asp His Gly Thr Val Gln Pro Gly Glu Thr
625                 630                 635                 640
Ile Gln Ser Gln Ile Lys Cys Thr Pro Ile Lys Thr Gly Pro Lys Lys
                645                 650                 655
Phe Ile Val Lys Leu Ser Ser Lys Gln Val Lys Glu Ile Asn Ala Gln
            660                 665                 670
Lys Ile Val Leu Ile Thr Lys
        675
```

```
<210> 777
<211> 5668
<212> DNA
<213> Homo sapiens

<400> 777
gtcacttagg aaaaggtgtc ctttcgggca gccgggctca gcatgaggaa cagaaggaat 60
gacactctgg acagcacccg gaccctgtac tccagcgcgt ctcggagcac agacttgtct 120
tacagtgaaa gcgacttggt gaattttatt caagcaaatt ttaagaaacg agaatgtgtc 180
ttctttacca aagattccaa ggccacggag aatgtgtgca agtgtggcta tgcccagagc 240
cagcacatgg aaggcaccca gatcaaccaa agtgagaaat ggaactacaa gaaacacacc 300
aaggaatttc ctaccgacgc ctttggggat attcagtttg agacactggg gaagaaaggg 360
aagtatatac gtctgtcctg cgacacggac gcggaaatcc tttacgagct gctgacccag 420
cactggcacc tgaaaacacc caacctggtc atttctgtga ccgggggcgc caagaacttc 480
gccctgaagc cgcgcatgcg caagatcttc agccggctca tctacatcgc gcagtccaaa 540
ggtgcttgga ttctcacggg aggcacccat tatggcctga cgaagtacat cggggaggtg 600
gtgagagata acaccatcag caggagttca gaggagaata ttgtggccat tggcatagca 660
gcttggggca tggtctccaa ccgggacacc ctcatcagga attgcgatgc tgagggctat 720
```

```
tttttagccc agtaccttat ggatgacttc acaagggatc cactgtatat cctggacaac 780
aaccacacac atttgctgct cgtggacaat ggctgtcatg gacatcccac tgtcgaagca 840
aagctccgga atcagctaga gaagcatatc tctgagcgca ctattcaaga ttccaactat 900
ggtggcaaga tccccattgt gtgttttgcc caaggaggtg gaaaagagac tttgaaagcc 960
atcaataccт ccatcaaaaa taaaattcct tgtgtggtgg tggaaggctc gggccggatc 1020
gctgatgtga tcgctagcct ggtggaggtg gaggatgccc cgacatcttc tgccgtcaag 1080
gagaagctgg tgcgcttttt accccgcacg gtgtcccggc tgtctgagga ggagactgag 1140
agttggatca aatggctcaa agaaattctc gaatgttctc acctattaac agttattaaa 1200
atggaagaag ctggggatga aattgtgagc aatgccatct cctacgctct atacaaagcc 1260
ttcagcacca gtgagcaaga caaggataac tggaatgggc agctgaagct tctgctggag 1320
tggaaccagc tggacttagc caatgatgag attttcacca atgaccgccg atgggagtct 1380
gctgaccttc aagaagtcat gtttacggct ctcataaagg acagacccaa gtttgtccgc 1440
ctctttctgg agaatggctt gaacctacgg aagtttctca cccatgatgt cctcactgaa 1500
ctcttctcca accacttcag cacgcttgtg taccggaatc tgcagatcgc caagaattcc 1560
tataatgatg ccctcctcac gtttgtctgg aaactggttg cgaacttccg aagaggcttc 1620
cggaaggaag acagaaatgg ccgggacgag atggacatag aactccacga cgtgtctcct 1680
attactcggc acccccctgca agctctcttc atctgggcca ttcttcagaa taagaaggaa 1740
ctctccaaag tcatttggga gcagaccagg ggctgcactc tggcagccct gggagccagc 1800
aagcttctga agactctggc caaagtgaag aacgacatca atgctgctgg ggagtccgag 1860
gagctggcta atgagtacga gacccgggct gttgagctgt tcactgagtg ttacagcagc 1920
gatgaagact tggcagaaca gctgctggtc tattcctgtg aagcttgggg tggaagcaac 1980
tgtctggagc tggcggtgga ggccacagac cagcatttca ccgcccagcc tggggtccag 2040
aatttcttt ctaagcaatg gtatggagag atttcccgag acaccaagaa ctggaagatt 2100
atcctgtgtc tgtttattat acccttggtg ggctgtggct ttgtatcatt taggaagaaa 2160
cctgtcgaca agcacaagaa gctgctttgg tactatgtgg cgttcttcac ctcccccttc 2220
gtggtcttct cctggaatgt ggtcttctac atcgccttcc tcctgctgtt tgcctacgtg 2280
ctgctcatgg atttccattc ggtgccacac ccccccgagc tggtcctgta ctcgctggtc 2340
tttgtcctct tctgtgatga agtgagacag tggtacgtaa atggggtgaa ttattttact 2400
gacctgtgga atgtgatgga cacgctgggg ctttttttact tcatagcagg aattgtattt 2460
cggctccact cttctaataa aagctctttg tattctggac gagtcatttt ctgtctggac 2520
tacattattt tcactctaag attgatccac atttttactg taagcagaaa cttaggaccc 2580
aagattataa tgctgcagag gatgctgatc gatgtgttct tcttcctgtt cctctttgcg 2640
gtgtggatgg tggcctttgg cgtggccagg caagggatcc ttaggcagaa tgagcagcgc 2700
tggaggtgga tattccgttc ggtcatctac gagccctacc tggccatgtt cggccaggtg 2760
cccagtgacg tggatggtac cacgtatgac tttgcccact gcaccttcac tgggaatgag 2820
tccaagccac tgtgtgtgga gctggatgag cacaacctgc cccggttccc cgagtggatc 2880
accatccccc tggtgtgcat ctacatgtta tccaccaaca tcctgctggt caacctgctg 2940
gtcgccatgt ttggctacac ggtgggcacc gtccaggaga acaatgacca ggtctggaag 3000
ttccagaggt acttcctggt gcaggagtac tgcagccgcc tcaatatccc cttccccttc 3060
atcgtcttcg cttacttcta catggtggtg aagaagtgct tcaagtgttg ctgcaaggag 3120
aaaaacatgg agtcttctgt ctgctgtttc aaaaatgaag acaatgagac tctggcatgg 3180
gagggtgtca tgaaggaaaa ctaccttgtc aagatcaaca caaaagccaa cgacacctca 3240
gaggaaatga ggcatcgatt tagacaactg gatacaaagc ttaatgatct caagggtctt 3300
ctgaaagaga ttgctaataa aatcaaataa aactgtatga aactctaatg gagaaaaatc 3360
taattatagc aagatcatat taaggaatgc tgatgaacaa ttttgctatc gactactaaa 3420
tgagagattt tcagacccct gggtacatgg tggatgattt taaatcaccc tagtgtgctg 3480
agaccttgag aataaagtgt gtgattggtt tcatacttga agacggatat aaaggaagaa 3540
tatttccttt atgtgtttct ccagaatggt gcctgtttct ctctgtgtct caatgcctgg 3600
gactggaggt tgatagttta agtgtgttct taccgcctcc tttttccttt aatcttattt 3660
ttgatgaaca catatatagg agaacatcta tcctatgaat aagaacctgg tcatgcttta 3720
ctcctgtatt gttattttgt tcatttccaa ttgattctct acttttccct tttttgtatt 3780
atgtgactaa ttagttggca tattgttaaa agtctctcaa attaggccag attctaaaac 3840
atgctgcagc aagaggaccc cgctctcttc aggaaaagtg ttttcatttc tcaggatgct 3900
tcttacctgt cagaggaggt gacaaggcag tctcttgctc tcttggactc accaggctcc 3960
tattgaagga accacccccca ttcctaaata tgtgaaaagt cgcccaaaat gcaaccttga 4020
aaggcactac tgactttgtt cttattggat actcctctta tttattattt ttccattaaa 4080
aataatagct ggctattata gaaaatttag accatacaga gatgtagaaa gaacataaat 4140
tgtccccatt accttaaggt aatcactgct aacaatttct ggatggtttt tcaagtctat 4200
```

```
tttttttcta tgtatgtctc aattctcttt caaaatttta cagaatgtta tcatactaca 4260
tatatacttt ttatgtaagc tttttcactt agtattttat caaatatgtt tttattatat 4320
tcatagcctt cttaaacatt atatcaataa ttgcataata ggcaacctct agcgattacc 4380
ataattttgc tcattgaagg ctatctccag ttgatcattg ggatgagcat ctttgtgcat 4440
gaatcctatt gctgtatttg ggaaaatttt ccaaggttag attccaataa atatctattt 4500
attattaaat attaaaatat cgatttatta ttaaaaccat ttataaggct ttttcataaa 4560
tgtatagcaa ataggaatta ttaacttgag cataagatat gagatacatg aacctgaact 4620
attaaaataa aatattatat ttaaccctag tttaagaaga agtcaatatg cttatttaaa 4680
tattatggat ggtgggcaga tcacttgagg tcaggagttc gagaccagcc tggccaacat 4740
ggcaaaacca catctctact aaaaataaaa aaattagctg ggtgtggtgg tgcactcctg 4800
taatcccagc tactcagaag gctgaggtac aagaattgct ggaacctggg aggcggaggt 4860
tgcagtgaac caagattgca ccactgcact ccagcccggg tgacagagtg agactccgac 4920
tgaaaataaa taaataaata aataaataaa taaataaata aatattatgg atggtgaagg 4980
gaatggtata gaattggaga gattatctta ctgaacacct gtagtcccag ctttctctgg 5040
aagtggtggt atttgagcag gatgtgcaca aggcaattga aatgcccata attagtttct 5100
cagctttgaa tacactataa actcagtggc tgaaggagga aattttagaa ggaagctact 5160
aaaagatcta atttgaaaaa ctacaaaagc attaactaaa aaagtttatt ttcctttgt 5220
ctgggcagta gtgaaaataa ctactcacaa cattcactat gtttgcaagg aattaacaca 5280
aataaaagat gcctttttac ttaaacgcca agacagaaaa cttgcccaat actgagaagc 5340
aacttgcatt agagagggaa ctgttaaatg ttttcaaccc agttcatctg gtggatgttt 5400
ttgcaggtta ctctgagaat tttgcttatg aaaaatcatt atttttagtg tagttcacaa 5460
taatgtattg aacatacttc taatcaaagg tgctatgtcc ttgtgtatgg tactaaatgt 5520
gtcctgtgta cttttgcaca actgagaatc ctgcggcttg gtttaatgag tgtgttcatg 5580
aaataaataa tggaggaatt gtcaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 5640
aaaaaaaaaa aaaaaaaaaa aaaaaaa                                     5668
```

<210> 778
<211> 1095
<212> PRT
<213> Homo sapiens

<400> 778

```
Met Arg Asn Arg Arg Asn Asp Thr Leu Asp Ser Thr Arg Thr Leu Tyr
                5                   10                  15
Ser Ser Ala Ser Arg Ser Thr Asp Leu Ser Tyr Ser Glu Ser Asp Leu
            20                  25                  30
Val Asn Phe Ile Gln Ala Asn Phe Lys Lys Arg Glu Cys Val Phe Phe
        35                  40                  45
Thr Lys Asp Ser Lys Ala Thr Glu Asn Val Cys Lys Cys Gly Tyr Ala
    50                  55                  60
Gln Ser Gln His Met Glu Gly Thr Gln Ile Asn Gln Ser Glu Lys Trp
65                  70                  75                  80
Asn Tyr Lys Lys His Thr Lys Glu Phe Pro Thr Asp Ala Phe Gly Asp
                85                  90                  95
Ile Gln Phe Glu Thr Leu Gly Lys Lys Gly Lys Tyr Ile Arg Leu Ser
            100                 105                 110
Cys Asp Thr Asp Ala Glu Ile Leu Tyr Glu Leu Leu Thr Gln His Trp
        115                 120                 125
His Leu Lys Thr Pro Asn Leu Val Ile Ser Val Thr Gly Gly Ala Lys
    130                 135                 140
Asn Phe Ala Leu Lys Pro Arg Met Arg Lys Ile Phe Ser Arg Leu Ile
145                 150                 155                 160
Tyr Ile Ala Gln Ser Lys Gly Ala Trp Ile Leu Thr Gly Gly Thr His
                165                 170                 175
Tyr Gly Leu Thr Lys Tyr Ile Gly Glu Val Val Arg Asp Asn Thr Ile
            180                 185                 190
Ser Arg Ser Ser Glu Glu Asn Ile Val Ala Ile Gly Ile Ala Ala Trp
        195                 200                 205
```

```
Gly Met Val Ser Asn Arg Asp Thr Leu Ile Arg Asn Cys Asp Ala Glu
    210                 215                 220
Gly Tyr Phe Leu Ala Gln Tyr Leu Met Asp Asp Phe Thr Arg Asp Pro
225                 230                 235                 240
Leu Tyr Ile Leu Asp Asn Asn His Thr His Leu Leu Leu Val Asp Asn
                245                 250                 255
Gly Cys His Gly His Pro Thr Val Glu Ala Lys Leu Arg Asn Gln Leu
            260                 265                 270
Glu Lys His Ile Ser Glu Arg Thr Ile Gln Asp Ser Asn Tyr Gly Gly
        275                 280                 285
Lys Ile Pro Ile Val Cys Phe Ala Gln Gly Gly Gly Lys Glu Thr Leu
    290                 295                 300
Lys Ala Ile Asn Thr Ser Ile Lys Asn Lys Ile Pro Cys Val Val Val
305                 310                 315                 320
Glu Gly Ser Gly Arg Ile Ala Asp Val Ile Ala Ser Leu Val Glu Val
                325                 330                 335
Glu Asp Ala Pro Thr Ser Ser Ala Val Lys Glu Lys Leu Val Arg Phe
            340                 345                 350
Leu Pro Arg Thr Val Ser Arg Leu Ser Glu Glu Glu Thr Glu Ser Trp
        355                 360                 365
Ile Lys Trp Leu Lys Glu Ile Leu Glu Cys Ser His Leu Leu Thr Val
    370                 375                 380
Ile Lys Met Glu Glu Ala Gly Asp Glu Ile Val Ser Asn Ala Ile Ser
385                 390                 395                 400
Tyr Ala Leu Tyr Lys Ala Phe Ser Thr Ser Glu Gln Asp Lys Asp Asn
                405                 410                 415
Trp Asn Gly Gln Leu Lys Leu Leu Leu Glu Trp Asn Gln Leu Asp Leu
            420                 425                 430
Ala Asn Asp Glu Ile Phe Thr Asn Asp Arg Arg Trp Glu Ser Ala Asp
        435                 440                 445
Leu Gln Glu Val Met Phe Thr Ala Leu Ile Lys Asp Arg Pro Lys Phe
    450                 455                 460
Val Arg Leu Phe Leu Glu Asn Gly Leu Asn Leu Arg Lys Phe Leu Thr
465                 470                 475                 480
His Asp Val Leu Thr Glu Leu Phe Ser Asn His Phe Ser Thr Leu Val
                485                 490                 495
Tyr Arg Asn Leu Gln Ile Ala Lys Asn Ser Tyr Asn Asp Ala Leu Leu
            500                 505                 510
Thr Phe Val Trp Lys Leu Val Ala Asn Phe Arg Arg Gly Phe Arg Lys
        515                 520                 525
Glu Asp Arg Asn Gly Arg Asp Glu Met Asp Ile Glu Leu His Asp Val
    530                 535                 540
Ser Pro Ile Thr Arg His Pro Leu Gln Ala Leu Phe Ile Trp Ala Ile
545                 550                 555                 560
Leu Gln Asn Lys Lys Glu Leu Ser Lys Val Ile Trp Glu Gln Thr Arg
                565                 570                 575
Gly Cys Thr Leu Ala Ala Leu Gly Ala Ser Lys Leu Leu Lys Thr Leu
            580                 585                 590
Ala Lys Val Lys Asn Asp Ile Asn Ala Ala Gly Glu Ser Glu Glu Leu
        595                 600                 605
Ala Asn Glu Tyr Glu Thr Arg Ala Val Glu Leu Phe Thr Glu Cys Tyr
    610                 615                 620
Ser Ser Asp Glu Asp Leu Ala Glu Gln Leu Leu Val Tyr Ser Cys Glu
625                 630                 635                 640
Ala Trp Gly Gly Ser Asn Cys Leu Glu Leu Ala Val Glu Ala Thr Asp
                645                 650                 655
Gln His Phe Thr Ala Gln Pro Gly Val Gln Asn Phe Leu Ser Lys Gln
            660                 665                 670
```

```
Trp Tyr Gly Glu Ile Ser Arg Asp Thr Lys Asn Trp Lys Ile Ile Leu
        675                 680                 685
Cys Leu Phe Ile Ile Pro Leu Val Gly Cys Gly Phe Val Ser Phe Arg
    690                 695                 700
Lys Lys Pro Val Asp Lys His Lys Lys Leu Leu Trp Tyr Tyr Val Ala
705                 710                 715                 720
Phe Phe Thr Ser Pro Phe Val Val Phe Ser Trp Asn Val Val Phe Tyr
                725                 730                 735
Ile Ala Phe Leu Leu Leu Phe Ala Tyr Val Leu Leu Met Asp Phe His
            740                 745                 750
Ser Val Pro His Pro Pro Glu Leu Val Leu Tyr Ser Leu Val Phe Val
        755                 760                 765
Leu Phe Cys Asp Glu Val Arg Gln Trp Tyr Val Asn Gly Val Asn Tyr
    770                 775                 780
Phe Thr Asp Leu Trp Asn Val Met Asp Thr Leu Gly Leu Phe Tyr Phe
785                 790                 795                 800
Ile Ala Gly Ile Val Phe Arg Leu His Ser Ser Asn Lys Ser Ser Leu
                805                 810                 815
Tyr Ser Gly Arg Val Ile Phe Cys Leu Asp Tyr Ile Ile Phe Thr Leu
            820                 825                 830
Arg Leu Ile His Ile Phe Thr Val Ser Arg Asn Leu Gly Pro Lys Ile
        835                 840                 845
Ile Met Leu Gln Arg Met Leu Ile Asp Val Phe Phe Phe Leu Phe Leu
    850                 855                 860
Phe Ala Val Trp Met Val Ala Phe Gly Val Ala Arg Gln Gly Ile Leu
865                 870                 875                 880
Arg Gln Asn Glu Gln Arg Trp Arg Trp Ile Phe Arg Ser Val Ile Tyr
                885                 890                 895
Glu Pro Tyr Leu Ala Met Phe Gly Gln Val Pro Ser Asp Val Asp Gly
            900                 905                 910
Thr Thr Tyr Asp Phe Ala His Cys Thr Phe Thr Gly Asn Glu Ser Lys
        915                 920                 925
Pro Leu Cys Val Glu Leu Asp Glu His Asn Leu Pro Arg Phe Pro Glu
    930                 935                 940
Trp Ile Thr Ile Pro Leu Val Cys Ile Tyr Met Leu Ser Thr Asn Ile
945                 950                 955                 960
Leu Leu Val Asn Leu Leu Val Ala Met Phe Gly Tyr Thr Val Gly Thr
                965                 970                 975
Val Gln Glu Asn Asn Asp Gln Val Trp Lys Phe Gln Arg Tyr Phe Leu
            980                 985                 990
Val Gln Glu Tyr Cys Ser Arg Leu Asn Ile Pro Phe Pro Phe Ile Val
        995                 1000                1005
Phe Ala Tyr Phe Tyr Met Val Val Lys Lys Cys Phe Lys Cys Cys Cys
    1010                1015                1020
Lys Glu Lys Asn Met Glu Ser Ser Val Cys Cys Phe Lys Asn Glu Asp
1025                1030                1035                1040
Asn Glu Thr Leu Ala Trp Glu Gly Val Met Lys Glu Asn Tyr Leu Val
                1045                1050                1055
Lys Ile Asn Thr Lys Ala Asn Asp Thr Ser Glu Glu Met Arg His Arg
            1060                1065                1070
Phe Arg Gln Leu Asp Thr Lys Leu Asn Asp Leu Lys Gly Leu Leu Lys
        1075                1080                1085
Glu Ile Ala Asn Lys Ile Lys
    1090                1095
```

<210> 779
<211> 3639

<212> DNA
<213> Homo sapiens

<400> 779
gattacgcaa gctatttagg tgacactata gaatwctcag cttgcatcaa gcttggtacc 60
gagctcggat ccctagtaac ggccgccagt gtgctggaat tcgcccttgc agccgggctc 120
agcatgagga acagaaggaa tgacactctg gacagcaccc ggaccctgta ctccagcgcg 180
tctcggagca cagacttgtc ttacagtgaa agcgacttgg tgaattttat tcaagcaaat 240
tttaagaaac gagaatgtgt cttctttacc aaagattcca aggccacgga gaatgtgtgc 300
aagtgtggct atgcccagag ccagcacatg gaaggcaccc agatcaacca aagtgagaaa 360
tggaactaca agaaacacac caaggaattt cctaccgacg cctttgggga tattcagttt 420
gagacactgg ggaagaaagg gaagtatata cgtctgtcct gcgacacgga cgcggaaatc 480
ctttacgagc tgctgaccca gcactggcac ctgaaaacac ccaacctggt catttctgtg 540
accgggggcg ccaagaactt cgccctgaag ccgcgcatgc gcaagatctt cagccggctc 600
atctacatcg cgcagtccaa aggtgcttgg attctcacgg gaggcaccca ttatggcctg 660
atgaagtaca tcggggaggt ggtgagagat aacaccatca gcaggagttc agaggagaat 720
attgtggcca ttggcatagc agcttggggc atggtctcca accgggacac cctcatcagg 780
aattgcgatg ctgagggcta ttttttagcc cagtacctta tggatgactt cacaagagat 840
ccactgtata tcctggacaa caaccacaca catttgctgc tcgtggacaa tggctgtcat 900
ggacatccca ctgtcgaagc aaagctccgg aatcagctag agaagtatat ctctgagcgc 960
actattcaag attccaacta tggtggcaag atccccattg tgtgttttgc ccaaggaggt 1020
ggaaaagaga ctttgaaagc catcaatacc tccatcaaaa ataaaattcc ttgtgtggtg 1080
gtggaaggct cgggccagat cgctgatgtg atcgctagcc tggtggaggt ggaggatgcc 1140
ctgacatctt ctgccgtcaa ggagaagctg gtgcgctttt taccccgcac ggtgtcccgg 1200
ctgcctgagg aggagactga gagttggatc aaatggctca aagaaattct cgaatgttct 1260
cacctattaa cagttattaa aatggaagaa gctggggatg aaattgtgag caatgccatc 1320
tcctacgctc tatacaaagc cttcagcacc agtgagcaag acaaggataa ctggaatggg 1380
cagctgaagc ttctgctgga gtggaaccag ctggacttag ccaatgatga gattttcacc 1440
aatgaccgcc gatgggagtc tgctgacctt caagaagtca tgtttacggc tctcataaag 1500
gacagaccca agtttgtccg cctctttctg gagaatggct tgaacctacg gaagtttctc 1560
acccatgatg tcctcactga actcttctcc aaccacttca gcacgcttgt gtaccggaat 1620
ctgcagatcg ccaagaattc ctataatgat gccctcctca cgtttgtctg gaaactggtt 1680
gcgaacttcc gaagaggctt ccggaaggaa gacagaaatg gccgggacga gatggacata 1740
gaactccacg acgtgtctcc tattactcgg cacccccctgc aagctctctt catctgggcc 1800
attcttcaga ataagaagga actctccaaa gtcatttggg agcagaccag ggggctgcact 1860
ctggcagccc tgggagccag caagcttctg aagactctgg ccaaagtgaa gaacgacatc 1920
aatgctgctg gggagtccga ggagctggct aatgagtacg agacccgggc tgttgagctg 1980
ttcactgagt gttacagcag cgatgaagac ttggcagaac agctgctggt ctattcctgt 2040
gaagcttggg gtggaagcaa ctgtctggag ctggcggtgg aggccacaga ccagcatttc 2100
atcgcccagc ctggggtcca gaattttctt tctaagcaat ggtatggaga gatttcccga 2160
gacaccaaga actggaagat tatcctgtgt ctgtttatta taccccttggt gggctgtggc 2220
tttgtatcat ttaggaagaa acctgtcgac aagcacaaga agctgctttg gtactatgtg 2280
gcgttcttca cctcccccctt cgtggtcttc tcctggaatg tggtcttcta catcgccttc 2340
ctcctgctgt ttgcctacgt gctgctcatg gatttccatt cggtgccaca cccccccgag 2400
ctggtcctgt actcgctggt ctttgtcctc ttctgtgatg aagtgagaca gtggtacgta 2460
aatggggtga attattttac tgacctgtgg aatgtgatgg acacgctggg gctttttttac 2520
ttcatagcag gaattgtatt tcggctccac tcttctaata aaagctcttt gtattctgga 2580
cgagtcattt tctgtctgga ctacattatt ttcactctaa gattgatcca catttttact 2640
gtaagcagaa acttaggacc caagattata atgctgcaga ggatgctgat cgatgtgttc 2700
ttcttcctgt tcctctttgc ggwgtggatg gtggcctttg gcgtggccag gcaagggatc 2760
cttaggcaga atgagcagcg ctggaggtgg atattccgtt cggtcatcta cgagccctac 2820
ctggccatgt tcggccaggt gcccagtgac gtggatggta ccacgtatga ctttgcccac 2880
tgcaccttca ctgggaatga gtccaagcca ctgtgtgtgg agctggatga gcacaacctg 2940
ccccggttcc ccgagtggat caccatcccc ctggtgtgca tctacatgtt atccaccaac 3000
atcctgctgg tcaacctgct ggtcgccatg tttggctaca cggtgggcac cgtccaggag 3060
aacaatgacc aggtctggaa gttccagagg tacttcctgg tgcaggagta ctgcagccgc 3120
ctcaatatcc ccttcccctt catcgtcttc gcttacttct acatggtggt gaagaagtgc 3180
ttcaagtgtt gctgcaagga gaaaaacatg gagtcttctg tctgctgttt caaaaatgaa 3240

```
gacaatgaga ctctggcatg ggagggtgtc atgaaggaaa actaccttgt caagatcaac 3300
acaaaagcca acgacacctc agaggaaatg aggcatcgat ttagacaact ggatacaaag 3360
cttaatgatc tcaagggtct tctgaaagag attgctaata aaatcaaata aaactgtatg 3420
aactctaatg gagaaaaatc taattatagc aagatcatat taaggaatgc tgatgaacaa 3480
ttttgctatc gactactaaa tgagagattt tcagacccct gggtacatgg tggatgattt 3540
taaatcaccc tagtgtgctg agaccttgag aataaagtgt gaagggcgaa ttctgcagat 3600
atccatcaca ctggcggccg ctcgagcatg catctagag                        3639

&lt;210&gt; 780
&lt;211&gt; 1095
&lt;212&gt; PRT
&lt;213&gt; Homo sapiens

&lt;220&gt;
&lt;221&gt; VARIANT
&lt;222&gt; (1)...(1095)
&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 780
Met Arg Asn Arg Arg Asn Asp Thr Leu Asp Ser Thr Arg Thr Leu Tyr
                 5                  10                  15
Ser Ser Ala Ser Arg Ser Thr Asp Leu Ser Tyr Ser Glu Ser Asp Leu
            20                  25                  30
Val Asn Phe Ile Gln Ala Asn Phe Lys Lys Arg Glu Cys Val Phe Phe
        35                  40                  45
Thr Lys Asp Ser Lys Ala Thr Glu Asn Val Cys Lys Cys Gly Tyr Ala
    50                  55                  60
Gln Ser Gln His Met Glu Gly Thr Gln Ile Asn Gln Ser Glu Lys Trp
65                  70                  75                  80
Asn Tyr Lys Lys His Thr Lys Glu Phe Pro Thr Asp Ala Phe Gly Asp
                85                  90                  95
Ile Gln Phe Glu Thr Leu Gly Lys Lys Gly Lys Tyr Ile Arg Leu Ser
            100                 105                 110
Cys Asp Thr Asp Ala Glu Ile Leu Tyr Glu Leu Leu Thr Gln His Trp
        115                 120                 125
His Leu Lys Thr Pro Asn Leu Val Ile Ser Val Thr Gly Gly Ala Lys
    130                 135                 140
Asn Phe Ala Leu Lys Pro Arg Met Arg Lys Ile Phe Ser Arg Leu Ile
145                 150                 155                 160
Tyr Ile Ala Gln Ser Lys Gly Ala Trp Ile Leu Thr Gly Gly Thr His
                165                 170                 175
Tyr Gly Leu Met Lys Tyr Ile Gly Glu Val Val Arg Asp Asn Thr Ile
            180                 185                 190
Ser Arg Ser Ser Glu Glu Asn Ile Val Ala Ile Gly Ile Ala Ala Trp
        195                 200                 205
Gly Met Val Ser Asn Arg Asp Thr Leu Ile Arg Asn Cys Asp Ala Glu
    210                 215                 220
Gly Tyr Phe Leu Ala Gln Tyr Leu Met Asp Asp Phe Thr Arg Asp Pro
225                 230                 235                 240
Leu Tyr Ile Leu Asp Asn Asn His Thr His Leu Leu Leu Val Asp Asn
                245                 250                 255
Gly Cys His Gly His Pro Thr Val Glu Ala Lys Leu Arg Asn Gln Leu
            260                 265                 270
Glu Lys Tyr Ile Ser Glu Arg Thr Ile Gln Asp Ser Asn Tyr Gly Gly
        275                 280                 285
Lys Ile Pro Ile Val Cys Phe Ala Gln Gly Gly Gly Lys Glu Thr Leu
    290                 295                 300
Lys Ala Ile Asn Thr Ser Ile Lys Asn Lys Ile Pro Cys Val Val Val
```

305 310 315 320
Glu Gly Ser Gly Gln Ile Ala Asp Val Ile Ala Ser Leu Val Glu Val
325 330 335
Glu Asp Ala Leu Thr Ser Ser Ala Val Lys Glu Lys Leu Val Arg Phe
340 345 350
Leu Pro Arg Thr Val Ser Arg Leu Pro Glu Glu Glu Thr Glu Ser Trp
355 360 365
Ile Lys Trp Leu Lys Glu Ile Leu Glu Cys Ser His Leu Leu Thr Val
370 375 380
Ile Lys Met Glu Glu Ala Gly Asp Glu Ile Val Ser Asn Ala Ile Ser
385 390 395 400
Tyr Ala Leu Tyr Lys Ala Phe Ser Thr Ser Glu Gln Asp Lys Asp Asn
405 410 415
Trp Asn Gly Gln Leu Lys Leu Leu Leu Glu Trp Asn Gln Leu Asp Leu
420 425 430
Ala Asn Asp Glu Ile Phe Thr Asn Asp Arg Arg Trp Glu Ser Ala Asp
435 440 445
Leu Gln Glu Val Met Phe Thr Ala Leu Ile Lys Asp Arg Pro Lys Phe
450 455 460
Val Arg Leu Phe Leu Glu Asn Gly Leu Asn Leu Arg Lys Phe Leu Thr
465 470 475 480
His Asp Val Leu Thr Glu Leu Phe Ser Asn His Phe Ser Thr Leu Val
485 490 495
Tyr Arg Asn Leu Gln Ile Ala Lys Asn Ser Tyr Asn Asp Ala Leu Leu
500 505 510
Thr Phe Val Trp Lys Leu Val Ala Asn Phe Arg Arg Gly Phe Arg Lys
515 520 525
Glu Asp Arg Asn Gly Arg Asp Glu Met Asp Ile Glu Leu His Asp Val
530 535 540
Ser Pro Ile Thr Arg His Pro Leu Gln Ala Leu Phe Ile Trp Ala Ile
545 550 555 560
Leu Gln Asn Lys Lys Glu Leu Ser Lys Val Ile Trp Glu Gln Thr Arg
565 570 575
Gly Cys Thr Leu Ala Ala Leu Gly Ala Ser Lys Leu Leu Lys Thr Leu
580 585 590
Ala Lys Val Lys Asn Asp Ile Asn Ala Ala Gly Glu Ser Glu Glu Leu
595 600 605
Ala Asn Glu Tyr Glu Thr Arg Ala Val Glu Leu Phe Thr Glu Cys Tyr
610 615 620
Ser Ser Asp Glu Asp Leu Ala Glu Gln Leu Leu Val Tyr Ser Cys Glu
625 630 635 640
Ala Trp Gly Gly Ser Asn Cys Leu Glu Leu Ala Val Glu Ala Thr Asp
645 650 655
Gln His Phe Ile Ala Gln Pro Gly Val Gln Asn Phe Leu Ser Lys Gln
660 665 670
Trp Tyr Gly Glu Ile Ser Arg Asp Thr Lys Asn Trp Lys Ile Ile Leu
675 680 685
Cys Leu Phe Ile Ile Pro Leu Val Gly Cys Gly Phe Val Ser Phe Arg
690 695 700
Lys Lys Pro Val Asp Lys His Lys Lys Leu Leu Trp Tyr Tyr Val Ala
705 710 715 720
Phe Phe Thr Ser Pro Phe Val Val Phe Ser Trp Asn Val Val Phe Tyr
725 730 735
Ile Ala Phe Leu Leu Leu Phe Ala Tyr Val Leu Leu Met Asp Phe His
740 745 750
Ser Val Pro His Pro Pro Glu Leu Val Leu Tyr Ser Leu Val Phe Val
755 760 765
Leu Phe Cys Asp Glu Val Arg Gln Trp Tyr Val Asn Gly Val Asn Tyr

```
    770                 775                 780
Phe Thr Asp Leu Trp Asn Val Met Asp Thr Leu Gly Leu Phe Tyr Phe
785                 790                 795                 800
Ile Ala Gly Ile Val Phe Arg Leu His Ser Ser Asn Lys Ser Ser Leu
                805                 810                 815
Tyr Ser Gly Arg Val Ile Phe Cys Leu Asp Tyr Ile Ile Phe Thr Leu
            820                 825                 830
Arg Leu Ile His Ile Phe Thr Val Ser Arg Asn Leu Gly Pro Lys Ile
        835                 840                 845
Ile Met Leu Gln Arg Met Leu Ile Asp Val Phe Phe Phe Leu Phe Leu
    850                 855                 860
Phe Ala Xaa Trp Met Val Ala Phe Gly Val Ala Arg Gln Gly Ile Leu
865                 870                 875                 880
Arg Gln Asn Glu Gln Arg Trp Arg Trp Ile Phe Arg Ser Val Ile Tyr
                885                 890                 895
Glu Pro Tyr Leu Ala Met Phe Gly Gln Val Pro Ser Asp Val Asp Gly
            900                 905                 910
Thr Thr Tyr Asp Phe Ala His Cys Thr Phe Thr Gly Asn Glu Ser Lys
        915                 920                 925
Pro Leu Cys Val Glu Leu Asp Glu His Asn Leu Pro Arg Phe Pro Glu
    930                 935                 940
Trp Ile Thr Ile Pro Leu Val Cys Ile Tyr Met Leu Ser Thr Asn Ile
945                 950                 955                 960
Leu Leu Val Asn Leu Leu Val Ala Met Phe Gly Tyr Thr Val Gly Thr
                965                 970                 975
Val Gln Glu Asn Asn Asp Gln Val Trp Lys Phe Gln Arg Tyr Phe Leu
            980                 985                 990
Val Gln Glu Tyr Cys Ser Arg Leu Asn Ile Pro Phe Pro Phe Ile Val
        995                 1000                1005
Phe Ala Tyr Phe Tyr Met Val Val Lys Lys Cys Phe Lys Cys Cys Cys
    1010                1015                1020
Lys Glu Lys Asn Met Glu Ser Ser Val Cys Cys Phe Lys Asn Glu Asp
1025                1030                1035                1040
Asn Glu Thr Leu Ala Trp Glu Gly Val Met Lys Glu Asn Tyr Leu Val
                1045                1050                1055
Lys Ile Asn Thr Lys Ala Asn Asp Thr Ser Glu Glu Met Arg His Arg
            1060                1065                1070
Phe Arg Gln Leu Asp Thr Lys Leu Asn Asp Leu Lys Gly Leu Leu Lys
        1075                1080                1085
Glu Ile Ala Asn Lys Ile Lys
    1090                1095
```

<210> 781
<211> 15
<212> PRT
<213> Homo sapiens

<400> 781

```
Arg Met Pro Thr Val Leu Gln Cys Val Asn Val Ser Val Val Ser
                5                   10                  15
```

<210> 782
<211> 45
<212> DNA
<213> Homo sapiens

<400> 782

agaatgccta ccgtgctgca gtgcgtgaac gtgtcggtgg tgtct 45

<210> 783
<211> 45
<212> DNA
<213> Homo sapiens

<400> 783
gagccaggga gccagatggt ggaggccagc ctctccgtac ggcac 45

<210> 784
<211> 45
<212> DNA
<213> Homo sapiens

<400> 784
gaggccgacc aagagccagg gagccagatg gtggaggcca gcctc 45

<210> 785
<211> 45
<212> DNA
<213> Homo sapiens

<400> 785
ggcctgcaca gtcttgaggc cgaccaagag ccagggagcc agatg 45

<210> 786
<211> 45
<212> DNA
<213> Homo sapiens

<400> 786
tacaccatcg ggctgggcct gcacagtctt gaggccgacc aagag 45

<210> 787
<211> 42
<212> DNA
<213> Homo sapiens

<400> 787
ttccagaact cctacaccat cgggctgggc ctgcacagtc tt 42

<210> 788
<211> 45
<212> DNA
<213> Homo sapiens

<400> 788
ctgtcagccg cacactgttt ccagaactcc tacaccatcg ggctg 45

<210> 789
<211> 45
<212> DNA
<213> Homo sapiens

<400> 789
catccgcagt gggtgctgtc agccgcacac tgtttccaga actcc 45

<210> 790
<211> 45
<212> DNA
<213> Homo sapiens

<400> 790
tcgggcgtcc tggtgcatcc gcagtgggtg ctgtcagccg cacac 45

<210> 791
<211> 45
<212> DNA
<213> Homo sapiens

<400> 791
aacgaattgt tctgctcggg cgtcctggtg catccgcagt gggtg 45

<210> 792
<211> 45
<212> DNA
<213> Homo sapiens

<400> 792
gcactggtca tggaaaacga attgttctgc tcgggcgtcc tggtg 45

<210> 793
<211> 51
<212> DNA
<213> Homo sapiens

<400> 793
tcgcagccct ggcaggcggc actggtcatg gaaaacgaat tgttctgctc g 51

<210> 794
<211> 45
<212> DNA
<213> Homo sapiens

<400> 794
atcagcattg cttcgcagtg ccctaccgcg ggaactctt gcctc 45

<210> 795
<211> 45
<212> DNA
<213> Homo sapiens

<400> 795
tccgtgtccg agtctgacac catccggagc atcagcattg cttcg 45

<210> 796
<211> 45
<212> DNA
<213> Homo sapiens

<400> 796
atcaagttgg acgaatccgt gtccgagtct gacaccatcc ggagc 45

<210> 797

<211> 45
<212> DNA
<213> Homo sapiens

<400> 797
aacgacctca tgctcatcaa gttggacgaa tccgtgtccg agtct 45

<210> 798
<211> 45
<212> DNA
<213> Homo sapiens

<400> 798
agacccttgc tcgctaacga cctcatgctc atcaagttgg acgaa 45

<210> 799
<211> 15
<212> PRT
<213> Homo sapiens

<400> 799
Glu Pro Gly Ser Gln Met Val Glu Ala Ser Leu Ser Val Arg His
5 10 15

<210> 800
<211> 15
<212> PRT
<213> Homo sapiens

<400> 800
Glu Ala Asp Gln Glu Pro Gly Ser Gln Met Val Glu Ala Ser Leu
5 10 15

<210> 801
<211> 15
<212> PRT
<213> Homo sapiens

<400> 801
Gly Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met
5 10 15

<210> 802
<211> 15
<212> PRT
<213> Homo sapiens

<400> 802
Tyr Thr Ile Gly Leu Gly Leu His Ser Leu Glu Ala Asp Gln Glu
5 10 15

<210> 803
<211> 14
<212> PRT

<213> Homo sapiens

<400> 803
Phe Gln Asn Ser Tyr Thr Ile Gly Leu Gly Leu His Ser Leu
5 10

<210> 804
<211> 15
<212> PRT
<213> Homo sapiens

<400> 804
Leu Ser Ala Ala His Cys Phe Gln Asn Ser Tyr Thr Ile Gly Leu
5 10 15

<210> 805
<211> 15
<212> PRT
<213> Homo sapiens

<400> 805
His Pro Gln Trp Val Leu Ser Ala Ala His Cys Phe Gln Asn Ser
5 10 15

<210> 806
<211> 15
<212> PRT
<213> Homo sapiens

<400> 806
Ser Gly Val Leu Val His Pro Gln Trp Val Leu Ser Ala Ala His
5 10 15

<210> 807
<211> 15
<212> PRT
<213> Homo sapiens

<400> 807
Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln Trp Val
5 10 15

<210> 808
<211> 15
<212> PRT
<213> Homo sapiens

<400> 808
Ala Leu Val Met Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val
5 10 15

<210> 809

<211> 17
<212> PRT
<213> Homo sapiens

<400> 809
Ser Gln Pro Trp Gln Ala Ala Leu Val Met Glu Asn Glu Leu Phe Cys
5 10 15

Ser

<210> 810
<211> 15
<212> PRT
<213> Homo sapiens

<400> 810
Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala Gly Asn Ser Cys Leu
5 10 15

<210> 811
<211> 15
<212> PRT
<213> Homo sapiens

<400> 811
Ser Val Ser Glu Ser Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser
5 10 15

<210> 812
<211> 15
<212> PRT
<213> Homo sapiens

<400> 812
Ile Lys Leu Asp Glu Ser Val Ser Glu Ser Asp Thr Ile Arg Ser
5 10 15

<210> 813
<211> 15
<212> PRT
<213> Homo sapiens

<400> 813
Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu Ser
5 10 15

<210> 814
<211> 15
<212> PRT
<213> Homo sapiens

<400> 814

Arg Pro Leu Leu Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu
5 10 15

<210> 815
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 815
ggaccagcat atgaggaaca gaaggaatga cactc 35

<210> 816
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 816
ccgctcgagt ccaccccaag cttcacagg 29

<210> 817
<211> 1959
<212> DNA
<213> Homo sapiens

<400> 817
atgaggaaca gaaggaatga cactctggac agcacccgga ccctgtactc cagcgcgtct 60
cggagcacag acttgtctta cagtgaaagc gacttggtga attttattca agcaaatttt 120
aagaaacgag aatgtgtctt ctttaccaaa gattccaagg ccacggagaa tgtgtgcaag 180
tgtggctatg cccagagcca gcacatggaa ggcacccaga tcaaccaaag tgagaaatgg 240
aactacaaga aacacaccaa ggaatttcct accgacgcct ttggggatat tcagtttgag 300
acactgggga agaaagggaa gtatatacgt ctgtcctgcg acacggacgc ggaaatcctt 360
tacgagctgc tgacccagca ctggcacctg aaaacaccca acctggtcat ttctgtgacc 420
gggggcgcca agaacttcgc cctgaagccg cgcatgcgca agatcttcag ccggctcatc 480
tacatcgcgc agtccaaagg tgcttggatt ctcacgggag gcacccatta tggcctgatg 540
aagtacatcg gggaggtggt gagagataac accatcagca ggagttcaga ggagaatatt 600
gtggccattg gcatagcagc ttggggcatg gtctccaacc gggacaccct catcaggaat 660
tgcgatgctg agggctattt tttagcccag taccttatgg atgacttcac aagagatcca 720
ctgtatatcc tggacaacaa ccacacacat ttgctgctcg tggacaatgg ctgtcatgga 780
catcccactg tcgaagcaaa gctccggaat cagctagaga agtatatctc tgagcgcact 840
attcaagatt ccaactatgg tggcaagatc cccattgtgt gttttgccca aggaggtgga 900
aaagagactt tgaaagccat caatacctcc atcaaaaata aaattccttg tgtggtggtg 960
gaaggctcgg gccagatcgc tgatgtgatc gctagcctgg tggaggtgga ggatgccctg 1020
acatcttctg ccgtcaagga gaagctggtg cgctttttac cccgcacggt gtcccggctg 1080
cctgaggagg agactgagag ttggatcaaa tggctcaaag aaattctcga atgttctcac 1140
ctattaacag ttattaaaat ggaagaagct ggggatgaaa ttgtgagcaa tgccatctcc 1200
tacgctctat acaaagcctt cagcaccagt gagcaagaca aggataactg gaatgggcag 1260
ctgaagcttc tgctggagtg gaaccagctg gacttagcca atgatgagat tttcaccaat 1320
gaccgccgat gggagtctgc tgaccttcaa gaagtcatgt ttacggctct cataaaggac 1380
agacccaagt ttgtccgcct ctttctggag aatggcttga acctacggaa gtttctcacc 1440
catgatgtcc tcactgaact cttctccaac cacttcagca cgcttgtgta ccggaatctg 1500

```
cagatcgcca agaattccta taatgatgcc ctcctcacgt ttgtctggaa actggttgcg 1560
aacttccgaa gaggcttccg gaaggaagac agaaatggcc gggacgagat ggacatagaa 1620
ctccacgacg tgtctcctat tactcggcac cccctgcaag ctctcttcat ctgggccatt 1680
cttcagaata agaaggaact ctccaaagtc atttgggagc agaccagggg ctgcactctg 1740
gcagccctgg gagccagcaa gcttctgaag actctggcca aagtgaagaa cgacatcaat 1800
gctgctgggg agtccgagga gctggctaat gagtacgaga cccgggctgt tgagctgttc 1860
actgagtgtt acagcagcga tgaagacttg gcagaacagc tgctggtcta ttcctgtgaa 1920
gcttggggtg gactcgagca ccaccaccac caccactga                        1959
```

<210> 818
<211> 652
<212> PRT
<213> Homo sapiens

<400> 818

```
Met Arg Asn Arg Arg Asn Asp Thr Leu Asp Ser Thr Arg Thr Leu Tyr
                    5                   10                  15
Ser Ser Ala Ser Arg Ser Thr Asp Leu Ser Tyr Ser Glu Ser Asp Leu
            20                  25                  30
Val Asn Phe Ile Gln Ala Asn Phe Lys Lys Arg Glu Cys Val Phe Phe
        35                  40                  45
Thr Lys Asp Ser Lys Ala Thr Glu Asn Val Cys Lys Cys Gly Tyr Ala
    50                  55                  60
Gln Ser Gln His Met Glu Gly Thr Gln Ile Asn Gln Ser Glu Lys Trp
65                  70                  75                  80
Asn Tyr Lys Lys His Thr Lys Glu Phe Pro Thr Asp Ala Phe Gly Asp
                85                  90                  95
Ile Gln Phe Glu Thr Leu Gly Lys Lys Gly Lys Tyr Ile Arg Leu Ser
            100                 105                 110
Cys Asp Thr Asp Ala Glu Ile Leu Tyr Glu Leu Leu Thr Gln His Trp
        115                 120                 125
His Leu Lys Thr Pro Asn Leu Val Ile Ser Val Thr Gly Gly Ala Lys
    130                 135                 140
Asn Phe Ala Leu Lys Pro Arg Met Arg Lys Ile Phe Ser Arg Leu Ile
145                 150                 155                 160
Tyr Ile Ala Gln Ser Lys Gly Ala Trp Ile Leu Thr Gly Gly Thr His
                165                 170                 175
Tyr Gly Leu Met Lys Tyr Ile Gly Glu Val Val Arg Asp Asn Thr Ile
            180                 185                 190
Ser Arg Ser Ser Glu Glu Asn Ile Val Ala Ile Gly Ile Ala Ala Trp
        195                 200                 205
Gly Met Val Ser Asn Arg Asp Thr Leu Ile Arg Asn Cys Asp Ala Glu
    210                 215                 220
Gly Tyr Phe Leu Ala Gln Tyr Leu Met Asp Asp Phe Thr Arg Asp Pro
225                 230                 235                 240
Leu Tyr Ile Leu Asp Asn Asn His Thr His Leu Leu Leu Val Asp Asn
                245                 250                 255
Gly Cys His Gly His Pro Thr Val Glu Ala Lys Leu Arg Asn Gln Leu
            260                 265                 270
Glu Lys Tyr Ile Ser Glu Arg Thr Ile Gln Asp Ser Asn Tyr Gly Gly
        275                 280                 285
Lys Ile Pro Ile Val Cys Phe Ala Gln Gly Gly Gly Lys Glu Thr Leu
    290                 295                 300
Lys Ala Ile Asn Thr Ser Ile Lys Asn Lys Ile Pro Cys Val Val Val
305                 310                 315                 320
Glu Gly Ser Gly Gln Ile Ala Asp Val Ile Ala Ser Leu Val Glu Val
                325                 330                 335
Glu Asp Ala Leu Thr Ser Ser Ala Val Lys Glu Lys Leu Val Arg Phe
```

```
            340                 345                 350
Leu Pro Arg Thr Val Ser Arg Leu Pro Glu Glu Glu Thr Glu Ser Trp
        355                 360                 365
Ile Lys Trp Leu Lys Glu Ile Leu Glu Cys Ser His Leu Leu Thr Val
    370                 375                 380
Ile Lys Met Glu Glu Ala Gly Asp Glu Ile Val Ser Asn Ala Ile Ser
385                 390                 395                 400
Tyr Ala Leu Tyr Lys Ala Phe Ser Thr Ser Glu Gln Asp Lys Asp Asn
                405                 410                 415
Trp Asn Gly Gln Leu Lys Leu Leu Leu Glu Trp Asn Gln Leu Asp Leu
            420                 425                 430
Ala Asn Asp Glu Ile Phe Thr Asn Asp Arg Arg Trp Glu Ser Ala Asp
        435                 440                 445
Leu Gln Glu Val Met Phe Thr Ala Leu Ile Lys Asp Arg Pro Lys Phe
    450                 455                 460
Val Arg Leu Phe Leu Glu Asn Gly Leu Asn Leu Arg Lys Phe Leu Thr
465                 470                 475                 480
His Asp Val Leu Thr Glu Leu Phe Ser Asn His Phe Ser Thr Leu Val
                485                 490                 495
Tyr Arg Asn Leu Gln Ile Ala Lys Asn Ser Tyr Asn Asp Ala Leu Leu
            500                 505                 510
Thr Phe Val Trp Lys Leu Val Ala Asn Phe Arg Arg Gly Phe Arg Lys
        515                 520                 525
Glu Asp Arg Asn Gly Arg Asp Glu Met Asp Ile Glu Leu His Asp Val
    530                 535                 540
Ser Pro Ile Thr Arg His Pro Leu Gln Ala Leu Phe Ile Trp Ala Ile
545                 550                 555                 560
Leu Gln Asn Lys Lys Glu Leu Ser Lys Val Ile Trp Glu Gln Thr Arg
                565                 570                 575
Gly Cys Thr Leu Ala Ala Leu Gly Ala Ser Lys Leu Leu Lys Thr Leu
            580                 585                 590
Ala Lys Val Lys Asn Asp Ile Asn Ala Ala Gly Glu Ser Glu Glu Leu
        595                 600                 605
Ala Asn Glu Tyr Glu Thr Arg Ala Val Glu Leu Phe Thr Glu Cys Tyr
    610                 615                 620
Ser Ser Asp Glu Asp Leu Ala Glu Gln Leu Leu Val Tyr Ser Cys Glu
625                 630                 635                 640
Ala Trp Gly Gly Leu Glu His His His His His His
                645                 650


<210> 819
<211> 132
<212> PRT
<213> Homo sapien

<400> 819
Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe
1               5                   10                  15
Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser
            20                  25                  30
Gly Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly
        35                  40                  45
Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val
    50                  55                  60
Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val
65                  70                  75                  80
Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala
```

```
                85                  90                  95
Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Asn Trp
            100                 105                 110
Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu
        115                 120                 125
Gly Pro Pro Ala
   130
```

<210> 820
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 820
```
ggggaattca tgatccggga gaaatttgcc cactgc                                36
```

<210> 821
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 821
```
gggctcgagt caggagtttg agaccagcct ggc                                   33
```

<210> 822
<211> 675
<212> DNA
<213> Homo sapiens

<400> 822
```
atgcatcacc atcaccatca cacggccgcg tccgataact tccagctgtc ccagggtggg 60
cagggattcg ccattccgat cgggcaggcg atggcgatcg cgggccagat caagcttccc 120
accgttcata tcgggcctac cgccttcctc ggcttgggtg ttgtcgacaa caacggcaac 180
ggcgcacgag tccaacgcgt ggtcgggagc gctccggcgg caagtctcgg catctccacc 240
ggcgacgtga tcaccgcggt cgacggcgct ccgatcaact cggccaccgc gatggcggac 300
gcgcttaacg ggcatcatcc cggtgacgtc atctcggtga cctggcaaac caagtcgggc 360
ggcacgcgta cagggaacgt gacattggcc gagggacccc cggccgaatt catgatccgg 420
gagaaatttg cccactgcac cgtgctaacc attgcacaca gattgaacac cattattgac 480
agcgacaaga taatggtttt agattcagga agactgaaag aatatgatga gccgtatgtt 540
ttgctgcaaa ataaagagag cctattttac aagatggtgc aacaactggg caaggcagaa 600
gccgctgccc tcactgaaac agcaaaacag agatggggtt tcaccatgtt ggccaggctg 660
gtctcaaact cctga                                                  675
```

<210> 823
<211> 291
<212> DNA
<213> Homo sapiens

<400> 823
atggggatcc gggagaaatt tgcccactgc accgtgctaa ccattgcaca cagattgaac 60
accattattg acagcgacaa gataatggtt ttagattcag gaagactgaa agaatatgat 120
gagccgtatg ttttgctgca aaataaagag agcctatttt acaagatggt gcaacaactg 180
ggcaaggcag aagccgctgc cctcactgaa acagcaaaac agagatgggg tttcaccatg 240
ttggccaggc tggtctcaaa ctccctcgag caccaccacc accaccactg a 291

<210> 824
<211> 1074
<212> DNA
<213> Homo sapiens

<400> 824
atgtcagcca ttgagagggt gtcagaggca atcgtcagca tccgaagaat ccagaccttt 60
ttgctacttg atgagatatc acagcgcaac cgtcagctgc cgtcagatgg taaaaagatg 120
gtgcatgtgc aggattttac tgctttttgg gataaggcat cagagacccc aactctacaa 180
ggcctttcct ttactgtcag acctggcgaa ttgttagctg tggtcggccc cgtgggagca 240
gggaagtcat cactgttaag tgccgtgctc ggggaattgg ccccaagtca cgggctggtc 300
agcgtgcatg gaagaattgc ctatgtgtct cagcagccct gggtgttctc gggaactctg 360
aggagtaata ttttatttgg gaagaaatac gaaaaggaac gatatgaaaa agtcataaag 420
gcttgtgctc tgaaaaagga tttacagctg ttggaggatg gtgatctgac tgtgatagga 480
gatcggggaa ccacgctgag tggagggcag aaagcacggg taaaccttgc aagagcagtg 540
tatcaagatg ctgacatcta tctcctggac gatcctctca gtgcagtaga tgcggaagtt 600
agcagacact tgttcgaact gtgtatttgt caaattttgc atgagaagat cacaatttta 660
gtgactcatc agttgcagta cctcaaagct gcaagtcaga ttctgatatt gaaagatggt 720
aaaatggtgc agaaggggac ttacactgag ttcctaaaat ctggtataga ttttggctcc 780
cttttaaaga aggataatga ggaaagtgaa caacctccag ttccaggaac tcccacacta 840
aggaatcgta ccttctcaga gtcttcggtt tggtctcaac aatcttctag accctccttg 900
aaagatggtg ctctggagag ccaagataca gagaatgtcc cagttacact atcagaggag 960
aaccgttctg aaggaaaagt tggttttcag gcctataaga attacttcag agctggtgct 1020
cactggattg tcttcatttt ccttattctc gagcaccacc accaccacca ctga 1074

<210> 825
<211> 224
<212> PRT
<213> Homo sapiens

<400> 825
Met His His His His His His Thr Ala Ala Ser Asp Asn Phe Gln Leu
5 10 15
Ser Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala
20 25 30
Ile Ala Gly Gln Ile Lys Leu Pro Thr Val His Ile Gly Pro Thr Ala
35 40 45
Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val
50 55 60
Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr
65 70 75 80
Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr
85 90 95
Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser
100 105 110
Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr
115 120 125
Leu Ala Glu Gly Pro Pro Ala Glu Phe Met Ile Arg Glu Lys Phe Ala
130 135 140
His Cys Thr Val Leu Thr Ile Ala His Arg Leu Asn Thr Ile Ile Asp

```
145                 150                 155                 160
Ser Asp Lys Ile Met Val Leu Asp Ser Gly Arg Leu Lys Glu Tyr Asp
                165                 170                 175
Glu Pro Tyr Val Leu Leu Gln Asn Lys Glu Ser Leu Phe Tyr Lys Met
            180                 185                 190
Val Gln Gln Leu Gly Lys Ala Glu Ala Ala Ala Leu Thr Glu Thr Ala
        195                 200                 205
Lys Gln Arg Trp Gly Phe Thr Met Leu Ala Arg Leu Val Ser Asn Ser
    210                 215                 220


<210> 826
<211> 357
<212> PRT
<213> Homo sapiens

<400> 826
Met Ser Ala Ile Glu Arg Val Ser Glu Ala Ile Val Ser Ile Arg Arg
                5                   10                  15
Ile Gln Thr Phe Leu Leu Leu Asp Glu Ile Ser Gln Arg Asn Arg Gln
            20                  25                  30
Leu Pro Ser Asp Gly Lys Lys Met Val His Val Gln Asp Phe Thr Ala
        35                  40                  45
Phe Trp Asp Lys Ala Ser Glu Thr Pro Thr Leu Gln Gly Leu Ser Phe
    50                  55                  60
Thr Val Arg Pro Gly Glu Leu Leu Ala Val Val Gly Pro Val Gly Ala
65                  70                  75                  80
Gly Lys Ser Ser Leu Leu Ser Ala Val Leu Gly Glu Leu Ala Pro Ser
                85                  90                  95
His Gly Leu Val Ser Val His Gly Arg Ile Ala Tyr Val Ser Gln Gln
            100                 105                 110
Pro Trp Val Phe Ser Gly Thr Leu Arg Ser Asn Ile Leu Phe Gly Lys
        115                 120                 125
Lys Tyr Glu Lys Glu Arg Tyr Glu Lys Val Ile Lys Ala Cys Ala Leu
    130                 135                 140
Lys Lys Asp Leu Gln Leu Leu Glu Asp Gly Asp Leu Thr Val Ile Gly
145                 150                 155                 160
Asp Arg Gly Thr Thr Leu Ser Gly Gly Gln Lys Ala Arg Val Asn Leu
                165                 170                 175
Ala Arg Ala Val Tyr Gln Asp Ala Asp Ile Tyr Leu Leu Asp Asp Pro
            180                 185                 190
Leu Ser Ala Val Asp Ala Glu Val Ser Arg His Leu Phe Glu Leu Cys
        195                 200                 205
Ile Cys Gln Ile Leu His Glu Lys Ile Thr Ile Leu Val Thr His Gln
    210                 215                 220
Leu Gln Tyr Leu Lys Ala Ala Ser Gln Ile Leu Ile Leu Lys Asp Gly
225                 230                 235                 240
Lys Met Val Gln Lys Gly Thr Tyr Thr Glu Phe Leu Lys Ser Gly Ile
                245                 250                 255
Asp Phe Gly Ser Leu Leu Lys Lys Asp Asn Glu Glu Ser Glu Gln Pro
            260                 265                 270
Pro Val Pro Gly Thr Pro Thr Leu Arg Asn Arg Thr Phe Ser Glu Ser
        275                 280                 285
Ser Val Trp Ser Gln Gln Ser Ser Arg Pro Ser Leu Lys Asp Gly Ala
    290                 295                 300
Leu Glu Ser Gln Asp Thr Glu Asn Val Pro Val Thr Leu Ser Glu Glu
305                 310                 315                 320
Asn Arg Ser Glu Gly Lys Val Gly Phe Gln Ala Tyr Lys Asn Tyr Phe
```

```
                    325                 330                 335
Arg Ala Gly Ala His Trp Ile Val Phe Ile Phe Leu Ile Leu Glu His
                340                 345                 350
His His His His His
            355

<210> 827
<211> 96
<212> PRT
<213> Homo sapiens

<400> 827
Met Gly Ile Arg Glu Lys Phe Ala His Cys Thr Val Leu Thr Ile Ala
                  5                  10                  15
His Arg Leu Asn Thr Ile Ile Asp Ser Asp Lys Ile Met Val Leu Asp
             20                  25                  30
Ser Gly Arg Leu Lys Glu Tyr Asp Glu Pro Tyr Val Leu Leu Gln Asn
         35                  40                  45
Lys Glu Ser Leu Phe Tyr Lys Met Val Gln Gln Leu Gly Lys Ala Glu
     50                  55                  60
Ala Ala Ala Leu Thr Glu Thr Ala Lys Gln Arg Trp Gly Phe Thr Met
 65                  70                  75                  80
Leu Ala Arg Leu Val Ser Asn Ser Leu Glu His His His His His His
                 85                  90                  95

<210> 828
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 828
cgcccatggg gatccgggag aaatttgccc actgc                              35


<210> 829
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 829
cgcctcgagg gagtttgaga ccagcctggc caaca                              35


<210> 830
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 830
```

gcatggacca tatgtcagcc attgagaggg tgtcagag 38

<210> 831
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 831
ccgctcgaga ataaggaaaa tgaagacaat ccag 34

<210> 832
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 832
gttgaattca tgcacgggcc ccaggtg 27

<210> 833
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 833
cccctcgagt cactatggtc tgcctcttga 30

<210> 834
<211> 915
<212> DNA
<213> Homo sapiens

<400> 834
atgcatcacc atcaccatca cacggccgcg tccgataact tccagctgtc ccagggtggg 60
cagggattcg ccattccgat cgggcaggcg atggcgatcg cgggccagat caagcttccc 120
accgttcata tcgggcctac cgccttcctc ggcttgggtg ttgtcgacaa caacggcaac 180
ggcgcacgag tccaacgcgt ggtcgggagc gctccggcgg caagtctcgg catctccacc 240
ggcgacgtga tcaccgcggt cgacggcgct ccgatcaact cggccaccgc gatggcggac 300
gcgcttaacg ggcatcatcc cggtgacgtc atctcggtga cctggcaaac caagtcgggc 360
ggcacgcgta cagggaacgt gacattggcc gagggacccc cggccgaatt catgcacggg 420
ccccaggtgc tggcacgctg ctccgagtgt gcttgtcctg ccttggctgc cacctctgcg 480
ggggtgcgtc tggagggggt ggaccggcca ccaaccttac ccagtcaagg aagtggatgg 540
ccatgttccc acagcctgag tggctgccac ctgatggctg atggagcaaa ggccttagga 600
aaagcagatg gcccttggcc ctaccttttt gttagaagaa ctgatgttcc atgtcctgca 660
gcgagtgagg ttggtggctg tgccccagc tcctggcgcg ccctcgcaga ggtgactggt 720
tgctctttgg gccctcttgg ccttgcccag catgcacaag cctcagtgct actactgtgc 780

tacaaatgga gccatatagg ggaaacgagc agccatctca ggagcaaggt gtatgctgcc 840
tttgggggct ccagtccttg cctcaagggt cttatgtcac tgtgggcttc ttggttgtca 900
agaggcagac catag 915

<210> 835
<211> 304
<212> PRT
<213> Homo sapiens

<400> 835
Met His His His His His His Thr Ala Ala Ser Asp Asn Phe Gln Leu
                5   10   15
Ser Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala
            20   25   30
Ile Ala Gly Gln Ile Lys Leu Pro Thr Val His Ile Gly Pro Thr Ala
        35   40   45
Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val
    50   55   60
Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr
65   70   75   80
Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr
                85   90   95
Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser
            100   105   110
Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr
        115   120   125
Leu Ala Glu Gly Pro Pro Ala Glu Phe Met His Gly Pro Gln Val Leu
    130   135   140
Ala Arg Cys Ser Glu Cys Ala Cys Pro Ala Leu Ala Ala Thr Ser Ala
145   150   155   160
Gly Val Arg Leu Glu Gly Val Asp Arg Pro Pro Thr Leu Pro Ser Gln
                165   170   175
Gly Ser Gly Trp Pro Cys Ser His Ser Leu Ser Gly Cys His Leu Met
            180   185   190
Ala Asp Gly Ala Lys Ala Leu Gly Lys Ala Asp Gly Pro Trp Pro Tyr
        195   200   205
Leu Phe Val Arg Arg Thr Asp Val Pro Cys Pro Ala Ala Ser Glu Val
    210   215   220
Gly Gly Cys Ala Pro Ser Ser Trp Arg Ala Leu Ala Glu Val Thr Gly
225   230   235   240
Cys Ser Leu Gly Pro Leu Gly Leu Ala Gln His Ala Gln Ala Ser Val
                245   250   255
Leu Leu Leu Cys Tyr Lys Trp Ser His Ile Gly Glu Thr Ser Ser His
            260   265   270
Leu Arg Ser Lys Val Tyr Ala Ala Phe Gly Gly Ser Ser Pro Cys Leu
        275   280   285
Lys Gly Leu Met Ser Leu Trp Ala Ser Trp Leu Ser Arg Gly Arg Pro
    290   295   300

<210> 836
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 836

cgaagtcacg tggaggccag cctc 24

<210> 837
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 837
cctgaccgaa ttcattaact ggcctggac 29

<210> 838
<211> 166
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (1)...(166)
<223> Xaa = Any Amino Acid

<400> 838
Met Gly His His His His His His Val Glu Ala Ser Leu Ser Val Arg
1 5 10 15
His Pro Glu Tyr Asn Arg Pro Leu Leu Ala Asn Asp Leu Met Leu Ile
20 25 30
Lys Leu Asp Glu Ser Val Ser Glu Ser Asp Thr Ile Arg Ser Ile Ser
35 40 45
Ile Ala Ser Gln Cys Pro Thr Ala Gly Asn Ser Cys Leu Val Ser Gly
50 55 60
Trp Gly Leu Leu Ala Asn Gly Arg Met Pro Thr Val Leu Gln Cys Val
65 70 75 80
Asn Val Ser Val Val Ser Glu Glu Val Cys Ser Lys Leu Tyr Asp Pro
85 90 95
Leu Tyr His Pro Ser Met Phe Cys Ala Gly Gly Gly Gln Xaa Gln Xaa
100 105 110
Asp Ser Cys Asn Gly Asp Ser Gly Gly Pro Leu Ile Cys Asn Gly Tyr
115 120 125
Leu Gln Gly Leu Val Ser Phe Gly Lys Ala Pro Cys Gly Gln Val Gly
130 135 140
Val Pro Gly Val Tyr Thr Asn Leu Cys Lys Phe Thr Glu Trp Ile Glu
145 150 155 160
Lys Thr Val Gln Ala Ser
165

<210> 839
<211> 504
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(504)
<223> n = A,T,C or G

<400> 839
atgggccatc atcatcatca tcacgtggag gccagcctct ccgtacggca cccagagtac 60
aacagaccct tgctcgctaa cgacctcatg ctcatcaagt tggacgaatc cgtgtccgag 120
tctgacacca tccggagcat cagcattgct tcgcagtgcc ctaccgcggg gaactcttgc 180
ctcgtttctg gctggggtct gctggcgaac ggcagaatgc ctaccgtgct gcagtgcgtg 240
aacgtgtcgg tggtgtctga ggaggtctgc agtaagctct atgacccgct gtaccacccc 300
agcatgttct gcgccggcgg agggcaaanac cagaangact cctgcaacgg tgactctggg 360
gggcccctga tctgcaacgg gtacttgcag ggccttgtgt ctttcggaaa agccccgtgt 420
ggccaagttg gcgtgccagg tgtctacacc aacctctgca aattcactga gtggatagag 480
aaaaccgtcc aggccagtta atga 504

<210> 840
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 840
ctcagggttc cggagccgcg g 21

<210> 841
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 841
ctatagaatt cattaccaaa aagctgggct ccagc 35

<210> 842
<211> 241
<212> PRT
<213> Homo sapiens

<400> 842
Met Gln His His His His His His Leu Arg Val Pro Glu Pro Arg Pro
1 5 10 15
Gly Glu Ala Lys Ala Glu Gly Ala Ala Pro Pro Thr Pro Ser Lys Pro
20 25 30
Leu Thr Ser Phe Leu Ile Gln Asp Ile Leu Arg Asp Gly Ala Gln Arg
35 40 45
Gln Gly Gly Arg Thr Ser Ser Gln Arg Gln Arg Asp Pro Glu Pro Glu
50 55 60
Pro Glu Pro Glu Pro Glu Gly Gly Arg Ser Arg Ala Gly Ala Gln Asn
65 70 75 80
Asp Gln Leu Ser Thr Gly Pro Arg Ala Ala Pro Glu Glu Ala Glu Thr
85 90 95
Leu Ala Glu Thr Glu Pro Glu Arg His Leu Gly Ser Tyr Leu Leu Asp
100 105 110
Ser Glu Asn Thr Ser Gly Ala Leu Pro Arg Leu Pro Gln Thr Pro Lys
115 120 125

```
Gln Pro Gln Lys Arg Ser Arg Ala Ala Phe Ser His Thr Gln Val Ile
    130                 135                 140
Glu Leu Glu Arg Lys Phe Ser His Gln Lys Tyr Leu Ser Ala Pro Glu
145                 150                 155                 160
Arg Ala His Leu Ala Lys Asn Leu Lys Leu Thr Glu Thr Gln Val Lys
                165                 170                 175
Ile Trp Phe Gln Asn Arg Arg Tyr Lys Thr Lys Arg Lys Gln Leu Ser
            180                 185                 190
Ser Glu Leu Gly Asp Leu Glu Lys His Ser Ser Leu Pro Ala Leu Lys
        195                 200                 205
Glu Glu Ala Phe Ser Arg Ala Ser Leu Val Ser Val Tyr Asn Ser Tyr
    210                 215                 220
Pro Tyr Tyr Pro Tyr Leu Tyr Cys Val Gly Ser Trp Ser Pro Ala Phe
225                 230                 235                 240
Trp
```

<210> 843
<211> 729
<212> DNA
<213> Homo sapiens

<400> 843

```
atgcagcatc accaccatca ccacctcagg gttccggagc cgcggcccgg ggaggcgaaa     60
gcggaggggg ccgcgccgcc gaccccgtcc aagccgctca cgtccttcct catccaggac    120
atcctgcggg acggcgcgca gcggcaaggc ggccgcacga gcagccagag acagcgcgac    180
ccggagccgg agccagagcc agagccagag ggaggacgca gccgcgccgg ggcgcagaac    240
gaccagctga gcaccgggcc ccgcgccgcg ccggatgagg ccgagacgct ggcagagacc    300
gagccagaaa ggcacttggg gtcttatctg ttggactctg aaaacacttc aggcgccctt    360
ccaaggcttc cccaaacccc taagcagccg cagaagcgct cccgagctgc cttctcccac    420
actcaggtga tcgagttgga gaggaagttc agccatcaga agtacctgtc ggcccctgaa    480
cgggcccacc tggccaagaa cctcaagctc acggagaccc aagtgaagat atggttccag    540
aacagacgct ataagactaa gcgaaagcag ctctcctcgg agctgggaga cttggagaag    600
cactcctttt tgccggccct gaaagaggag gccttctccc gggcctccct ggtctccgtg    660
tataacagct atccttacta cccatacctg cactgcgtgg gcagctggag cccagctttt    720
tggtaatga                                                            729
```

<210> 844
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 844

```
ctactaagcg ctggagtgag ggatcag                                         27
```

<210> 845
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 845
catcgagaat tcactactct ctgactagat gtc 33

<210> 846
<211> 161
<212> PRT
<213> Homo sapiens

<400> 846
Met Gln His His His His His His Ala Gly Val Arg Asp Gln Gly Gln
1 5 10 15
Gly Ala Arg Trp Pro His Thr Gly Lys Arg Gly Pro Leu Leu Gln Gly
20 25 30
Leu Thr Trp Ala Thr Gly Gly His Cys Phe Ser Ser Glu Glu Ser Gly
35 40 45
Ala Val Asp Gly Ala Gly Gln Lys Lys Asp Arg Ala Trp Leu Arg Cys
50 55 60
Pro Glu Ala Val Ala Gly Phe Pro Leu Gly Ser Asp Cys Arg Glu Gly
65 70 75 80
Gly Arg Gln Gly Cys Gly Gly Ser Asp Asp Glu Asp Asp Leu Gly Val
85 90 95
Ala Pro Gly Leu Ala Pro Ala Trp Ala Leu Thr Gln Pro Pro Ser Gln
100 105 110
Ser Pro Gly Pro Gln Ser Leu Pro Ser Thr Pro Ser Ser Ile Trp Pro
115 120 125
Gln Trp Val Ile Leu Ile Thr Glu Leu Thr Ile Pro Ser Pro Ala His
130 135 140
Gly Pro Pro Trp Leu Pro Asn Ala Leu Glu Arg Gly His Leu Val Arg
145 150 155 160
Glu

<210> 847
<211> 489
<212> DNA
<213> Homo sapiens

<400> 847
atgcagcatc accaccatca ccacgctgga gtgagggatc aggggcaggg cgcgagatgg 60
cctcacacag ggaagagagg gcccctcctg cagggcctca cctgggccac aggaggacac 120
tgcttttcct ctgaggagtc aggagctgtg gatggtgctg gacagaagaa ggacagggcc 180
tggctcaggt gtccagaggc tgtcgctggc ttccctttgg gatcagactg cagggaggga 240
gggcggcagg gttgtggggg gagtgacgat gaggatgacc tgggggtggc tccaggcctt 300
gcccctgcct gggccctcac ccagcctccc tcacagtctc ctggccctca gtctctcccc 360
tccactccat cctccatctg gcctcagtgg gtcattctga tcactgaact gaccataccc 420
agccctgccc acggccctcc atggctcccc aatgccctgg agaggggaca tctagtcaga 480
gagtagtga 489

<210> 848
<211> 132
<212> PRT
<213> Homo sapiens

<400> 848
Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe

```
 1               5                   10                  15
Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser
            20                  25                  30
Gly Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly
        35                  40                  45
Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val
    50                  55                  60
Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val
65                  70                  75                  80
Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala
                85                  90                  95
Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Asn Trp
            100                 105                 110
Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu
        115                 120                 125
Gly Pro Pro Ala
    130
```

<210> 849
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 849
ggggaattca tcacctatgt gccgcctctg c 31

<210> 850
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 850
gggctcgagt cactcgccca cgaaatccgt gtaaaacagc 40

<210> 851
<211> 1203
<212> DNA
<213> Homo sapiens

<400> 851
atgcatcacc atcaccatca cacggccgcg tccgataact tccagctgtc ccagggtggg 60
cagggattcg ccattccgat cgggcaggcg atggcgatcg cgggccagat caagcttccc 120
accgttcata tcgggcctac cgccttcctc ggcttgggtg ttgtcgacaa caacggcaac 180
ggcgcacgag tccaacgcgt ggtcgggagc gctccggcgg caagtctcgg catctccacc 240
ggcgacgtga tcaccgcggt cgacggcgct ccgatcaact cggccaccgc gatggcggac 300
gcgcttaacg ggcatcatcc cggtgacgtc atctcggtga cctggcaaac caagtcgggc 360
ggcacgcgta cagggaacgt gacattggcc gagggacccc cggccgaatt catcacctat 420
gtgccgcctc tgctgctgga agtgggggta gaggagaagt tcatgaccat ggtgctgggc 480
attggtccag tgctgggcct ggtctgtgtc ccgctcctag gctcagccag tgaccactgg 540
cgtggacgct atggccgccg ccggcccttc atctgggcac tgtccttggg catcctgctg 600

```
agcctctttc tcatcccaag ggccggctgg ctagcagggc tgctgtgccc ggatcccagg 660
cccctggagc tggcactgct catcctgggc gtggggctgc tggacttctg tggccaggtg 720
tgcttcactc cactggaggc cctgctctct gacctcttcc gggacccgga ccactgtcgc 780
caggcctact ctgtctatgc cttcatgatc agtcttgggg gctgcctggg ctacctcctg 840
cctgccattg actgggacac cagtgccctg gccccctacc tgggcaccca ggaggagtgc 900
ctctttggcc tgctcaccct catcttcctc acctgcgtag cagccacact gctggtggct 960
gaggaggcag cgctgggccc caccgagcca gcagaagggc tgtcggcccc ctccttgtcg 1020
ccccactgct gtccatgccg ggcccgcttg gctttccgga acctgggcgc cctgcttccc 1080
cggctgcacc agctgtgctg ccgcatgccc cgcaccctgc gccggctctt cgtggctgag 1140
ctgtgcagct ggatggcact catgaccttc acgctgtttt acacggattt cgtgggcgag 1200
tga                                                               1203
```

<210> 852
<211> 400
<212> PRT
<213> Homo sapiens

<400> 852

```
Met His His His His His His Thr Ala Ala Ser Asp Asn Phe Gln Leu
                    5                   10                  15
Ser Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala
                20                  25                  30
Ile Ala Gly Gln Ile Lys Leu Pro Thr Val His Ile Gly Pro Thr Ala
            35                  40                  45
Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val
        50                  55                  60
Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr
65                  70                  75                  80
Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr
                85                  90                  95
Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser
            100                 105                 110
Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr
        115                 120                 125
Leu Ala Glu Gly Pro Pro Ala Glu Phe Ile Thr Tyr Val Pro Pro Leu
    130                 135                 140
Leu Leu Glu Val Gly Val Glu Glu Lys Phe Met Thr Met Val Leu Gly
145                 150                 155                 160
Ile Gly Pro Val Leu Gly Leu Val Cys Val Pro Leu Leu Gly Ser Ala
                165                 170                 175
Ser Asp His Trp Arg Gly Arg Tyr Gly Arg Arg Arg Pro Phe Ile Trp
            180                 185                 190
Ala Leu Ser Leu Gly Ile Leu Leu Ser Leu Phe Leu Ile Pro Arg Ala
        195                 200                 205
Gly Trp Leu Ala Gly Leu Leu Cys Pro Asp Pro Arg Pro Leu Glu Leu
    210                 215                 220
Ala Leu Leu Ile Leu Gly Val Gly Leu Leu Asp Phe Cys Gly Gln Val
225                 230                 235                 240
Cys Phe Thr Pro Leu Glu Ala Leu Leu Ser Asp Leu Phe Arg Asp Pro
                245                 250                 255
Asp His Cys Arg Gln Ala Tyr Ser Val Tyr Ala Phe Met Ile Ser Leu
            260                 265                 270
Gly Gly Cys Leu Gly Tyr Leu Leu Pro Ala Ile Asp Trp Asp Thr Ser
        275                 280                 285
Ala Leu Ala Pro Tyr Leu Gly Thr Gln Glu Glu Cys Leu Phe Gly Leu
    290                 295                 300
Leu Thr Leu Ile Phe Leu Thr Cys Val Ala Ala Thr Leu Leu Val Ala
305                 310                 315                 320
```

```
Glu Glu Ala Ala Leu Gly Pro Thr Glu Pro Ala Glu Gly Leu Ser Ala
                325                 330                 335
Pro Ser Leu Ser Pro His Cys Cys Pro Cys Arg Ala Arg Leu Ala Phe
            340                 345                 350
Arg Asn Leu Gly Ala Leu Leu Pro Arg Leu His Gln Leu Cys Cys Arg
        355                 360                 365
Met Pro Arg Thr Leu Arg Arg Leu Phe Val Ala Glu Leu Cys Ser Trp
    370                 375                 380
Met Ala Leu Met Thr Phe Thr Leu Phe Tyr Thr Asp Phe Val Gly Glu
385                 390                 395                 400

<210> 853
<211> 20
<212> PRT
<213> Homo sapiens

<400> 853
Leu Leu Pro Pro Pro Pro Ala Leu Cys Gly Ala Ser Ala Cys Asp Val
                  5                  10                  15
Ser Val Arg Val
             20

<210> 854
<211> 60
<212> DNA
<213> Homo sapiens

<400> 854
ctgctcccac ctccacccgc gctctgcggg gcctctgcct gtgatgtctc cgtacgtgtg 60

<210> 855
<211> 10
<212> PRT
<213> Homo sapiens

<400> 855
Ala Ser Ala Cys Asp Val Ser Val Arg Val
                  5                  10

<210> 856
<211> 30
<212> DNA
<213> Homo sapiens

<400> 856
gcctctgcct gtgatgtctc cgtacgtgtg                                  30


<210> 857
<211> 9
<212> PRT
<213> Homo sapiens

<400> 857
Ala Ser Ala Cys Asp Val Ser Val Arg
 1               5

<210> 858
```

<211> 9
<212> PRT
<213> Homo sapiens

<400> 858
Ser Ala Cys Asp Val Ser Val Arg Val
5

<210> 859
<211> 27
<212> DNA
<213> Homo sapiens

<400> 859
tctgcctgtg atgtctccgt acgtgtg 27

<210> 860
<211> 19
<212> PRT
<213> Homo sapiens

<400> 860
Gly Ile Gly Pro Val Leu Gly Leu Val Cys Val Pro Leu Leu Gly Ser
5 10 15
Ala Ser Asp

<210> 861
<211> 19
<212> PRT
<213> Homo sapiens

<400> 861
Val Pro Pro Leu Leu Leu Glu Val Gly Val Glu Glu Lys Phe Met Thr
5 10 15
Met Val Leu

<210> 862
<211> 19
<212> PRT
<213> Homo sapiens

<400> 862
Met Val Gln Arg Leu Trp Val Ser Arg Leu Leu Arg His Arg Lys Ala
5 10 15
Gln Leu Leu

<210> 863
<211> 57
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(57)
<223> n = A,T,C or G

<400> 863
ggnathggnc cngtnytngg nytngtntgy gtnccnytny tnggnwsngc nwsngay 57

<210> 864
<211> 57
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(57)
<223> n = A,T,C or G

<400> 864
gtnccnccny tnytnytnga rgtnggngtn gargaraart tyatgacnat ggtnytn 57

<210> 865
<211> 57
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(57)
<223> n = A,T,C or G

<400> 865
atggtncarm gnytntgggt nwsnmgnytn ytnmgncaym gnaargcnca rytnytn 57

<210> 866
<211> 9
<212> PRT
<213> Homo sapiens

<400> 866
Val Leu Gln Cys Val Asn Val Ser Val
1 5

<210> 867
<211> 9
<212> PRT
<213> Homo sapiens

<400> 867
Arg Met Pro Thr Val Leu Gln Cys Val
1 5

<210> 868
<211> 9
<212> PRT
<213> Homo sapiens

<400> 868
Asn Leu Cys Lys Phe Thr Glu Trp Ile
1 5

<210> 869
<211> 9
<212> PRT
<213> Homo sapiens

<400> 869
Met Leu Ile Lys Leu Asp Glu Ser Val
1 5

<210> 870
<211> 9
<212> PRT
<213> Homo sapiens

<400> 870
Leu Leu Ala Asn Asp Leu Met Leu Ile
1 5

<210> 871
<211> 10
<212> PRT
<213> Homo sapiens

<400> 871
Leu Leu Ala Asn Gly Arg Met Pro Thr Val
1 5 10

<210> 872
<211> 10
<212> PRT
<213> Homo sapiens

<400> 872
Leu Met Leu Ile Lys Leu Asp Glu Ser Val
1 5 10

<210> 873
<211> 10
<212> PRT
<213> Homo sapiens

<400> 873
Val Leu Gln Cys Val Asn Val Ser Val Val
1 5 10

<210> 874
<211> 10
<212> PRT
<213> Homo sapiens

<400> 874
Gly Leu Leu Ala Asn Gly Arg Met Pro Thr
1 5 10

<210> 875
<211> 10
<212> PRT

<213> Homo sapiens

<400> 875
Thr Val Leu Gln Cys Val Asn Val Ser Val
1 5 10

<210> 876
<211> 9
<212> PRT
<213> Homo sapiens

<400> 876
Gly Val Leu Val His Pro Gln Trp Val
1 5

<210> 877
<211> 9
<212> PRT
<213> Homo sapiens

<400> 877
Val Leu Val His Pro Gln Trp Val Leu
1 5

<210> 878
<211> 1195
<212> DNA
<213> Homo sapiens

<400> 878
ccgagactca cggtcaagct aaggcgaaga gtgggtggct gaagccatac tattttatag 60
aattaatgga aagcagaaaa gacatcacaa accaagaaga actttggaaa atgaagccta 120
ggagaaattt agaagaagac gattatttgc ataaggacac gggagagacc agcatgctaa 180
aaagacctgt gcttttgcat ttgcaccaaa cagcccatgc tgatgaattt gactgccctt 240
cagaacttca gcacacacag gaactctttc cacagtggca cttgccaatt aaaatagctg 300
ctattatagc atctctgact ttctttaca ctcttctgag ggaagtaatt cacccttag 360
caacttccca tcaacaatat ttttataaaa ttccaatcct ggtcatcaac aaagtcttgc 420
caatggtttc catcactctc ttggcattgg tttacctgcc aggtgtgata gcagcaattg 480
tccaacttca taatggaacc aagtataaga agtttccaca ttggttggat aagtggatgt 540
taacaagaaa gcagtttggg cttctcagtt tcttttttgc tgtactgcat gcaatttata 600
gtctgtctta cccaatgagg cgatcctaca gatacaagtt gctaaactgg gcatatcaac 660
aggtccaaca aaataaagaa gatgcctgga ttgagcatga tgtttggaga atggagattt 720
atgtgtctct gggaattgtg ggattggcaa tactggctct gttggctgtg acatctattc 780
catctgtgag tgactctttg acatggagag aatttcacta tattcagagc aagctaggaa 840
ttgtttccct tctactgggc acaatacacg cattgatttt tgcctggaat aagtggatag 900
atataaaaca atttgtatgg tatacacctc caacttttat gatagctgtt ttccttccaa 960
ttgttgtcct gatatttaaa agcatactat tcctgccatg cttgaggaag aagatactga 1020
agattagaca tggttgggaa gacgtcacca aaattaacaa aactgagata tgttcccagt 1080
tgtagaatta ctgtttacac acatttttgt tcaatattga tatattttat caccaacatt 1140
tcaagtttgt atttgttaat aaaatgatta ttcaaggaaa aaaaaaaaaa aaaaa 1195

<210> 879
<211> 339
<212> PRT
<213> Homo sapiens

<400> 879
Met Glu Ser Arg Lys Asp Ile Thr Asn Gln Glu Glu Leu Trp Lys Met
                5   10   15
Lys Pro Arg Arg Asn Leu Glu Glu Asp Asp Tyr Leu His Lys Asp Thr
            20   25   30
Gly Glu Thr Ser Met Leu Lys Arg Pro Val Leu Leu His Leu His Gln
        35   40   45
Thr Ala His Ala Asp Glu Phe Asp Cys Pro Ser Glu Leu Gln His Thr
    50   55   60
Gln Glu Leu Phe Pro Gln Trp His Leu Pro Ile Lys Ile Ala Ala Ile
65   70   75   80
Ile Ala Ser Leu Thr Phe Leu Tyr Thr Leu Leu Arg Glu Val Ile His
                85   90   95
Pro Leu Ala Thr Ser His Gln Gln Tyr Phe Tyr Lys Ile Pro Ile Leu
            100   105   110
Val Ile Asn Lys Val Leu Pro Met Val Ser Ile Thr Leu Leu Ala Leu
        115   120   125
Val Tyr Leu Pro Gly Val Ile Ala Ala Ile Val Gln Leu His Asn Gly
    130   135   140
Thr Lys Tyr Lys Lys Phe Pro His Trp Leu Asp Lys Trp Met Leu Thr
145   150   155   160
Arg Lys Gln Phe Gly Leu Leu Ser Phe Phe Phe Ala Val Leu His Ala
                165   170   175
Ile Tyr Ser Leu Ser Tyr Pro Met Arg Arg Ser Tyr Arg Tyr Lys Leu
            180   185   190
Leu Asn Trp Ala Tyr Gln Gln Val Gln Gln Asn Lys Glu Asp Ala Trp
        195   200   205
Ile Glu His Asp Val Trp Arg Met Glu Ile Tyr Val Ser Leu Gly Ile
    210   215   220
Val Gly Leu Ala Ile Leu Ala Leu Leu Ala Val Thr Ser Ile Pro Ser
225   230   235   240
Val Ser Asp Ser Leu Thr Trp Arg Glu Phe His Tyr Ile Gln Ser Lys
                245   250   255
Leu Gly Ile Val Ser Leu Leu Leu Gly Thr Ile His Ala Leu Ile Phe
            260   265   270
Ala Trp Asn Lys Trp Ile Asp Ile Lys Gln Phe Val Trp Tyr Thr Pro
        275   280   285
Pro Thr Phe Met Ile Ala Val Phe Leu Pro Ile Val Val Leu Ile Phe
    290   295   300
Lys Ser Ile Leu Phe Leu Pro Cys Leu Arg Lys Lys Ile Leu Lys Ile
305   310   315   320
Arg His Gly Trp Glu Asp Val Thr Lys Ile Asn Lys Thr Glu Ile Cys
                325   330   335
Ser Gln Leu

<210> 880
<211> 2172
<212> DNA
<213> Homo sapiens

<400> 880
aaaattgaat attgagatac cattctttag tgttaccttt tttacccaca tgtgtttctg 60
aaaatattgg aattttattc atcttaaaaa ttggacccgg ccttatttac catctttaat 120
ccatttttagt actatgggtg agtacatgga attgaagtct ggcttaaatc ttcagaaagt 180
tatatatcta ttttatttta tttttttgag acagagtctc gctgtgtcac ccaggctgga 240
gtgcggtgcc acaatcttgg ctcactgcaa cctctgagtc ccaggttcaa gcgatactca 300
tgcctcggcc tcctgagtag ctgggactac aggcgtgcac caccacatct ggctaatctt 360
tttttgtatt tttagtagag acggggtttc actgtggtct ccatctcctg acctcgtgat 420

ccgcctgcct cccaaagtgc tgggattaca ggcatgagcc accgcacaca gctgggactg 480
ggtaatttat aaagaaaaga ggtttaatga ctcacagttc cgcatggctg gagaggcctc 540
aggaaactta caatcatggt ggaaggcgaa ggggaagcaa ggcacgtctt acatggtggc 600
aggagagaac gagtgagggg ggagactgcc acaaactttt ttttttgag acaagagtct 660
ggccctgttg cccaggctgg agtgcagtgg catgatctca gctcactgca acctctgcct 720
cacaggttca agcaattctc atgcctcagc ctcccgcata gctgggacca caggtatgca 780
ccaccacacc tagctaattt ttgtagtttt agtagagatg gggtctcact atgttgctca 840
ggctggtcta aaactcctgg gctccagcaa tccgcctgcc ttggcctccc aaagtgctgg 900
ggttacaggc ataagccacc acatccagcc tgccacatac ttttaaacta tcaggtctca 960
tgagaactca tgcactatca caagaatagc atggggaaaa tcccccccat aatccaatca 1020
cctcccacca ggtctcctcc gacacgtggg attgggtggg gacacagagc caaaccgtat 1080
cagatgctgc aggggctggg gacactgaga ccactcagac ctggtgtctc tgtcactctt 1140
ctgggctctg tctgtctcca ggacctccct ccccttccat ggtatagaag gaaagtgctg 1200
taaggtgcaa attgcacagg aactccttaa gacatacatc atccactcag cagttttagg 1260
ttcgcagcaa aatggagtgg aaggaacaga aatttcctgt gcacccctcc ccgctgtctc 1320
cgccatatcg gcatcctgca tccagagtgg tggactggtt acaggctatg aacctacact 1380
gatgcggcac caccacccag agtccacggg ttatgttggt tcacatttac tcttgctgtg 1440
gtatggtcta taggtttgga cagatgtccg ataatccttt ttacattttg gcatccttgg 1500
gtagctcgtc ttgtaggaat ggacttgctt caaagtggag gcaggcagat ccttcagacg 1560
ggtatatgga gccctgtttt cagttgcttt tctaattctc tcttatcgtt tacctcaaaa 1620
tcttcctgag gtctcgcttc cttttaaaat ccttgtctac tttgcagcat cactctgaca 1680
ctccattgat tcctcagcac ctactgacta cacggttagg agtgcaaggg tagaattcat 1740
gttttattca tctttgggtc tgtagcaccc agcaaagtgc tcagtaaatg cgcagtaatt 1800
gatttgacct ctgaacaaat acacactgta ctaagaatct acacaccgaa agacaaaaac 1860
aagacaaatt tgagtgctac aggtgtcacg cttggcatca cacatgtgcc tgtgtattcc 1920
tctaggtggt taccaggagc tctgccactg catgtccact agtgacgggt tcgctccacc 1980
accccagctg ggtagccgct gctctcacat aaggggtcca attaaaattg ccaggaataa 2040
attcccccgg actttgactt ctcaagagct aagaaggttt gctgagtatt ctggcatgat 2100
gtttggtgat caaacaactg ctggccaaaa atgatgagta tttcccctc ttgctgaaga 2160
tgtgctccat ac 2172

<210> 881
<211> 2455
<212> DNA
<213> Homo sapiens

<400> 881
cagcttaaaa atggtttctt gaaatcagtg attagcattc actcaccagt acccctacta 60
aggggtaggc actggtttgt actcctggga atacaggagt acaccagaat ttatttctgc 120
ttattgcttt tgttgcaaat gccgtggctt catctgagga attctagaat tcagagggtg 180
tagccctcca ctctgctgtc ttgctatctg ctctcattgc atccgtttaa cctgcattct 240
gaaagatgtt tctcaggttt ttccttgacg atttcttct tttctgattc tgacaatgtt 300
ttaaatcatt gtactgtggt tatcatttct ctgcatttat tttacccatc ttcctttgta 360
acttgtccta ttgtctttta atttctgcct gttctttatg gctttcaact tcataaataa 420
catgttttct caaatctctt tgtgaattcc agagagggcc aggcacggtg gctcacatct 480
gtaatcccag cactttgggg aggctgagac gggtggatca cttgaggtca ggagtttgag 540
accagcctgg ccaacatggt gaaatcccgt ttcactaaaa atacaaaaat tacccaggca 600
tggtggcggg cgcctgtaat cccaggtact cgggaggctg agggaggaga atcgcttgaa 660
cctgggaggc tgagggagga gaatcgcttg aacccgggag gcagaggttg cagtgaaccg 720
agatcatgtt gctgcactcc agcctggtca acagagcaag actctgcctc aaaaacaaac 780
aaataaacaa acaaacaaac aaaacagaga gattttgctg caatgtacaa ggagcaattt 840
gctcctttaa aaaaataatt tttggccagg cacagtggct cacacctgta atcccagcac 900
tttgggaagc caaggtgggt ggatcatttg aggtcaggag tttgagatca gcctggccaa 960
catggtgaaa cactatctct attaaaaata caaaaatgtg ctcagtgtgg tggtgcacat 1020
ctgtaatctc agcctcccgc atagctggga ccacaggtat gcaccaccac acctagctaa 1080
tttttgtagt tttagtagag atggggtctc actatgttgc tcaggctggt ctaaaactcc 1140
tggctccag caatccgcct gccttggcct cccaaagtgc tggggttaca ggcataagcc 1200
accacatcca gcctgccaca tacttttaaa ctatcaggtc tcatgagaac tcatgcacta 1260

tcacaagaat agcatgggga aaatcccccc cataatccaa tcacctccca ccaggtctcc 1320
tccgacacgt gggattgggt ggggacacag agccaaaccg tatcagatgc tgcaggggct 1380
ggggacactg agaccactca gacctggtgt ctctgtcact cttctgggct ctgtctgtct 1440
ccaggacctc cctccccttc catggtatag aaggaaagtg ctgtaaggtg caaattgcac 1500
aggaactcct taagacatac atcatccact cagcagtttt aggttcgcag caaaatggag 1560
tggaaggaac agaaatttcc tgtgcacccc tccccgctgt ctccgccata tcggcatcct 1620
gcatccagag tggtggactg gttacaggct atgaacctac actgatgcgg caccaccacc 1680
cagagtccac aggttatgtt ggttcacatt tactcttgct gtggtatggt ctataggttt 1740
ggacagatgt ccgataatcc tttttacatt ttggcatcct tgggtagctc gtcttgtagg 1800
aatggacttg cttcaaagtg gaggcaggca gatccttcag acgggtatat ggagccctgt 1860
tttcagttgc ttttctaatt ctctcttatc gtttacctca aaatcttcct gaggtctcgc 1920
ttcctttttaa aatccttgtc tactttgcag catcactctg acactccatt gattcctcag 1980
cacctactga ctacacggtt aggagtgcaa gggtagaatt catgttttat tcatctttgg 2040
gtctgtagca cccagcaaag tgctcagtaa atgcgcagta attgatttga cctctgaaca 2100
aatacacact gtactaagaa tctacacacc gaaagacaaa aacaagacaa atttgagtgc 2160
tacaggtgtc acgcttggca tcacacatgt gcctgtgtat tcctctaggt ggttaccagg 2220
agctctgcca ctgcatgtcc actagtgacg ggttcgctcc accaccccag ctgggtagcc 2280
gctgctctca cataaggggt ccaattaaaa ttgccaggaa taaattcccc cggactttga 2340
cttctcaaga gctaagaagg tttgctgagt attctggcat gatgtttggt gatcaaacaa 2400
ctgctggcca aaaatgatga gtatttcccc ctcttgctga agatgtgctc catac 2455

<210> 882
<211> 2455
<212> DNA
<213> Homo sapiens

<400> 882
cagcttaaaa atggtttctt gaaatcagtg attagcattc actcaccagt accccctacta 60
aggggtaggc actggtttgt actcctggga atacaggagt acaccagaat ttatttctgc 120
ttattgcttt tgttgcaaat gccgtggctt catctgagga attctagaat tcagagggtg 180
tagccctcca ctctgctgtc ttgctatctg ctctcattgc atccgtttaa cctgcattct 240
gaaagatgtt tctcaggttt ttccttgacg attttcttct tttctgattc tgacaatgtt 300
ttaaatcatt gtactgtggt tatcatttct ctgcatttat tttacccatc ttcctttgta 360
acttgtccta ttgtctttta atttctgcct gttctttatg gctttcaact tcataaataa 420
catgttttct caaatctctt tgtgaattcc agagagggcc aggcacggtg gctcacatct 480
gtaatcccag cactttgggg aggctgagac gggtggatca cttgaggtca ggagtttgag 540
accagcctgg ccaacatggt gaaatcccgt ttcactaaaa atacaaaaat tacccaggca 600
tggtggcggg cgcctgtaat cccaggtact cgggaggctg agggaggaga atcgcttgaa 660
cctgggaggc tgagggagga gaatcgcttg aacccgggag gcagaggttg cagtgaaccg 720
agatcatgtt gctgcactcc agcctggtca acagagcaag actctgcctc aaaaacaaac 780
aaataaacaa acaaacaaac aaaacagaga gattttgctg caatgtacaa ggagcaattt 840
gctcctttaa aaaaataatt tttggccagg cacagtggct cacacctgta atcccagcac 900
tttgggaagc caaggtgggt ggatcatttg aggtcaggag tttgagatca gcctggccaa 960
catggtgaaa cactatctct attaaaaata caaaaatgtg ctcagtgtgg tggtgcacat 1020
ctgtaatctc agcctcccgc atagctggga ccacaggtat gcaccaccac acctagctaa 1080
tttttgtagt tttagtagag atggggtctc actatgttgc tcaggctggt ctaaaactcc 1140
tgggctccag caatccgcct gccttggcct cccaaagtgc tggggttaca ggcataagcc 1200
accacatcca gcctgccaca tacttttaaa ctatcaggtc tcatgagaac tcatgcacta 1260
tcacaagaat agcatgggga aaatcccccc cataatccaa tcacctccca ccaggtctcc 1320
tccgacacgt gggattgggt ggggacacag agccaaaccg tatcagatgc tgcaggggct 1380
ggggacactg agaccactca gacctggtgt ctctgtcact cttctgggct ctgtctgtct 1440
ccaggacctc cctccccttc catggtatag aaggaaagtg ctgtaaggtg caaattgcac 1500
aggaactcct taagacatac atcatccact cagcagtttt aggttcgcag caaaatggag 1560
tggaaggaac agaaatttcc tgtgcacccc tccccgctgt ctccgccata tcggcatcct 1620
gcatccagag tggtggactg gttacaggct atgaacctac actgatgcgg caccaccacc 1680
cagagtccac aggttatgtt ggttcacatt tactcttgct gtggtatggt ctataggttt 1740
ggacagatgt ccgataatcc tttttacatt ttggcatcct tgggtagctc gtcttgtagg 1800
aatggacttg cttcaaagtg gaggcaggca gatccttcag acgggtatat ggagccctgt 1860

```
tttcagttgc ttttctaatt ctctcttatc gtttacctca aaatcttcct gaggtctcgc 1920
ttccttttaa aatccttgtc tactttgcag catcactctg acactccatt gattcctcag 1980
cacctactga ctacacggtt aggagtgcaa gggtagaatt catgttttat tcatctttgg 2040
gtctgtagca cccagcaaag tgctcagtaa atgcgcagta attgatttga cctctgaaca 2100
aatacacact gtactaagaa tctacacacc gaaagacaaa aacaagacaa atttgagtgc 2160
tacaggtgtc acgcttggca tcacacatgt gcctgtgtat tcctctaggt ggttaccagg 2220
agctctgcca ctgcatgtcc actagtgacg ggttcgctcc accaccccag ctgggtagcc 2280
gctgctctca cataaggggt ccaattaaaa ttgccaggaa taaattcccc cggactttga 2340
cttctcaaga gctaagaagg tttgctgagt attctggcat gatgtttggt gatcaaacaa 2400
ctgctggcca aaaatgatga gtatttcccc ctcttgctga agatgtgctc catac      2455

<210> 883
<211> 62
<212> PRT
<213> Homo sapiens

<400> 883
Met Thr His Ser Ser Ala Trp Leu Glu Arg Pro Gln Glu Thr Tyr Asn
                5                   10                  15
His Gly Gly Arg Arg Arg Gly Ser Lys Ala Arg Leu Thr Trp Trp Gln
            20                  25                  30
Glu Arg Thr Ser Glu Gly Gly Asp Cys His Lys Leu Phe Phe Phe Glu
        35                  40                  45
Thr Arg Val Trp Pro Cys Cys Pro Gly Trp Ser Ala Val Ala
    50                  55                  60

<210> 884
<211> 135
<212> PRT
<213> Homo sapiens

<400> 884
Met Val Glu Gly Glu Gly Glu Ala Arg His Val Leu His Gly Gly Arg
                5                   10                  15
Arg Glu Arg Val Arg Gly Glu Thr Ala Thr Asn Phe Phe Phe Leu Arg
            20                  25                  30
Gln Glu Ser Gly Pro Val Ala Gln Ala Gly Val Gln Trp His Asp Leu
        35                  40                  45
Ser Ser Leu Gln Pro Leu Pro His Arg Phe Lys Gln Phe Ser Cys Leu
    50                  55                  60
Ser Leu Pro His Ser Trp Asp His Arg Tyr Ala Pro Pro His Leu Ala
65                  70                  75                  80
Asn Phe Cys Ser Phe Ser Arg Asp Gly Val Ser Leu Cys Cys Ser Gly
                85                  90                  95
Trp Ser Lys Thr Pro Gly Leu Gln Gln Ser Ala Cys Leu Gly Leu Pro
            100                 105                 110
Lys Cys Trp Gly Tyr Arg His Lys Pro Pro His Pro Ala Cys His Ile
        115                 120                 125
Leu Leu Asn Tyr Gln Val Ser
    130                 135

<210> 885
<211> 77
<212> PRT
<213> Homo sapiens

<400> 885
Met His Tyr His Lys Asn Ser Met Gly Lys Ile Pro Pro Ile Ile Gln
```

```
                    5                   10                  15
Ser Pro Pro Thr Arg Ser Pro Pro Thr Arg Gly Ile Gly Trp Gly His
            20                  25                  30
Arg Ala Lys Pro Tyr Gln Met Leu Gln Gly Leu Gly Thr Leu Arg Pro
        35                  40                  45
Leu Arg Pro Gly Val Ser Val Thr Leu Leu Gly Ser Val Cys Leu Gln
    50                  55                  60
Asp Leu Pro Pro Leu Pro Trp Tyr Arg Arg Lys Val Leu
65                  70                  75
```

<210> 886
<211> 60
<212> PRT
<213> Homo sapiens

<400> 886

```
Met Leu Val His Ile Tyr Ser Cys Cys Gly Met Val Tyr Arg Phe Gly
                5                   10                  15
Gln Met Ser Asp Asn Pro Phe Tyr Ile Leu Ala Ser Leu Gly Ser Ser
            20                  25                  30
Ser Cys Arg Asn Gly Leu Ala Ser Lys Trp Arg Gln Ala Asp Pro Ser
        35                  40                  45
Asp Gly Tyr Met Glu Pro Cys Phe Gln Leu Leu Phe
    50                  55                  60
```

<210> 887
<211> 76
<212> PRT
<213> Homo sapiens

<400> 887

```
Met Cys Leu Cys Ile Pro Leu Gly Gly Tyr Gln Glu Leu Cys His Cys
                5                   10                  15
Met Ser Thr Ser Asp Gly Phe Ala Pro Pro Pro Gln Leu Gly Ser Arg
            20                  25                  30
Cys Ser His Ile Arg Gly Pro Ile Lys Ile Ala Arg Asn Lys Phe Pro
        35                  40                  45
Arg Thr Leu Thr Ser Gln Glu Leu Arg Arg Phe Ala Glu Tyr Ser Gly
    50                  55                  60
Met Met Phe Gly Asp Gln Thr Thr Ala Gly Gln Lys
65                  70                  75
```

<210> 888
<211> 76
<212> PRT
<213> Homo sapiens

<400> 888

```
Met Val Lys Ser Arg Phe Thr Lys Asn Thr Lys Ile Thr Gln Ala Trp
                5                   10                  15
Trp Arg Ala Pro Val Ile Pro Gly Thr Arg Glu Ala Glu Gly Gly Glu
            20                  25                  30
Ser Leu Glu Pro Gly Arg Leu Arg Glu Glu Asn Arg Leu Asn Pro Gly
        35                  40                  45
Gly Arg Gly Cys Ser Glu Pro Arg Ser Cys Cys Cys Thr Pro Ala Trp
    50                  55                  60
Ser Thr Glu Gln Asp Ser Ala Ser Lys Thr Asn Lys
65                  70                  75
```

<210> 889
<211> 80
<212> PRT
<213> Homo sapiens

<400> 889
Met Leu Leu His Ser Ser Leu Val Asn Arg Ala Arg Leu Cys Leu Lys
5 10 15
Asn Lys Gln Ile Asn Lys Gln Thr Asn Lys Thr Glu Arg Phe Cys Cys
20 25 30
Asn Val Gln Gly Ala Ile Cys Ser Phe Lys Lys Ile Ile Phe Gly Gln
35 40 45
Ala Gln Trp Leu Thr Pro Val Ile Pro Ala Leu Trp Glu Ala Lys Val
50 55 60
Gly Gly Ser Phe Glu Val Arg Ser Leu Arg Ser Ala Trp Pro Thr Trp
65 70 75 80

<210> 890
<211> 72
<212> PRT
<213> Homo sapiens

<400> 890
Met His Tyr His Lys Asn Ser Met Gly Lys Ile Pro Pro His Asn Pro
5 10 15
Ile Thr Ser His Gln Val Ser Ser Asp Thr Trp Asp Trp Val Gly Thr
20 25 30
Gln Ser Gln Thr Val Ser Asp Ala Ala Gly Ala Gly Asp Thr Glu Thr
35 40 45
Thr Gln Thr Trp Cys Leu Cys His Ser Ser Gly Leu Cys Leu Ser Pro
50 55 60
Gly Pro Pro Ser Pro Ser Met Val
65 70

<210> 891
<211> 77
<212> PRT
<213> Homo sapiens

<400> 891
Met His Tyr His Lys Asn Ser Met Gly Lys Ile Pro Pro Ile Ile Gln
5 10 15
Ser Pro Pro Thr Arg Ser Pro Pro Thr Arg Gly Ile Gly Trp Gly His
20 25 30
Arg Ala Lys Pro Tyr Gln Met Leu Gln Gly Leu Gly Thr Leu Arg Pro
35 40 45
Leu Arg Pro Gly Val Ser Val Thr Leu Leu Gly Ser Val Cys Leu Gln
50 55 60
Asp Leu Pro Pro Leu Pro Trp Tyr Arg Arg Lys Val Leu
65 70 75

<210> 892
<211> 60
<212> PRT
<213> Homo sapiens

<400> 892

```
Met Leu Val His Ile Tyr Ser Cys Cys Gly Met Val Tyr Arg Phe Gly
                5                   10                  15
Gln Met Ser Asp Asn Pro Phe Tyr Ile Leu Ala Ser Leu Gly Ser Ser
            20                  25                  30
Ser Cys Arg Asn Gly Leu Ala Ser Lys Trp Arg Gln Ala Asp Pro Ser
        35                  40                  45
Asp Gly Tyr Met Glu Pro Cys Phe Gln Leu Leu Phe
    50                  55                  60
```

<210> 893
<211> 76
<212> PRT
<213> Homo sapiens

<400> 893

```
Met Cys Leu Cys Ile Pro Leu Gly Gly Tyr Gln Glu Leu Cys His Cys
                5                   10                  15
Met Ser Thr Ser Asp Gly Phe Ala Pro Pro Pro Gln Leu Gly Ser Arg
            20                  25                  30
Cys Ser His Ile Arg Gly Pro Ile Lys Ile Ala Arg Asn Lys Phe Pro
        35                  40                  45
Arg Thr Leu Thr Ser Gln Glu Leu Arg Arg Phe Ala Glu Tyr Ser Gly
    50                  55                  60
Met Met Phe Gly Asp Gln Thr Thr Ala Gly Gln Lys
65                  70                  75
```

<210> 894
<211> 2479
<212> DNA
<213> Homo sapiens

<400> 894

```
gtcatattga acattccaga tacctatcat tactcgatgc tgttgataac agcaagatgg 60
ctttgaactc agggtcacca ccagctattg gaccttacta tgaaaaccat ggataccaac 120
cggaaaaccc ctatcccgca cagcccactg tggtccccac tgtctacgag gtgcatccgg 180
ctcagtacta cccgtccccc gtgccccagt acgccccgag ggtcctgacg caggcttcca 240
accccgtcgt ctgcacgcag cccaaatccc catccgggac agtgtgcacc tcaaagacta 300
agaaagcact gtgcatcacc ttgaccctgg ggaccttcct cgtgggagct gcgctggccg 360
ctggcctact ctggaagttc atgggcagca agtgctccaa ctctgggata gagtgcgact 420
cctcaggtac ctgcatcaac ccctctaact ggtgtgatgg cgtgtcacac tgccccggcg 480
gggaggacga gaatcggtgt gttcgcctct acggaccaaa cttcatcctt cagatgtact 540
catctcagag gaagtcctgg caccctgtgt gccaagacga ctggaacgag aactacgggc 600
gggcggcctg cagggacatg ggctataaga ataattttta ctctagccaa ggaatagtgg 660
atgacagcgg atccaccagc tttatgaaac tgaacacaag tgccggcaat gtcgatatct 720
ataaaaaact gtaccacagt gatgcctgtt cttcaaaagc agtggtttct ttacgctgtt 780
tagcctgcgg ggtcaacttg aactcaagcc gccagagcag gatcgtgggc ggtgagagcg 840
cgctcccggg ggcctggccc tggcaggtca gcctgcacgt ccagaacgtc cacgtgtgcg 900
gaggctccat catcaccccc gagtggatcg tgacagccgc ccactgcgtg gaaaaacctc 960
ttaacaatcc atggcattgg acggcatttg cggggatttt gagacaatct ttcatgttct 1020
atggagccgg ataccaagta caaaaagtga tttctcatcc aaattatgac tccaagacca 1080
agaacaatga cattgcgctg atgaagctgc agaagcctct gactttcaac gacctagtga 1140
aaccagtgtg tctgcccaac ccaggcatga tgctgcagcc agaacagctc tgctggattt 1200
ccgggtgggg ggccaccgag gagaaaggga agacctcaga agtgctgaac gctgccaagg 1260
tgcttctcat tgagacacag agatgcaaca gcagatatgt ctatgacaac ctgatcacac 1320
cagccatgat ctgtgccggc ttcctgcagg ggaacgtcga ttcttgccag ggtgacagtg 1380
gagggcctct ggtcacttcg aacaacaata tctggtggct gataggggat acaagctggg 1440
gttctggctg tgccaaagct tacagaccag gagtgtacgg gaatgtgatg gtattcacgg 1500
actggattta tcgacaaatg aaggcaaacg gctaatccac atggtcttcg tccttgacgt 1560
```

cgttttacaa gaaaacaatg gggctggttt tgcttccccg tgcatgattt actcttagag 1620
atgattcaga ggtcacttca tttttattaa acagtgaact tgtctggctt tggcactctc 1680
tgccatactg tgcaggctgc agtggctccc ctgcccagcc tgctctccct aacccccttgt 1740
ccgcaagggg tgatggccgg ctggttgtgg gcactggcgg tcaattgtgg aaggaagagg 1800
gttggaggct gcccccattg agatcttcct gctgagtcct ttccaggggc caattttgga 1860
tgagcatgga gctgtcactt ctcagctgct ggatgacttg agatgaaaaa ggagagacat 1920
ggaaagggag acagccaggt ggcacctgca gcggctgccc tctggggcca cttggtagtg 1980
tccccagcct acttcacaag gggattttgc tgatgggttc ttagagcctt agcagccctg 2040
gatggtggcc agaaataaag ggaccagccc ttcatgggtg gtgacgtggt agtcacttgt 2100
aaggggaaca gaaacatttt tgttcttatg gggtgagaat atagacagtg cccttggtgc 2160
gagggaagca attgaaaagg aacttgccct gagcactcct ggtgcaggtc tccacctgca 2220
cattgggtgg ggctcctggg agggagactc agccttcctc ctcatcctcc ctgaccctgc 2280
tcctagcacc ctggagagtg aatgcccctt ggtccctggc agggcgccaa gtttggcacc 2340
atgtcggcct cttcaggcct gatagtcatt ggaaattgag gtccatgggg gaaatcaagg 2400
atgctcagtt taaggtacac tgtttccatg ttatgtttct acacattgat ggtggtgacc 2460
ctgagttcaa agccatctt 2479

<210> 895
<211> 492
<212> PRT
<213> Homo sapiens

<400> 895
Met Ala Leu Asn Ser Gly Ser Pro Pro Ala Ile Gly Pro Tyr Tyr Glu
1 5 10 15
Asn His Gly Tyr Gln Pro Glu Asn Pro Tyr Pro Ala Gln Pro Thr Val
20 25 30
Val Pro Thr Val Tyr Glu Val His Pro Ala Gln Tyr Tyr Pro Ser Pro
35 40 45
Val Pro Gln Tyr Ala Pro Arg Val Leu Thr Gln Ala Ser Asn Pro Val
50 55 60
Val Cys Thr Gln Pro Lys Ser Pro Ser Gly Thr Val Cys Thr Ser Lys
65 70 75 80
Thr Lys Lys Ala Leu Cys Ile Thr Leu Thr Leu Gly Thr Phe Leu Val
85 90 95
Gly Ala Ala Leu Ala Ala Gly Leu Leu Trp Lys Phe Met Gly Ser Lys
100 105 110
Cys Ser Asn Ser Gly Ile Glu Cys Asp Ser Ser Gly Thr Cys Ile Asn
115 120 125
Pro Ser Asn Trp Cys Asp Gly Val Ser His Cys Pro Gly Gly Glu Asp
130 135 140
Glu Asn Arg Cys Val Arg Leu Tyr Gly Pro Asn Phe Ile Leu Gln Met
145 150 155 160
Tyr Ser Ser Gln Arg Lys Ser Trp His Pro Val Cys Gln Asp Asp Trp
165 170 175
Asn Glu Asn Tyr Gly Arg Ala Ala Cys Arg Asp Met Gly Tyr Lys Asn
180 185 190
Asn Phe Tyr Ser Ser Gln Gly Ile Val Asp Asp Ser Gly Ser Thr Ser
195 200 205
Phe Met Lys Leu Asn Thr Ser Ala Gly Asn Val Asp Ile Tyr Lys Lys
210 215 220
Leu Tyr His Ser Asp Ala Cys Ser Ser Lys Ala Val Val Ser Leu Arg
225 230 235 240
Cys Leu Ala Cys Gly Val Asn Leu Asn Ser Ser Arg Gln Ser Arg Ile
245 250 255
Val Gly Gly Glu Ser Ala Leu Pro Gly Ala Trp Pro Trp Gln Val Ser
260 265 270
Leu His Val Gln Asn Val His Val Cys Gly Gly Ser Ile Ile Thr Pro

```
        275                 280                 285
Glu Trp Ile Val Thr Ala Ala His Cys Val Glu Lys Pro Leu Asn Asn
    290                 295                 300
Pro Trp His Trp Thr Ala Phe Ala Gly Ile Leu Arg Gln Ser Phe Met
305                 310                 315                 320
Phe Tyr Gly Ala Gly Tyr Gln Val Gln Lys Val Ile Ser His Pro Asn
                325                 330                 335
Tyr Asp Ser Lys Thr Lys Asn Asn Asp Ile Ala Leu Met Lys Leu Gln
            340                 345                 350
Lys Pro Leu Thr Phe Asn Asp Leu Val Lys Pro Val Cys Leu Pro Asn
        355                 360                 365
Pro Gly Met Met Leu Gln Pro Glu Gln Leu Cys Trp Ile Ser Gly Trp
    370                 375                 380
Gly Ala Thr Glu Glu Lys Gly Lys Thr Ser Glu Val Leu Asn Ala Ala
385                 390                 395                 400
Lys Val Leu Leu Ile Glu Thr Gln Arg Cys Asn Ser Arg Tyr Val Tyr
                405                 410                 415
Asp Asn Leu Ile Thr Pro Ala Met Ile Cys Ala Gly Phe Leu Gln Gly
            420                 425                 430
Asn Val Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Thr Ser
        435                 440                 445
Asn Asn Asn Ile Trp Trp Leu Ile Gly Asp Thr Ser Trp Gly Ser Gly
    450                 455                 460
Cys Ala Lys Ala Tyr Arg Pro Gly Val Tyr Gly Asn Val Met Val Phe
465                 470                 475                 480
Thr Asp Trp Ile Tyr Arg Gln Met Lys Ala Asn Gly
                485                 490
```

<210> 896
<211> 683
<212> DNA
<213> Homo sapiens

<400> 896

```
gtcatattga acattccaga tacctatcat tactcgatgc tgttgataac agcaagatgg 60
ctttgaactc agggtcacca ccagctattg gaccttacta tgaaaaccat ggataccaac 120
cggaaaaccc ctatcccgca cagcccactg tggtccccac tgtctacgag gtgcatccgg 180
ctcagtacta cccgtccccc gtgccccagt acgccccgag ggtcctgacg caggcttcca 240
accccgtcgt ctgcacgcag cccaaatccc catccgggac agtgtgcacc tcaaagacta 300
agaaagcact gtgcatcacc ttgaccctgg ggaccttcct cgtgggagct gcgctggccg 360
ctggcctact ctggaagttc atgggcagca agtgctccaa ctctgggata gagtgcgact 420
cctcaggtac ctgcatcaac ccctctaact ggtgtgatgg cgtgtcacac tgccccggcg 480
gggaggacga gaatcggtgt gttcgcctct acggaccaaa cttcatcctt cagatgtact 540
catctcagag gaagtcctgg caccctgtgt gccaagacga ctggaacgag aactacggc 600
gggcggcctg cagggacatg ggctataaga ataattttta ctctagccaa ggaatagtgg 660
atgacagcgg atccaccagc ttt                                         683
```

<210> 897
<211> 209
<212> PRT
<213> Homo sapiens

<400> 897

```
Met Ala Leu Asn Ser Gly Ser Pro Pro Ala Ile Gly Pro Tyr Tyr Glu
 1               5                  10                  15
```

Asn His Gly Tyr Gln Pro Glu Asn Pro Tyr Pro Ala Gln Pro Thr Val
20 25 30
Val Pro Thr Val Tyr Glu Val His Pro Ala Gln Tyr Tyr Pro Ser Pro
35 40 45
Val Pro Gln Tyr Ala Pro Arg Val Leu Thr Gln Ala Ser Asn Pro Val
50 55 60
Val Cys Thr Gln Pro Lys Ser Pro Ser Gly Thr Val Cys Thr Ser Lys
65 70 75 80
Thr Lys Lys Ala Leu Cys Ile Thr Leu Thr Leu Gly Thr Phe Leu Val
85 90 95
Gly Ala Ala Leu Ala Ala Gly Leu Leu Trp Lys Phe Met Gly Ser Lys
100 105 110
Cys Ser Asn Ser Gly Ile Glu Cys Asp Ser Ser Gly Thr Cys Ile Asn
115 120 125
Pro Ser Asn Trp Cys Asp Gly Val Ser His Cys Pro Gly Gly Glu Asp
130 135 140
Glu Asn Arg Cys Val Arg Leu Tyr Gly Pro Asn Phe Ile Leu Gln Met
145 150 155 160
Tyr Ser Ser Gln Arg Lys Ser Trp His Pro Val Cys Gln Asp Asp Trp
165 170 175
Asn Glu Asn Tyr Gly Arg Ala Ala Cys Arg Asp Met Gly Tyr Lys Asn
180 185 190
Asn Phe Tyr Ser Ser Gln Gly Ile Val Asp Asp Ser Gly Ser Thr Ser
195 200 205
Phe

<210> 898
<211> 27
<212> PRT
<213> Homo sapiens

<400> 898
Val Gly Glu Gly Leu Tyr Gln Gly Val Pro Arg Ala Glu Pro Gly Thr
1 5 10 15
Glu Ala Arg Arg His Tyr Asp Glu Gly Val Arg
20 25

<210> 899
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 899
ggatccgccg ccaccatgtc actttctagc ctgct 35

<210> 900
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 900

gtcgactcag ctggaccaca gccgcag 27

<210> 901
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 901
ggatccgccg ccaccatggg ctgcaggctg ctct 34

<210> 902
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 902
gtcgactcag aaatcctttc tcttgac 27

<210> 903
<211> 936
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...()
<223> n = A,T,C or G

<400> 903
atgggctgca ggctgntctg ctgtgcggtt ctctgtctcc tgggagcggt ccccatggaa 60
acgggagtta cgcagacacc aagacacctg gtcatgggaa tgacaaataa gaagtctttg 120
aaatgtgaac aacatctggg tcataacgct atgtattggt acaagcaaag tgctaagaag 180
ccactggagc tcatgtttgt ctacagtctt gaagaacggg ttgaaaacaa cagtgtgcca 240
agtcgcttct cacctgaatg ccccaacagc tctcacttat tccttcacct acacaccctg 300
cagccagaag actcggccct gtatctctgc gccagcagcc aagaccggac aagcagctcc 360
tacgagcagt acttcgggcc gggcaccagg ctcacggtca cagaggacct gaaaaacgtg 420
ttcccacccg aggtcgctgt gtttgagcca tcagaagcag agatctccca cacccaaaag 480
gccacactgg tgtgcctggc cacaggcttc taccccgacc acgtggagct gagctggtgg 540
gtgaatggga aggaggtgca cagtggggtc agcacagacc cgcagcccct caaggagcag 600
cccgccctca atgactccag atactgcctg agcagccgcc tgagggtctc ggccaccttc 660
tggcagaacc cccgcaacca cttccgctgt caagtccagt tctacgggct ctcggagaat 720
gacgagtgga cccaggatag ggccaaacct gtcacccaga tcgtcagcgc cgaggcctgg 780
ggtagagcag actgtggctt cacctccgag tcttaccagc aaggggtcct gtctgccacc 840
atcctctatg agatcttgct agggaaggcc accttgtatg ccgtgctggt cagtgccctc 900
gtgctgatgg ccatggtcaa gagaaaggat ttctga 936

<210> 904
<211> 834
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...()
<223> n = A,T,C or G

<400> 904
atgtcacttt ctagcctgct naaggtggtc acagcttcac tgtggctagg acctggcatt 60
gcccagaaga taactcaaac ccaaccagga atgttcgtgc aggaaaagga ggctgtgact 120
ctggactgca catatgacac cagtgatcaa agttatggtc tcttctggta caagcagccc 180
agcagtgggg aaatgatttt tcttatttat caggggtctt atgacgagca aaatgcaaca 240
gaaggtcgct actcattgaa tttccagaag gcaagaaaat ccgccaacct tgtcatctcc 300
gcttcacaac tgggggactc agcaatgtat ttctgtgcaa tgagagaggg cgcgggagga 360
ggaaacaaac tcacctttgg gacaggcact cagctaaaag tggaactcaa tatccagaac 420
cctgaccctg ccgtgtacca gctgagagac tctaaatcca gtgacaagtc tgtctgccta 480
ttcaccgatt ttgattctca aacaaatgtg tcacaaagta aggattctga tgtgtatatc 540
acagacaaaa ctgtgctaga catgaggtct atggacttca agagcaacag tgctgtggcc 600
tggagcaaca aatctgactt tgcatgtgca aacgccttca acaacagcat tattccagaa 660
gacaccttct tccccagccc agaaagttcc tgtgatgtca agctggtcga gaaaagcttt 720
gaaacagata cgaacctaaa ctttcaaaac ctgtcagtga ttgggttccg aatcctcctc 780
ctgaaagtgg ccgggtttaa tctgctcatg acgctgcggc tgtggtccag ctga 834

<210> 905
<211> 311
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(311)
<223> Xaa = Any amino acid

<400> 905
Met Gly Cys Arg Leu Xaa Cys Cys Ala Val Leu Cys Leu Leu Gly Ala
1 5 10 15
Val Pro Met Glu Thr Gly Val Thr Gln Thr Pro Arg His Leu Val Met
20 25 30
Gly Met Thr Asn Lys Lys Ser Leu Lys Cys Glu Gln His Leu Gly His
35 40 45
Asn Ala Met Tyr Trp Tyr Lys Gln Ser Ala Lys Lys Pro Leu Glu Leu
50 55 60
Met Phe Val Tyr Ser Leu Glu Glu Arg Val Glu Asn Asn Ser Val Pro
65 70 75 80
Ser Arg Phe Ser Pro Glu Cys Pro Asn Ser Ser His Leu Phe Leu His
85 90 95
Leu His Thr Leu Gln Pro Glu Asp Ser Ala Leu Tyr Leu Cys Ala Ser
100 105 110
Ser Gln Asp Arg Thr Ser Ser Ser Tyr Glu Gln Tyr Phe Gly Pro Gly
115 120 125
Thr Arg Leu Thr Val Thr Glu Asp Leu Lys Asn Val Phe Pro Pro Glu
130 135 140
Val Ala Val Phe Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys
145 150 155 160
Ala Thr Leu Val Cys Leu Ala Thr Gly Phe Tyr Pro Asp His Val Glu
165 170 175
Leu Ser Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr
180 185 190
Asp Pro Gln Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr
195 200 205

```
Cys Leu Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn Pro
    210                 215                 220
Arg Asn His Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn
225                 230                 235                 240
Asp Glu Trp Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser
                245                 250                 255
Ala Glu Ala Trp Gly Arg Ala Asp Cys Gly Phe Thr Ser Glu Ser Tyr
            260                 265                 270
Gln Gln Gly Val Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly
        275                 280                 285
Lys Ala Thr Leu Tyr Ala Val Leu Val Ser Ala Leu Val Leu Met Ala
    290                 295                 300
Met Val Lys Arg Lys Asp Phe
305                 310
```

<210> 906
<211> 277
<212> PRT
<213> Homo sapiens

<400> 906

```
Met Ser Leu Ser Ser Leu Leu Lys Val Val Thr Ala Ser Leu Trp Leu
                5                   10                  15
Gly Pro Gly Ile Ala Gln Lys Ile Thr Gln Thr Gln Pro Gly Met Phe
            20                  25                  30
Val Gln Glu Lys Glu Ala Val Thr Leu Asp Cys Thr Tyr Asp Thr Ser
        35                  40                  45
Asp Gln Ser Tyr Gly Leu Phe Trp Tyr Lys Gln Pro Ser Ser Gly Glu
    50                  55                  60
Met Ile Phe Leu Ile Tyr Gln Gly Ser Tyr Asp Glu Gln Asn Ala Thr
65                  70                  75                  80
Glu Gly Arg Tyr Ser Leu Asn Phe Gln Lys Ala Arg Lys Ser Ala Asn
                85                  90                  95
Leu Val Ile Ser Ala Ser Gln Leu Gly Asp Ser Ala Met Tyr Phe Cys
            100                 105                 110
Ala Met Arg Glu Gly Ala Gly Gly Gly Asn Lys Leu Thr Phe Gly Thr
        115                 120                 125
Gly Thr Gln Leu Lys Val Glu Leu Asn Ile Gln Asn Pro Asp Pro Ala
    130                 135                 140
Val Tyr Gln Leu Arg Asp Ser Lys Ser Ser Asp Lys Ser Val Cys Leu
145                 150                 155                 160
Phe Thr Asp Phe Asp Ser Gln Thr Asn Val Ser Gln Ser Lys Asp Ser
                165                 170                 175
Asp Val Tyr Ile Thr Asp Lys Thr Val Leu Asp Met Arg Ser Met Asp
            180                 185                 190
Phe Lys Ser Asn Ser Ala Val Ala Trp Ser Asn Lys Ser Asp Phe Ala
        195                 200                 205
Cys Ala Asn Ala Phe Asn Asn Ser Ile Ile Pro Glu Asp Thr Phe Phe
    210                 215                 220
Pro Ser Pro Glu Ser Ser Cys Asp Val Lys Leu Val Glu Lys Ser Phe
225                 230                 235                 240
Glu Thr Asp Thr Asn Leu Asn Phe Gln Asn Leu Ser Val Ile Gly Phe
                245                 250                 255
Arg Ile Leu Leu Leu Lys Val Ala Gly Phe Asn Leu Leu Met Thr Leu
            260                 265                 270
Arg Leu Trp Ser Ser
        275
```

<210> 907
<211> 1536
<212> DNA
<213> Homo sapiens

<400> 907
atgtacaacc tgttgctgtc ctacgacaga catggggacc acctgcagcc cctggacctc 60
gtgcccaatc accagggtct cacccctttc aagctggctg gagtggaggg taacactgtg 120
atgtttcagc acctgatgca gaagcggaag cacacccagt ggacgtatgg accactgacc 180
tcgactctct atgacctcac agagatcgac tcctcagggg atgagcagtc cctgctggaa 240
cttatcatca ccaccaagaa gcgggaggct cgccagatcc tggaccagac gccggtgaag 300
gagctggtga gcctcaagtg gaagcggtac gggcggccgt acttctgcat gctgggtgcc 360
atatatctgc tgtacatcat ctgcttcacc atgtgctgca tctaccgccc cctcaagccc 420
aggaccaata accgcacgag cccccgggac aacaccctct tacagcagaa gctacttcag 480
gaagcctaca tgacccctaa ggacgatatc cggctggtcg gggagctggt gactgtcatt 540
ggggctatca tcatcctgct ggtagaggtt ccagacatct tcagaatggg ggtcactcgc 600
ttctttggac agaccatcct tgggggccca ttccatgtcc tcatcatcac ctatgccttc 660
atggtgctgg tgaccatggt gatgcggctc atcagtgcca gcggggaggt ggtacccatg 720
tcctttgcac tcgtgctggg ctggtgcaac gtcatgtact tcgcccgagg attccagatg 780
ctaggcccct tcaccatcat gattcagaag atgatttttg gcgacctgat gcgattctgc 840
tggctgatgg ctgtggtcat cctgggcttt gcttcagcct tctatatcat cttccagaca 900
gaggaccccg aggagctagg ccacttctac gactacccca tggccctgtt cagcaccttc 960
gagctgttcc ttaccatcat cgatggccca gccaactaca acgtggacct gcccttcatg 1020
tacagcatca cctatgctgc ctttgccatc atcgccacac tgctcatgct caacctcctc 1080
attgccatga tgggcgacac tcactggcga gtggcccatg agcgggatga gctgtggagg 1140
gcccagattg tggccaccac ggtgatgctg gagcggaagc tgcctcgctg cctgtggcct 1200
cgctccggga tctgcggacg ggagtatggc ctgggagacc gctggttcct gcgggtggaa 1260
gacaggcaag atctcaaccg gcagcggatc caacgctacg cacaggcctt ccacacccgg 1320
ggctctgagg atttggacaa agactcagtg gaaaaactag agctgggctg tcccttcagc 1380
cccccacctgt cccttcctat gccctcagtg tctcgaagta cctcccgcag cagtgccaat 1440
tgggaaaggc ttcggcaagg gaccctgagg agagacctgc gtgggataat caacaggggt 1500
ctggaggacg gggagagctg ggaatatcag atctga 1536

<210> 908
<211> 1533
<212> DNA
<213> Homo sapiens

<400> 908
atgtacaacc tgttgctgtc ctacgacaga catggggacc acctgcagcc cctggacctc 60
gtgcccaatc accagggtct cacccctttc aagctggctg gagtggaggg taacactgtg 120
atgtttcagc acctgatgca gaagcggaag cacacccagt ggacgtatgg accactgacc 180
tcgactctct atgacctcac agagatcgac tcctcagggg atgagcagtc cctgctggaa 240
cttatcatca ccaccaagaa gcgggaggct cgccagatcc tggaccagac gccggtgaag 300
gagctggtga gcctcaagtg gaagcggtac gggcggccgt acttctgcat gctgggtgcc 360
atatatctgc tgtacatcat ctgcttcacc atgtgctgca tctaccgccc cctcaagccc 420
aggaccaata accgcacgag cccccgggac aacaccctct tacagcagaa gctacttcag 480
gaagcctaca tgacccctaa ggacgatatc cggctggtcg gggagctggt gactgtcatt 540
ggggctatca tcatcctgct ggtagaggtt ccagacatct tcagaatggg ggtcactcgc 600
ttctttggac agaccatcct tgggggccca ttccatgtcc tcatcatcac ctatgccttc 660
atggtgctgg tgaccatggt gatgcggctc atcagtgcca gcggggaggt ggtacccatg 720
tcctttgcac tcgtgctggg ctggtgcaac gtcatgtact tcgcccgagg attccagatg 780
ctaggcccct tcaccatcat gattcagaag atgatttttg gcgacctgat gcgattctgc 840
tggctgatgg ctgtggtcat cctgggcttt gcttcagcct tctatatcat cttccagaca 900
gaggaccccg aggagctagg ccacttctac gactacccca tggccctgtt cagcaccttc 960
gagctgttcc ttaccatcat cgatggccca gccaactaca acgtggacct gcccttcatg 1020
tacagcatca cctatgctgc ctttgccatc atcgccacac tgctcatgct caacctcctc 1080

```
attgccatga tgggcgacac tcactggcga gtggcccatg agcgggatga gctgtggagg 1140
gcccagattg tggccaccac ggtgatgctg gagcggaagc tgcctcgctg cctgtggcct 1200
cgctccggga tctgcggacg ggagtatggc ctgggagacc gctggttcct gcgggtggaa 1260
gacaggcaag atctcaaccg gcagcggatc caacgctacg cacaggcctt ccacacccgg 1320
ggctctgagg atttggacaa agactcagtg gaaaaactag agctgggctg tcccttcagc 1380
ccccacctgt cccttcctat gccctcagtg tctcgaagta cctcccgcag cagtgccaat 1440
tgggaaaggc ttcggcaagg gaccctgagg agagacctgc gtgggataat caacaggggt 1500
ctggaggacg gggagagctg ggaatatcag atc                              1533
```

<210> 909
<211> 511
<212> PRT
<213> Homo sapiens

<400> 909

```
Met Tyr Asn Leu Leu Leu Ser Tyr Asp Arg His Gly Asp His Leu Gln
                5                   10                  15
Pro Leu Asp Leu Val Pro Asn His Gln Gly Leu Thr Pro Phe Lys Leu
            20                  25                  30
Ala Gly Val Glu Gly Asn Thr Val Met Phe Gln His Leu Met Gln Lys
        35                  40                  45
Arg Lys His Thr Gln Trp Thr Tyr Gly Pro Leu Thr Ser Thr Leu Tyr
    50                  55                  60
Asp Leu Thr Glu Ile Asp Ser Ser Gly Asp Glu Gln Ser Leu Leu Glu
65                  70                  75                  80
Leu Ile Ile Thr Thr Lys Lys Arg Glu Ala Arg Gln Ile Leu Asp Gln
                85                  90                  95
Thr Pro Val Lys Glu Leu Val Ser Leu Lys Trp Lys Arg Tyr Gly Arg
            100                 105                 110
Pro Tyr Phe Cys Met Leu Gly Ala Ile Tyr Leu Leu Tyr Ile Ile Cys
        115                 120                 125
Phe Thr Met Cys Cys Ile Tyr Arg Pro Leu Lys Pro Arg Thr Asn Asn
    130                 135                 140
Arg Thr Ser Pro Arg Asp Asn Thr Leu Leu Gln Gln Lys Leu Leu Gln
145                 150                 155                 160
Glu Ala Tyr Met Thr Pro Lys Asp Asp Ile Arg Leu Val Gly Glu Leu
                165                 170                 175
Val Thr Val Ile Gly Ala Ile Ile Ile Leu Leu Val Glu Val Pro Asp
            180                 185                 190
Ile Phe Arg Met Gly Val Thr Arg Phe Phe Gly Gln Thr Ile Leu Gly
        195                 200                 205
Gly Pro Phe His Val Leu Ile Ile Thr Tyr Ala Phe Met Val Leu Val
    210                 215                 220
Thr Met Val Met Arg Leu Ile Ser Ala Ser Gly Glu Val Val Pro Met
225                 230                 235                 240
Ser Phe Ala Leu Val Leu Gly Trp Cys Asn Val Met Tyr Phe Ala Arg
                245                 250                 255
Gly Phe Gln Met Leu Gly Pro Phe Thr Ile Met Ile Gln Lys Met Ile
            260                 265                 270
Phe Gly Asp Leu Met Arg Phe Cys Trp Leu Met Ala Val Val Ile Leu
        275                 280                 285
Gly Phe Ala Ser Ala Phe Tyr Ile Ile Phe Gln Thr Glu Asp Pro Glu
    290                 295                 300
Glu Leu Gly His Phe Tyr Asp Tyr Pro Met Ala Leu Phe Ser Thr Phe
305                 310                 315                 320
Glu Leu Phe Leu Thr Ile Ile Asp Gly Pro Ala Asn Tyr Asn Val Asp
                325                 330                 335
Leu Pro Phe Met Tyr Ser Ile Thr Tyr Ala Ala Phe Ala Ile Ile Ala
```

340 345 350
Thr Leu Leu Met Leu Asn Leu Leu Ile Ala Met Met Gly Asp Thr His
355 360 365
Trp Arg Val Ala His Glu Arg Asp Glu Leu Trp Arg Ala Gln Ile Val
370 375 380
Ala Thr Thr Val Met Leu Glu Arg Lys Leu Pro Arg Cys Leu Trp Pro
385 390 395 400
Arg Ser Gly Ile Cys Gly Arg Glu Tyr Gly Leu Gly Asp Arg Trp Phe
405 410 415
Leu Arg Val Glu Asp Arg Gln Asp Leu Asn Arg Gln Arg Ile Gln Arg
420 425 430
Tyr Ala Gln Ala Phe His Thr Arg Gly Ser Glu Asp Leu Asp Lys Asp
435 440 445
Ser Val Glu Lys Leu Glu Leu Gly Cys Pro Phe Ser Pro His Leu Ser
450 455 460
Leu Pro Met Pro Ser Val Ser Arg Ser Thr Ser Arg Ser Ser Ala Asn
465 470 475 480
Trp Glu Arg Leu Arg Gln Gly Thr Leu Arg Arg Asp Leu Arg Gly Ile
485 490 495
Ile Asn Arg Gly Leu Glu Asp Gly Glu Ser Trp Glu Tyr Gln Ile
500 505 510

<210> 910
<211> 134
<212> PRT
<213> Homo sapiens

<400> 910
Met Tyr Asn Leu Leu Leu Ser Tyr Asp Arg His Gly Asp His Leu Gln
5 10 15
Pro Leu Asp Leu Val Pro Asn His Gln Gly Leu Thr Pro Phe Lys Leu
20 25 30
Ala Gly Val Glu Gly Asn Thr Val Met Phe Gln His Leu Met Gln Lys
35 40 45
Arg Lys His Thr Gln Trp Thr Tyr Gly Pro Leu Thr Ser Thr Leu Tyr
50 55 60
Asp Leu Thr Glu Ile Asp Ser Ser Gly Asp Glu Gln Ser Leu Leu Glu
65 70 75 80
Leu Ile Ile Thr Thr Lys Lys Arg Glu Ala Arg Gln Ile Leu Asp Gln
85 90 95
Thr Pro Val Lys Glu Leu Val Ser Leu Lys Trp Lys Arg Tyr Gly Arg
100 105 110
Pro Tyr Phe Cys Met Leu Gly Ala Ile Tyr Leu Leu Tyr Ile Ile Cys
115 120 125
Phe Thr Met Cys Cys Ile
130

<210> 911
<211> 55
<212> PRT
<213> Homo sapiens

<400> 911
Ala Tyr Arg Pro Leu Lys Pro Arg Thr Asn Asn Arg Thr Ser Pro Arg
5 10 15
Asp Asn Thr Leu Leu Gln Gln Lys Leu Leu Gln Glu Ala Tyr Met Thr
20 25 30
Pro Lys Asp Asp Ile Arg Leu Val Gly Glu Leu Val Thr Val Ile Gly

          35   40   45
Ala Ile Ile Ile Leu Leu Val
     50   55

<210> 912
<211> 39
<212> PRT
<213> Homo sapiens

<400> 912
Glu Val Pro Asp Ile Phe Arg Met Gly Val Thr Arg Phe Phe Gly Gln
                  5   10   15
Thr Ile Leu Gly Gly Pro Phe His Val Leu Ile Ile Thr Tyr Ala Phe
             20   25   30
Met Val Leu Val Thr Met Val
         35

<210> 913
<211> 19
<212> PRT
<213> Homo sapiens

<400> 913
Met Arg Leu Ile Ser Ala Ser Gly Glu Val Val Pro Met Ser Phe Ala
                  5   10   15
Leu Val Leu

<210> 914
<211> 52
<212> PRT
<213> Homo sapiens

<400> 914
Gly Trp Cys Asn Val Met Tyr Phe Ala Arg Gly Phe Gln Met Leu Gly
                  5   10   15
Pro Phe Thr Ile Met Ile Gln Lys Met Ile Phe Gly Asp Leu Met Arg
             20   25   30
Phe Cys Trp Leu Met Ala Val Val Ile Leu Gly Phe Ala Ser Ala Phe
         35   40   45
Tyr Ile Ile Phe
     50

<210> 915
<211> 213
<212> PRT
<213> Homo sapiens

<400> 915
Gln Thr Glu Asp Pro Glu Glu Leu Gly His Phe Tyr Asp Tyr Pro Met
                  5   10   15
Ala Leu Phe Ser Thr Phe Glu Leu Phe Leu Thr Ile Ile Asp Gly Pro
             20   25   30
Ala Asn Tyr Asn Val Asp Leu Pro Phe Met Tyr Ser Ile Thr Tyr Ala
         35   40   45
Ala Phe Ala Ile Ile Ala Thr Leu Leu Met Leu Asn Leu Leu Ile Ala
     50   55   60
Met Met Gly Asp Thr His Trp Arg Val Ala His Glu Arg Asp Glu Leu

```
65                  70                  75                  80
Trp Arg Ala Gln Ile Val Ala Thr Thr Val Met Leu Glu Arg Lys Leu
                85                  90                  95
Pro Arg Cys Leu Trp Pro Arg Ser Gly Ile Cys Gly Arg Glu Tyr Gly
            100                 105                 110
Leu Gly Asp Arg Trp Phe Leu Arg Val Glu Asp Arg Gln Asp Leu Asn
        115                 120                 125
Arg Gln Arg Ile Gln Arg Tyr Ala Gln Ala Phe His Thr Arg Gly Ser
    130                 135                 140
Glu Asp Leu Asp Lys Asp Ser Val Glu Lys Leu Glu Leu Gly Cys Pro
145                 150                 155                 160
Phe Ser Pro His Leu Ser Leu Pro Met Pro Ser Val Ser Arg Ser Thr
                165                 170                 175
Ser Arg Ser Ser Ala Asn Trp Glu Arg Leu Arg Gln Gly Thr Leu Arg
            180                 185                 190
Arg Asp Leu Arg Gly Ile Ile Asn Arg Gly Leu Glu Asp Gly Glu Ser
        195                 200                 205
Trp Glu Tyr Gln Ile
    210
```

```
<210> 916
<211> 1302
<212> DNA
<213> Homo sapiens

<400> 916
tggacaaagg gggtcacaca ttccttccat acggttgagc ctctacctgc ctggtgctgg 60
tcacagttca gcttcttcat gatggtggat cccaatggca atgaatccag tgctacatac 120
ttcatcctaa taggcctccc tggtttagaa gaggctcagt tctggttggc cttcccattg 180
tgctccctct accttattgc tgtgctaggt aacttgacaa tcatctacat tgtgcggact 240
gagcacagcc tgcatgagcc catgtatata tttctttgca tgctttcagg cattgacatc 300
ctcatctcca cctcatccat gcccaaaatg ctggccatct tctggttcaa ttccactacc 360
atccagtttg atgcttgtct gctacagatg tttgccatcc actccttatc tggcatggaa 420
tccacagtgc tgctggccat ggcttttgac cgctatgtgg ccatctgtca cccactgcgc 480
catgccacag tacttacgtt gcctcgtgtc accaaaattg gtgtggctgc tgtggtgcgg 540
ggggctgcac tgatggcacc ccttcctgtc ttcatcaagc agctgcccctt ctgccgctcc 600
aatatccttt cccattccta ctgcctacac caagatgtca tgaagctggc ctgtgatgat 660
atccgggtca atgtcgtcta tggccttatc gtcatcatct ccgccattgg cctggactca 720
cttctcatct ccttctcata tctgcttatt cttaagactg tgttgggctt gacacgtgaa 780
gcccaggcca aggcatttgg cacttgcgtc tctcatgtgt gtgctgtgtt catattctat 840
gtacctttca ttggattgtc catggtgcat cgctttagca agcggcgtga ctctccgctg 900
cccgtcatct tggccaatat ctatctgctg gttcctcctg tgctcaaccc aattgtctat 960
ggagtgaaga caaaggagat tcgacagcgc atccttcgac ttttccatgt ggccacacac 1020
gcttcagagc cctaggtgtc agtgatcaaa cttcttttcc attcagagtc ctctgattca 1080
gattttaatg ttaacatttt ggaagacagt attcagaaaa aaaatttcct taataaaaat 1140
acaactcaga tccttcaaat atgaaactgg ttggggaatc tccatttttt caatattatt 1200
ttcttctttg ttttcttgct acatataatt attaataccc tgactaggtt gtggtttgag 1260
ggttattact tttcatttta ccatgcagtc caaatctaaa ct                   1302

<210> 917
<211> 2061
<212> DNA
<213> Homo sapiens

<400> 917
acgattcgac agcgcatcct tcgacttttc catgtggcca cacacgcttc agagccctag 60
gtgtcagtga tcaaacttct tttccattca gagtcctctg attcagattt taatgttaac 120
```

attttggaag acagtattca gaaaaaaaat ttccttaata aaaatacaac tcagatcctt 180
caaatatgaa actggttggg gaatctccat tttttcaata ttattttctt ctttgttttc 240
ttgctacata taattattaa taccctgact aggttgtggt tggagggtta ttacttttca 300
ttttaccatg cagtccaaat ctaaactgct tctactgatg gtttacagca ttctgagata 360
agaatggtac atctagagaa catttgccaa aggcctaagc acggcaaagg aaaataaaca 420
cagaatataa taaaatgaga taatctagct taaaactata acttcctctt cagaactccc 480
aaccacattg gatctcagaa aaatgctgtc ttcaaaatga cttctacaga gaagaaataa 540
tttttcctct ggacactagc acttaagggg aagattggaa gtaaagcctt gaaaagagta 600
catttaccta cgttaatgaa agttgacaca ctgttctgag agttttcaca gcatatggac 660
cctgtttttc ctatttaatt ttcttatcaa ccctttaatt aggcaaagat attattagta 720
ccctcattgt agccatggga aaattgatgt tcagtgggga tcagtgaatt aaatggggtc 780
atacaagtat aaaaattaaa aaaaaaggac ttcatgccca atctcatatg atgtggaaga 840
actgttagag agaccaacag ggtagtgggt tagagatttc cagagtctta catttctag 900
aggaggtatt taatttcttc tcactcatcc agtgttgtat ttaggaattt cctggcaaca 960
gaactcatgg ctttaatccc actagctatt gcttattgtc ctggtccaat tgccaattac 1020
ctgtgtcttg gaagaagtga tttctaggtt caccattatg gaagattctt attcagaaag 1080
tctgcatagg gcttatagca agttatttat ttttaaaagt tccataggtg attctgatag 1140
gcagtgaggt tagggagcca ccagttatga tgggaagtat ggaatggcag gtcttgaaga 1200
taacattggc cttttgagtg tgactcgtag ctggaaagtg agggaatctt caggaccatg 1260
ctttatttgg ggctttgtgc agtatggaac agggactttg agaccaggaa agcaatctga 1320
cttaggcatg ggaatcaggc atttttgctt ctgaggggct attaccaagg gttaataggt 1380
ttcatcttca acaggatatg acaacagtgt taaccaagaa actcaaatta caaatactaa 1440
aacatgtgat catatatgtg gtaagtttca ttttcttttt caatcctcag gttccctgat 1500
atggattcct ataacatgct ttcatcccct tttgtaatgg atatcatatt tggaaatgcc 1560
tatttaatac ttgtatttgc tgctggactg taagcccatg agggcactgt ttattattga 1620
atgtcatctc tgttcatcat tgactgctct ttgctcatca ttgaatcccc cagcaaagtg 1680
cctagaacat aatagtgctt atgcttgaca ccggttattt ttcatcaaac ctgattcctt 1740
ctgtcctgaa cacatagcca ggcaatttc cagccttctt tgagttgggt attattaaat 1800
tctggccatt acttccaatg tgagtggaag tgacatgtgc aatttctata cctggctcat 1860
aaaaccctcc catgtgcagc ctttcatgtt gacattaaat gtgacttggg aagctatgtg 1920
ttacacagag taaatcacca gaagcctgga tttctgaaaa aactgtgcag agccaaacct 1980
ctgtcatttg caactcccac ttgtatttgt acgaggcagt tggataagtg aaaaataaag 2040
tactattgtg tcaagtctct g 2061

<210> 918
<211> 957
<212> DNA
<213> Homo sapiens

<400> 918
atgatggtgg atcccaatgg caatgaatcc agtgctacat acttcatcct aataggcctc 60
cctggtttag aagaggctca gttctggttg gccttcccat tgtgctccct ctaccttatt 120
gctgtgctag gtaacttgac aatcatctac attgtgcgga ctgagcacag cctgcatgag 180
cccatgtata tatttctttg catgctttca ggcattgaca tcctcatctc cacctcatcc 240
atgcccaaaa tgctggccat cttctggttc aattccacta ccatccagtt tgatgcttgt 300
ctgctacaga tgtttgccat ccactcctta tctggcatgg aatccacagt gctgctggcc 360
atggcttttg accgctatgt ggccatctgt cacccactgc gccatgccac agtacttacg 420
ttgcctcgtg tcaccaaaat tggtgtggct gctgtggtgc gggggctgc actgatggca 480
ccccttcctg tcttcatcaa gcagctgccc ttctgccgct ccaatatcct ttcccattcc 540
tactgcctac accaagatgt catgaagctg gcctgtgatg atatccgggt caatgtcgtc 600
tatggcctta tcgtcatcat ctccgccatt ggcctggact cacttctcat ctccttctca 660
tatctgctta ttcttaagac tgtgttgggc ttgacacgtg aagcccaggc caaggcattt 720
ggcacttgcg tctctcatgt gtgtgctgtg ttcatattct atgtaccttt cattggattg 780
tccatggtgc atcgctttag caagcggcgt gactctccgc tgcccgtcat cttggccaat 840
atctatctgc tggttcctcc tgtgctcaac ccaattgtct atggagtgaa gacaaaggag 900
attcgacagc gcatccttcg acttttccat gtggccacac acgcttcaga gccctag 957

<210> 919

<211> 954
<212> DNA
<213> Homo sapiens

<400> 919
atgatggtgg atcccaatgg caatgaatcc agtgctacat acttcatcct aataggcctc 60
cctggtttag aagaggctca gttctggttg gccttcccat tgtgctccct ctaccttatt 120
gctgtgctag gtaacttgac aatcatctac attgtgcgga ctgagcacag cctgcatgag 180
cccatgtata tatttctttg catgctttca ggcattgaca tcctcatctc cacctcatcc 240
atgcccaaaa tgctggccat cttctggttc aattccacta ccatccagtt tgatgcttgt 300
ctgctacaga tgtttgccat ccactcctta tctggcatgg aatccacagt gctgctggcc 360
atggcttttg accgctatgt ggccatctgt cacccactgc gccatgccac agtacttacg 420
ttgcctcgtg tcaccaaaat tggtgtggct gctgtggtgc ggggggctgc actgatggca 480
ccccttcctg tcttcatcaa gcagctgccc ttctgccgct ccaatatcct ttcccattcc 540
tactgcctac accaagatgt catgaagctg gcctgtgatg atatccgggt caatgtcgtc 600
tatggcctta tcgtcatcat ctccgccatt ggcctggact cacttctcat ctccttctca 660
tatctgctta ttcttaagac tgtgttgggc ttgacacgtg aagcccaggc caaggcattt 720
ggcacttgcg tctctcatgt gtgtgctgtg ttcatattct atgtaccttt cattggattg 780
tccatggtgc atcgctttag caagcggcgt gactctccgc tgcccgtcat cttggccaat 840
atctatctgc tggttcctcc tgtgctcaac ccaattgtct atggagtgaa gacaaaggag 900
attcgacagc gcatccttcg acttttccat gtggccacac acgcttcaga gccc 954

<210> 920
<211> 318
<212> PRT
<213> Homo sapiens

<400> 920
Met Met Val Asp Pro Asn Gly Asn Glu Ser Ser Ala Thr Tyr Phe Ile
5 10 15
Leu Ile Gly Leu Pro Gly Leu Glu Glu Ala Gln Phe Trp Leu Ala Phe
20 25 30
Pro Leu Cys Ser Leu Tyr Leu Ile Ala Val Leu Gly Asn Leu Thr Ile
35 40 45
Ile Tyr Ile Val Arg Thr Glu His Ser Leu His Glu Pro Met Tyr Ile
50 55 60
Phe Leu Cys Met Leu Ser Gly Ile Asp Ile Leu Ile Ser Thr Ser Ser
65 70 75 80
Met Pro Lys Met Leu Ala Ile Phe Trp Phe Asn Ser Thr Thr Ile Gln
85 90 95
Phe Asp Ala Cys Leu Leu Gln Met Phe Ala Ile His Ser Leu Ser Gly
100 105 110
Met Glu Ser Thr Val Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala
115 120 125
Ile Cys His Pro Leu Arg His Ala Thr Val Leu Thr Leu Pro Arg Val
130 135 140
Thr Lys Ile Gly Val Ala Ala Val Val Arg Gly Ala Ala Leu Met Ala
145 150 155 160
Pro Leu Pro Val Phe Ile Lys Gln Leu Pro Phe Cys Arg Ser Asn Ile
165 170 175
Leu Ser His Ser Tyr Cys Leu His Gln Asp Val Met Lys Leu Ala Cys
180 185 190
Asp Asp Ile Arg Val Asn Val Val Tyr Gly Leu Ile Val Ile Ile Ser
195 200 205
Ala Ile Gly Leu Asp Ser Leu Leu Ile Ser Phe Ser Tyr Leu Leu Ile
210 215 220
Leu Lys Thr Val Leu Gly Leu Thr Arg Glu Ala Gln Ala Lys Ala Phe
225 230 235 240

```
Gly Thr Cys Val Ser His Val Cys Ala Val Phe Ile Phe Tyr Val Pro
                245                 250                 255
Phe Ile Gly Leu Ser Met Val His Arg Phe Ser Lys Arg Arg Asp Ser
            260                 265                 270
Pro Leu Pro Val Ile Leu Ala Asn Ile Tyr Leu Leu Val Pro Pro Val
        275                 280                 285
Leu Asn Pro Ile Val Tyr Gly Val Lys Thr Lys Glu Ile Arg Gln Arg
    290                 295                 300
Ile Leu Arg Leu Phe His Val Ala Thr His Ala Ser Glu Pro
305                 310                 315

<210> 921
<211> 28
<212> PRT
<213> Homo sapiens

<400> 921
Met Met Val Asp Pro Asn Gly Asn Glu Ser Ser Ala Thr Tyr Phe Ile
                5                   10                  15
Leu Ile Gly Leu Pro Gly Leu Glu Glu Ala Gln Phe
            20                  25

<210> 922
<211> 9
<212> PRT
<213> Homo sapiens

<400> 922
Arg Thr Glu His Ser Leu His Glu Pro
                5

<210> 923
<211> 21
<212> PRT
<213> Homo sapiens

<400> 923
Lys Met Leu Ala Ile Phe Trp Phe Asn Ser Thr Thr Ile Gln Phe Asp
                5                   10                  15
Ala Cys Leu Leu Gln
            20

<210> 924
<211> 20
<212> PRT
<213> Homo sapiens

<400> 924
Asp Arg Tyr Val Ala Ile Cys His Pro Leu Arg His Ala Thr Val Leu
                5                   10                  15
Thr Leu Pro Arg
            20

<210> 925
<211> 37
<212> PRT
<213> Homo sapiens
```

<400> 925
Phe Ile Lys Gln Leu Pro Phe Cys Arg Ser Asn Ile Leu Ser His Ser
5 10 15
Tyr Cys Leu His Gln Asp Val Met Lys Leu Ala Cys Asp Asp Ile Arg
20 25 30
Val Asn Val Val Tyr
35

<210> 926
<211> 13
<212> PRT
<213> Homo sapiens

<400> 926
Lys Thr Val Leu Gly Leu Thr Arg Glu Ala Gln Ala Lys
5 10

<210> 927
<211> 10
<212> PRT
<213> Homo sapiens

<400> 927
Val His Arg Phe Ser Lys Arg Arg Asp Ser
5 10

<210> 928
<211> 22
<212> PRT
<213> Homo sapiens

<400> 928
Lys Thr Lys Glu Ile Arg Gln Arg Ile Leu Arg Leu Phe His Val Ala
5 10 15

Thr His Ala Ser Glu Pro
20

<210> 929
<211> 3245
<212> DNA
<213> Homo sapiens

<400> 929
gtcgacccac gcgtccgcgc gagctaagca ggaggcggag gcggaggcgg agggcgaggg 60
gcggggagcg ccgcctggag cgcggcaggt catattgaac attccagata cctatcatta 120
ctcgatgctg ttgataacag caagatggct ttgaactcag ggtcaccacc agctattgga 180
ccttactatg aaaaccatgg ataccaaccg gaaaacccct atcccgcaca gcccactgtg 240
gtccccactg tctacgaggt gcatccggct cagtactacc cgtcccccgt gccccagtac 300
gccccgaggg tcctgacgca ggcttccaac cccgtcgtct gcacgcagcc caaatcccca 360
tccgggacag tgtgcacctc aaagactaag aaagcactgt gcatcacctt gaccctgggg 420
accttcctcg tgggagctgc gctggccgct ggcctactct ggaagttcat gggcagcaag 480
tgctccaact ctgggataga gtgcgactcc tcaggtacct gcatcaaccc ctctaactgg 540
tgtgatggcg tgtcacactg ccccggcggg gaggacgaga atcggtgtgt tcgcctctac 600
ggatcaaact tcatccttca ggtgtactca tctcagagga agtcctggca ccctgtgtgc 660
caagacgact ggaacgagaa ctacgggcgg gcggcctgca gggacatggg ctataagaat 720
aatttttact ctagccaagg aatagtggat gacagcggat ccaccagctt tatgaaactg 780

aacacaagtg ccggcaatgt cgatatctat aaaaaactgt accacagtga tgcctgttct 840
tcaaaagcag tggtttcttt acgctgtata gcctgcgggg tcaacttgaa ctcaagccgc 900
cagagcagga ttgtgggcgg cgagagcgcg ctcccggggg cctggccctg gcaggtcagc 960
ctgcacgtcc agaacgtcca cgtgtgcgga ggctccatca tcaccccga gtggatcgtg 1020
acagccgccc actgcgtgga aaaacctctt aacaatccat ggcattggac ggcatttgcg 1080
gggatttga gacaatcttt catgttctat ggagccggat accaagtaga aaaagtgatt 1140
tctcatccaa attatgactc caagaccaag aacaatgaca ttgcgctgat gaagctgcag 1200
aagcctctga ctttcaacga cctagtgaaa ccagtgtgtc tgcccaaccc aggcatgatg 1260
ctgcagccag aacagctctg ctggatttcc gggtgggggg ccaccgagga gaaagggaag 1320
acctcagaag tgctgaacgc tgccaaggtg cttctcattg agacacagag atgcaacagc 1380
agatatgtct atgacaacct gatcacacca gccatgatct gtgccggctt cctgcagggg 1440
aacgtcgatt cttgccaggg tgacagtgga gggcctctgg tcacttcgaa gaacaatatc 1500
tggtggctga taggggatac aagctggggt tctggctgtg ccaaagctta cagaccagga 1560
gtgtacggga atgtgatggt attcacggac tggatttatc gacaaatgag ggcagacggc 1620
taatccacat ggtcttcgtc cttgacgtcg ttttacaaga aaacaatggg gctggttttg 1680
cttccccgtg catgatttac tcttagagat gattcagagg tcacttcatt tttattaaac 1740
agtgaacttg tctggctttg gcactctctg ccattctgtg caggctgcag tggctcccct 1800
gcccagcctg ctctccctaa ccccttgtcc gcaaggggtg atggccggct ggttgtgggc 1860
actggcggtc aagtgtggag gagaggggtg gaggctgccc cattgagatc ttcctgctga 1920
gtcctttcca ggggccaatt ttggatgagc atggagctgt cacctctcag ctgctggatg 1980
acttgagatg aaaaaggaga gacatggaaa gggagacagc caggtggcac ctgcagcggc 2040
tgccctctgg ggccacttgg tagtgtcccc agcctacctc tccacaaggg gattttgctg 2100
atgggttctt agagccttag cagccctgga tggtggccag aaataaaggg accagccctt 2160
catgggtggt gacgtggtag tcacttgtaa ggggaacaga aacattttg ttcttatggg 2220
gtgagaatat agacagtgcc cttggtgcga gggaagcaat tgaaaaggaa cttgccctga 2280
gcactcctgg tgcaggtctc cacctgcaca ttgggtgggg ctcctgggag ggagactcag 2340
ccttcctcct catcctccct gaccctgctc ctagcaccct ggagagtgca catgcccctt 2400
ggtcctggca gggcgccaag tctggcacca tgttggcctc ttcaggcctg ctagtcactg 2460
gaaattgagg tccatggggg aaatcaagga tgctcagttt aaggtacact gtttccatgt 2520
tatgtttcta cacattgcta cctcagtgct cctggaaact tagcttttga tgtctccaag 2580
tagtccacct tcatttaact ctttgaaact gtatcatctt tgccaagtaa gagtggtggc 2640
ctatttcagc tgctttgaca aaatgactgg ctcctgactt aacgttctat aaatgaatgt 2700
gctgaagcaa agtgcccatg gtggcggcga agaagagaaa gatgtgtttt gttttggact 2760
ctctgtggtc ccttccaatg ctgtgggttt ccaaccaggg gaagggtccc ttttgcattg 2820
ccaagtgcca taaccatgag cactactcta ccatggttct gcctcctggc caagcaggct 2880
ggtttgcaag aatgaaatga atgattctac agctaggact taaccttgaa atggaaagtc 2940
ttgcaatccc atttgcagga tccgtctgtg cacatgcctc tgtagagagc agcattccca 3000
gggaccttgg aaacagttgg cactgtaagg tgcttgctcc ccaagacaca tcctaaaagg 3060
tgttgtaatg gtgaaaacgt cttccttctt tattgcccct tcttatttat gtgaacaact 3120
gtttgtcttt ttttgtatct tttttaaact gtaaagttca attgtgaaaa tgaatatcat 3180
gcaaataaat tatgcgattt ttttttcaaa gtaaaaaaaa aaaaaaaaaa aaaaagggcg 3240
gccgc 3245

<210> 930
<211> 1479
<212> DNA
<213> Homo sapiens

<400> 930
atggctttga actcagggtc accaccagct attggacctt actatgaaaa ccatggatac 60
caaccggaaa acccctatcc cgcacagccc actgtggtcc ccactgtcta cgaggtgcat 120
ccggctcagt actacccgtc ccccgtgccc cagtacgccc cgagggtcct gacgcaggct 180
tccaaccccg tcgtctgcac gcagcccaaa tccccatccg ggacagtgtg cacctcaaag 240
actaagaaag cactgtgcat caccttgacc ctggggacct tcctcgtggg agctgcgctg 300
gccgctggcc tactctggaa gttcatgggc agcaagtgct ccaactctgg gatagagtgc 360
gactcctcag gtacctgcat caacccctct aactggtgtg atggcgtgtc acactgcccc 420
ggcggggagg acgagaatcg gtgtgttcgc ctctacggat caaacttcat ccttcaggtg 480

tactcatctc agaggaagtc ctggcaccct gtgtgccaag acgactggaa cgagaactac 540
gggcgggcgg cctgcaggga catgggctat aagaataatt tttactctag ccaaggaata 600
gtggatgaca gcggatccac cagctttatg aaactgaaca caagtgccgg caatgtcgat 660
atctataaaa aactgtacca cagtgatgcc tgttcttcaa aagcagtggt ttctttacgc 720
tgtatagcct gcggggtcaa cttgaactca agccgccaga gcaggattgt gggcggcgag 780
agcgcgctcc cggggggcctg gccctggcag gtcagcctgc acgtccagaa cgtccacgtg 840
tgcggaggct ccatcatcac ccccgagtgg atcgtgacag ccgcccactg cgtggaaaaa 900
cctcttaaca atccatggca ttggacggca tttgcgggga ttttgagaca atctttcatg 960
ttctatggag ccggatacca agtagaaaaa gtgatttctc atccaaatta tgactccaag 1020
accaagaaca atgacattgc gctgatgaag ctgcagaagc ctctgacttt caacgaccta 1080
gtgaaaccag tgtgtctgcc caacccaggc atgatgctgc agccagaaca gctctgctgg 1140
atttccgggt gggggccac cgaggagaaa gggaagacct cagaagtgct gaacgctgcc 1200
aaggtgcttc tcattgagac acagagatgc aacagcagat atgtctatga caacctgatc 1260
acaccagcca tgatctgtgc cggcttcctg caggggaacg tcgattcttg ccagggtgac 1320
agtggagggc ctctggtcac ttcgaagaac aatatctggt ggctgatagg ggatacaagc 1380
tggggttctg gctgtgccaa agcttacaga ccaggagtgt acgggaatgt gatggtattc 1440
acggactgga tttatcgaca aatgagggca gacggctaa 1479

<210> 931
<211> 1476
<212> DNA
<213> Homo sapiens

<400> 931
atggctttga actcagggtc accaccagct attggacctt actatgaaaa ccatggatac 60
caaccggaaa acccctatcc cgcacagccc actgtggtcc ccactgtcta cgaggtgcat 120
ccggctcagt actacccgtc ccccgtgccc cagtacgccc cgagggtcct gacgcaggct 180
tccaaccccg tcgtctgcac gcagcccaaa tccccatccg ggacagtgtg cacctcaaag 240
actaagaaag cactgtgcat caccttgacc ctggggacct tcctcgtggg agctgcgctg 300
gccgctggcc tactctggaa gttcatgggc agcaagtgct ccaactctgg gatagagtgc 360
gactcctcag gtacctgcat caacccctct aactggtgtg atggcgtgtc acactgcccc 420
ggcgggggagg acgagaatcg gtgtgttcgc ctctacggat caaacttcat ccttcaggtg 480
tactcatctc agaggaagtc ctggcaccct gtgtgccaag acgactggaa cgagaactac 540
gggcgggcgg cctgcaggga catgggctat aagaataatt tttactctag ccaaggaata 600
gtggatgaca gcggatccac cagctttatg aaactgaaca caagtgccgg caatgtcgat 660
atctataaaa aactgtacca cagtgatgcc tgttcttcaa aagcagtggt ttctttacgc 720
tgtatagcct gcggggtcaa cttgaactca agccgccaga gcaggattgt gggcggcgag 780
agcgcgctcc cggggggcctg gccctggcag gtcagcctgc acgtccagaa cgtccacgtg 840
tgcggaggct ccatcatcac ccccgagtgg atcgtgacag ccgcccactg cgtggaaaaa 900
cctcttaaca atccatggca ttggacggca tttgcgggga ttttgagaca atctttcatg 960
ttctatggag ccggatacca agtagaaaaa gtgatttctc atccaaatta tgactccaag 1020
accaagaaca atgacattgc gctgatgaag ctgcagaagc ctctgacttt caacgaccta 1080
gtgaaaccag tgtgtctgcc caacccaggc atgatgctgc agccagaaca gctctgctgg 1140
atttccgggt gggggccac cgaggagaaa gggaagacct cagaagtgct gaacgctgcc 1200
aaggtgcttc tcattgagac acagagatgc aacagcagat atgtctatga caacctgatc 1260
acaccagcca tgatctgtgc cggcttcctg caggggaacg tcgattcttg ccagggtgac 1320
agtggagggc ctctggtcac ttcgaagaac aatatctggt ggctgatagg ggatacaagc 1380
tggggttctg gctgtgccaa agcttacaga ccaggagtgt acgggaatgt gatggtattc 1440
acggactgga tttatcgaca aatgagggca gacggc 1476

<210> 932
<211> 492
<212> PRT
<213> Homo sapiens

<400> 932

```
Met Ala Leu Asn Ser Gly Ser Pro Pro Ala Ile Gly Pro Tyr Tyr Glu
                5                  10                  15
Asn His Gly Tyr Gln Pro Glu Asn Pro Tyr Pro Ala Gln Pro Thr Val
            20                  25                  30
Val Pro Thr Val Tyr Glu Val His Pro Ala Gln Tyr Tyr Pro Ser Pro
        35                  40                  45
Val Pro Gln Tyr Ala Pro Arg Val Leu Thr Gln Ala Ser Asn Pro Val
    50                  55                  60
Val Cys Thr Gln Pro Lys Ser Pro Ser Gly Thr Val Cys Thr Ser Lys
65                  70                  75                  80
Thr Lys Lys Ala Leu Cys Ile Thr Leu Thr Leu Gly Thr Phe Leu Val
                85                  90                  95
Gly Ala Ala Leu Ala Ala Gly Leu Leu Trp Lys Phe Met Gly Ser Lys
            100                 105                 110
Cys Ser Asn Ser Gly Ile Glu Cys Asp Ser Ser Gly Thr Cys Ile Asn
        115                 120                 125
Pro Ser Asn Trp Cys Asp Gly Val Ser His Cys Pro Gly Gly Glu Asp
    130                 135                 140
Glu Asn Arg Cys Val Arg Leu Tyr Gly Ser Asn Phe Ile Leu Gln Val
145                 150                 155                 160
Tyr Ser Ser Gln Arg Lys Ser Trp His Pro Val Cys Gln Asp Asp Trp
                165                 170                 175
Asn Glu Asn Tyr Gly Arg Ala Ala Cys Arg Asp Met Gly Tyr Lys Asn
            180                 185                 190
Asn Phe Tyr Ser Ser Gln Gly Ile Val Asp Asp Ser Gly Ser Thr Ser
        195                 200                 205
Phe Met Lys Leu Asn Thr Ser Ala Gly Asn Val Asp Ile Tyr Lys Lys
    210                 215                 220
Leu Tyr His Ser Asp Ala Cys Ser Ser Lys Ala Val Val Ser Leu Arg
225                 230                 235                 240
Cys Ile Ala Cys Gly Val Asn Leu Asn Ser Ser Arg Gln Ser Arg Ile
                245                 250                 255
Val Gly Gly Glu Ser Ala Leu Pro Gly Ala Trp Pro Trp Gln Val Ser
            260                 265                 270
Leu His Val Gln Asn Val His Val Cys Gly Gly Ser Ile Ile Thr Pro
        275                 280                 285
Glu Trp Ile Val Thr Ala Ala His Cys Val Glu Lys Pro Leu Asn Asn
    290                 295                 300
Pro Trp His Trp Thr Ala Phe Ala Gly Ile Leu Arg Gln Ser Phe Met
305                 310                 315                 320
Phe Tyr Gly Ala Gly Tyr Gln Val Glu Lys Val Ile Ser His Pro Asn
                325                 330                 335
Tyr Asp Ser Lys Thr Lys Asn Asn Asp Ile Ala Leu Met Lys Leu Gln
            340                 345                 350
Lys Pro Leu Thr Phe Asn Asp Leu Val Lys Pro Val Cys Leu Pro Asn
        355                 360                 365
Pro Gly Met Met Leu Gln Pro Glu Gln Leu Cys Trp Ile Ser Gly Trp
    370                 375                 380
Gly Ala Thr Glu Glu Lys Gly Lys Thr Ser Glu Val Leu Asn Ala Ala
385                 390                 395                 400
Lys Val Leu Leu Ile Glu Thr Gln Arg Cys Asn Ser Arg Tyr Val Tyr
                405                 410                 415
Asp Asn Leu Ile Thr Pro Ala Met Ile Cys Ala Gly Phe Leu Gln Gly
            420                 425                 430
Asn Val Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Thr Ser
        435                 440                 445
Lys Asn Asn Ile Trp Trp Leu Ile Gly Asp Thr Ser Trp Gly Ser Gly
    450                 455                 460
```

Cys Ala Lys Ala Tyr Arg Pro Gly Val Tyr Gly Asn Val Met Val Phe
465 470 475 480
Thr Asp Trp Ile Tyr Arg Gln Met Arg Ala Asp Gly
485 490

<210> 933
<211> 100
<212> PRT
<213> Homo sapiens

<400> 933
Met Ala Leu Asn Ser Gly Ser Pro Pro Ala Ile Gly Pro Tyr Tyr Glu
5 10 15
Asn His Gly Tyr Gln Pro Glu Asn Pro Tyr Pro Ala Gln Pro Thr Val
20 25 30
Val Pro Thr Val Tyr Glu Val His Pro Ala Gln Tyr Tyr Pro Ser Pro
35 40 45
Val Pro Gln Tyr Ala Pro Arg Val Leu Thr Gln Ala Ser Asn Pro Val
50 55 60
Val Cys Thr Gln Pro Lys Ser Pro Ser Gly Thr Val Cys Thr Ser Lys
65 70 75 80
Thr Lys Lys Ala Leu Cys Ile Thr Leu Thr Leu Gly Thr Phe Leu Val
85 90 95
Gly Ala Ala Leu
100

<210> 934
<211> 393
<212> PRT
<213> Homo sapiens

<400> 934
Leu Ala Ala Gly Leu Leu Trp Lys Phe Met Gly Ser Lys Cys Ser Asn
5 10 15
Ser Gly Ile Glu Cys Asp Ser Ser Gly Thr Cys Ile Asn Pro Ser Asn
20 25 30
Trp Cys Asp Gly Val Ser His Cys Pro Gly Gly Glu Asp Glu Asn Arg
35 40 45
Cys Val Arg Leu Tyr Gly Ser Asn Phe Ile Leu Gln Val Tyr Ser Ser
50 55 60
Gln Arg Lys Ser Trp His Pro Val Cys Gln Asp Asp Trp Asn Glu Asn
65 70 75 80
Tyr Gly Arg Ala Ala Cys Arg Asp Met Gly Tyr Lys Asn Asn Phe Tyr
85 90 95
Ser Ser Gln Gly Ile Val Asp Asp Ser Gly Ser Thr Ser Phe Met Lys
100 105 110
Leu Asn Thr Ser Ala Gly Asn Val Asp Ile Tyr Lys Lys Leu Tyr His
115 120 125
Ser Asp Ala Cys Ser Ser Lys Ala Val Val Ser Leu Arg Cys Ile Ala
130 135 140
Cys Gly Val Asn Leu Asn Ser Ser Arg Gln Ser Arg Ile Val Gly Gly
145 150 155 160
Glu Ser Ala Leu Pro Gly Ala Trp Pro Trp Gln Val Ser Leu His Val
165 170 175
Gln Asn Val His Val Cys Gly Gly Ser Ile Ile Thr Pro Glu Trp Ile
180 185 190

```
Val Thr Ala Ala His Cys Val Glu Lys Pro Leu Asn Asn Pro Trp His
        195                 200                 205
Trp Thr Ala Phe Ala Gly Ile Leu Arg Gln Ser Phe Met Phe Tyr Gly
    210                 215                 220
Ala Gly Tyr Gln Val Glu Lys Val Ile Ser His Pro Asn Tyr Asp Ser
225                 230                 235                 240
Lys Thr Lys Asn Asn Asp Ile Ala Leu Met Lys Leu Gln Lys Pro Leu
                245                 250                 255
Thr Phe Asn Asp Leu Val Lys Pro Val Cys Leu Pro Asn Pro Gly Met
            260                 265                 270
Met Leu Gln Pro Glu Gln Leu Cys Trp Ile Ser Gly Trp Gly Ala Thr
        275                 280                 285
Glu Glu Lys Gly Lys Thr Ser Glu Val Leu Asn Ala Ala Lys Val Leu
    290                 295                 300
Leu Ile Glu Thr Gln Arg Cys Asn Ser Arg Tyr Val Tyr Asp Asn Leu
305                 310                 315                 320
Ile Thr Pro Ala Met Ile Cys Ala Gly Phe Leu Gln Gly Asn Val Asp
                325                 330                 335
Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Thr Ser Lys Asn Asn
            340                 345                 350
Ile Trp Trp Leu Ile Gly Asp Thr Ser Trp Gly Ser Gly Cys Ala Lys
        355                 360                 365
Ala Tyr Arg Pro Gly Val Tyr Gly Asn Val Met Val Phe Thr Asp Trp
    370                 375                 380
Ile Tyr Arg Gln Met Arg Ala Asp Gly
385                 390
```

<210> 935
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR Primer

<400> 935
gtgctgtggg agtccccgcg gc 22

<210> 936
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR Primer

<400> 936
cgtgaactcg agtcattaga ttaacctcgt ggacgc 36

<210> 937
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR Primer

<400> 937
gtgctgtggg agtccccgcg gc 22

<210> 938
<211> 1158
<212> DNA
<213> Homo sapiens

<400> 938
catatgcagc atcaccacca tcaccacgtg ctgtgggagt ccccgcggca gtgcagcagc 60
tggacacttt gcgagggctt ttgctggctg ctgctgctgc ccgtcatgct actcatcgta 120
gcccgcccgg tgaagctcgc tgctttccct acctccttaa gtgactgcca aacgcccacc 180
ggctggaatt gctctggtta tgatgacaga gaaaatgatc tcttcctctg tgacaccaac 240
acctgtaaat ttgatgggga atgtttaaga attggagaca ctgtgacttg cgtctgtcag 300
ttcaagtgca acaatgacta tgtgcctgtg tgtggctcca atggggagag ctaccagaat 360
gagtgttacc tgcgacaggc tgcatgcaaa cagcagagtg agatacttgt ggtgtcagaa 420
ggatcatgtg ccacagatgc aggatcagga tctggagatg gagtccatga aggctctgga 480
gaaactagtc aaaaggagac atccacctgt gatatttgcc agtttggtgc agaatgtgac 540
gaagatgccg aggatgtctg gtgtgtgtgt aatattgact gttctcaaac caacttcaat 600
cccctctgcg cttctgatgg gaaatcttat gataatgcat gccaaatcaa agaagcatcg 660
tgtcagaaac aggagaaaat tgaagtcatg tctttgggtc gatgtcaaga taacacaact 720
acaactacta agtctgaaga tgggcattat gcaagaacag attatgcaga gaatgctaac 780
aaattagaag aaagtgccag agaacaccac ataccttgtc cggaacatta caatggcttc 840
tgcatgcatg ggaagtgtga gcattctatc aatatgcagg agccatcttg caggtgtgat 900
gctggttata ctggacaaca ctgtgaaaaa aaggactaca gtgttctata cgttgttccc 960
ggtcctgtac gatttcagta tgtcttaatc gcagctgtga ttggaacaat tcagattgct 1020
gtcatctgtg tggtggtcct ctgcatcaca aggaaatgcc ccagaagcaa cagaattcac 1080
agacagaagc aaaatacagg gcactacagt tcagacaata caacaagagc gtccacgagg 1140
ttaatctaat gactcgag 1158

<210> 939
<211> 1020
<212> DNA
<213> Homo sapiens

<400> 939
atgcagcatc accaccatca ccacgactgc caaacgccca ccggctggaa ttgctctggt 60
tatgatgaca gagaaaatga tctcttcctc tgtgacacca acacctgtaa atttgatggg 120
gaatgtttaa gaattggaga cactgtgact tgcgtctgtc agttcaagtg caacaatgac 180
tatgtgcctg tgtgtggctc caatggggag agctaccaga atgagtgtta cctgcgacag 240
gctgcatgca aacagcagag tgagatactt gtggtgtcag aaggatcatg tgccacagat 300
gcaggatcag gatctggaga tggagtccat gaaggctctg gagaaactag tcaaaaggag 360
acatccacct gtgatatttg ccagtttggt gcagaatgtg acgaagatgc cgaggatgtc 420
tggtgtgtgt gtaatattga ctgttctcaa accaacttca atcccctctg cgcttctgat 480
gggaaatctt atgataatgc atgccaaatc aaagaagcat cgtgtcagaa acaggagaaa 540
attgaagtca tgtctttggg tcgatgtcaa gataacacaa ctacaactac taagtctgaa 600
gatgggcatt atgcaagaac agattatgca gagaatgcta acaaattaga agaaagtgcc 660
agagaacacc acataccttg tccggaacat tacaatggct tctgcatgca tgggaagtgt 720
gagcattcta tcaatatgca ggagccatct tgcaggtgtg atgctggtta tactggacaa 780
cactgtgaaa aaaaggacta cagtgttcta tacgttgttc ccggtcctgt acgatttcag 840
tatgtcttaa tcgcagctgt gattggaaca attcagattg ctgtcatctg tgtggtggtc 900
ctctgcatca caaggaaatg ccccagaagc aacagaattc acagacagaa gcaaaataca 960
gggcactaca gttcagacaa tacaacaaga gcgtccacga ggttaatcta atgactcgag 1020

<210> 940
<211> 336

<212> PRT
<213> Homo sapiens

<400> 940
Met Gln His His His His His His Asp Cys Gln Thr Pro Thr Gly Trp
5 10 15
Asn Cys Ser Gly Tyr Asp Asp Arg Glu Asn Asp Leu Phe Leu Cys Asp
20 25 30
Thr Asn Thr Cys Lys Phe Asp Gly Glu Cys Leu Arg Ile Gly Asp Thr
35 40 45
Val Thr Cys Val Cys Gln Phe Lys Cys Asn Asn Asp Tyr Val Pro Val
50 55 60
Cys Gly Ser Asn Gly Glu Ser Tyr Gln Asn Glu Cys Tyr Leu Arg Gln
65 70 75 80
Ala Ala Cys Lys Gln Gln Ser Glu Ile Leu Val Val Ser Glu Gly Ser
85 90 95
Cys Ala Thr Asp Ala Gly Ser Gly Ser Gly Asp Gly Val His Glu Gly
100 105 110
Ser Gly Glu Thr Ser Gln Lys Glu Thr Ser Thr Cys Asp Ile Cys Gln
115 120 125
Phe Gly Ala Glu Cys Asp Glu Asp Ala Glu Asp Val Trp Cys Val Cys
130 135 140
Asn Ile Asp Cys Ser Gln Thr Asn Phe Asn Pro Leu Cys Ala Ser Asp
145 150 155 160
Gly Lys Ser Tyr Asp Asn Ala Cys Gln Ile Lys Glu Ala Ser Cys Gln
165 170 175
Lys Gln Glu Lys Ile Glu Val Met Ser Leu Gly Arg Cys Gln Asp Asn
180 185 190
Thr Thr Thr Thr Thr Lys Ser Glu Asp Gly His Tyr Ala Arg Thr Asp
195 200 205
Tyr Ala Glu Asn Ala Asn Lys Leu Glu Glu Ser Ala Arg Glu His His
210 215 220
Ile Pro Cys Pro Glu His Tyr Asn Gly Phe Cys Met His Gly Lys Cys
225 230 235 240
Glu His Ser Ile Asn Met Gln Glu Pro Ser Cys Arg Cys Asp Ala Gly
245 250 255
Tyr Thr Gly Gln His Cys Glu Lys Lys Asp Tyr Ser Val Leu Tyr Val
260 265 270
Val Pro Gly Pro Val Arg Phe Gln Tyr Val Leu Ile Ala Ala Val Ile
275 280 285
Gly Thr Ile Gln Ile Ala Val Ile Cys Val Val Val Leu Cys Ile Thr
290 295 300
Arg Lys Cys Pro Arg Ser Asn Arg Ile His Arg Gln Lys Gln Asn Thr
305 310 315 320
Gly His Tyr Ser Ser Asp Asn Thr Thr Arg Ala Ser Thr Arg Leu Ile
325 330 335

<210> 941
<211> 381
<212> PRT
<213> Homo sapiens

<400> 941
Met Gln His His His His His His Val Leu Trp Glu Ser Pro Arg Gln
5 10 15
Cys Ser Ser Trp Thr Leu Cys Glu Gly Phe Cys Trp Leu Leu Leu Leu
20 25 30

```
Pro Val Met Leu Leu Ile Val Ala Arg Pro Val Lys Leu Ala Ala Phe
        35                  40                  45
Pro Thr Ser Leu Ser Asp Cys Gln Thr Pro Thr Gly Trp Asn Cys Ser
    50                  55                  60
Gly Tyr Asp Asp Arg Glu Asn Asp Leu Phe Leu Cys Asp Thr Asn Thr
65                  70                  75                  80
Cys Lys Phe Asp Gly Glu Cys Leu Arg Ile Gly Asp Thr Val Thr Cys
                85                  90                  95
Val Cys Gln Phe Lys Cys Asn Asn Asp Tyr Val Pro Val Cys Gly Ser
            100                 105                 110
Asn Gly Glu Ser Tyr Gln Asn Glu Cys Tyr Leu Arg Gln Ala Ala Cys
        115                 120                 125
Lys Gln Gln Ser Glu Ile Leu Val Val Ser Glu Gly Ser Cys Ala Thr
    130                 135                 140
Asp Ala Gly Ser Gly Ser Gly Asp Gly Val His Glu Gly Ser Gly Glu
145                 150                 155                 160
Thr Ser Gln Lys Glu Thr Ser Thr Cys Asp Ile Cys Gln Phe Gly Ala
                165                 170                 175
Glu Cys Asp Glu Asp Ala Glu Asp Val Trp Cys Val Cys Asn Ile Asp
            180                 185                 190
Cys Ser Gln Thr Asn Phe Asn Pro Leu Cys Ala Ser Asp Gly Lys Ser
        195                 200                 205
Tyr Asp Asn Ala Cys Gln Ile Lys Glu Ala Ser Cys Gln Lys Gln Glu
    210                 215                 220
Lys Ile Glu Val Met Ser Leu Gly Arg Cys Gln Asp Asn Thr Thr Thr
225                 230                 235                 240
Thr Thr Lys Ser Glu Asp Gly His Tyr Ala Arg Thr Asp Tyr Ala Glu
                245                 250                 255
Asn Ala Asn Lys Leu Glu Glu Ser Ala Arg Glu His His Ile Pro Cys
            260                 265                 270
Pro Glu His Tyr Asn Gly Phe Cys Met His Gly Lys Cys Glu His Ser
        275                 280                 285
Ile Asn Met Gln Glu Pro Ser Cys Arg Cys Asp Ala Gly Tyr Thr Gly
    290                 295                 300
Gln His Cys Glu Lys Lys Asp Tyr Ser Val Leu Tyr Val Val Pro Gly
305                 310                 315                 320
Pro Val Arg Phe Gln Tyr Val Leu Ile Ala Ala Val Ile Gly Thr Ile
                325                 330                 335
Gln Ile Ala Val Ile Cys Val Val Val Leu Cys Ile Thr Arg Lys Cys
            340                 345                 350
Pro Arg Ser Asn Arg Ile His Arg Gln Lys Gln Asn Thr Gly His Tyr
        355                 360                 365
Ser Ser Asp Asn Thr Thr Arg Ala Ser Thr Arg Leu Ile
    370                 375                 380
```

<210> 942
<211> 45
<212> DNA
<213> Homo sapiens

<400> 942
ctgctggcga acggcagaat gcctaccgtg ctgcagtgcg tgaac 45

<210> 943
<211> 15
<212> PRT
<213> Homo sapiens

<400> 943
Leu Leu Ala Asn Gly Arg Met Pro Thr Val Leu Gln Cys Val Asn
1 5 10 15